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(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MOD-ULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

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METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or tarreets that inhibit lung cancer or related conditions.

BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides, hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

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Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include onthe-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the beyond the bounds where surgery and curative intent can be undertaken. Hoever, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

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and account for more than 75% of all lung cancers. Non-small cell tumors that are localized at the time of presentation can sometimes be cured with surgery and/or radiotherapy, but usually are not identified until significant metastasis has occurred, which are typically not very responsive to surgical, chemotherapy, or radiation treatment.

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of veffective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

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SUMMARY OF THE INVENTION

The present invention provides nucleotide sequences of genes that are up- and downregulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as
targets for screening for therapeutic compounds that modulate lung cancer, such as
antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins
can be used for a number of purposes. Examples include early detection of lung cancers,
monitoring and early detection of relapse following treatment of lung cancers, monitoring
response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy
of lung cancers, selecting patients for postoperative chemotherapy or radiation therapy,
selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early
detection of precancerous lesions of the lung. Examples of benign or precancerous lesions
include: atelectasis, emphysema, brochitis, chronic obstructive pulmonary disease, fibrosis,
hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and

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the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancerassociated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evalated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

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biological sample from a patient undergoing the therapeutic treatment; and (ii) determining
the level of a lung cancer-associated antibody in the biological sample by contacting the
biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes
to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the
polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the
efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

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In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

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In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

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WO 02/086443 very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based 5 upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseases lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

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Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancerassociated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

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have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

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WO 02/086443 PCT/US02/12476 same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

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Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) <u>Current Protocols in Molecular Biology</u>.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

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An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

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In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations." which are one species of

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conservatively modified variations. Every nucleic acid sequence herein which encodes a
polypeptide also describes silent variations of the nucleic acid. In certain contexts each
codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and
TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a
functionally similar molecule. Accordingly, a silent variation of a nucleic acid which
encodes a polypeptide is implicit in a described sequence with respect to the expression
product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) <u>Molecular Biology of the Cell</u> (3rd ed.) and Cantor and Schimmel (1980) <u>Biophysical Chemistry Part I: The Conformation of Biological Macromolecules</u>. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

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"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or Omethylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and 10 linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing 15 one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (Tm) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in Tm for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

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strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleotide and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) L. Immunol. Meth., 40:219-230; and Nygren (1982) L. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

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WO 02/086443 PCT/US02/12476 using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond 5 formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by pentide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

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WO 02/086443 PCT/US02/12476 recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein

made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid

indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two

or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

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The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in 5 "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) 10 at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or 15 other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% 20 SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C 25 to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and 30 Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

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occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice 5 background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein: measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein

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WO 02/086443 expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences. 5 measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, B-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

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WO 02/086443 PCT/US02/12476 preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, 5 anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

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WO 02/086443 PCT/US02/12476 for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab 5 which itself is a light chain joined to VH-CH1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

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variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to downregulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant diseasemay be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of hing cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

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nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

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WO 02/086443 etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as 5 described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression he disease specific to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in nonmalignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) Nucleic Acids Research 26:1-7 and http://www.nchi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) Genome Res. 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are downregulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

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WO 02/086443 or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

Informatics

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The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

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pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, genedisease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multidimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxevanis and Oeullette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds., 2000) Bioinformatics: Methods and Protocols: Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

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WO 02/086443 Approach: Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet: Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic senaration coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

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be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences

determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

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MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

15 Characteristics of lung cancer-associated proteins

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.). For example, many intracellular proteins averenzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, mucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

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WO 02/086443 PCT/US02/12476 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins.

Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains.

For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain.

However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

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 $WO~02/086443 \\ PCT/US02/12476 \\ localization and number of transmembrane domains within the protein may be predicted (see,$

e.g., PSORT web site http://psort.nibb.ac.jp/).

The extracellular domains of transmembrane proteins are diverse; however, conserved

notifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GFI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

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PCT/US02/12476 signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, sax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, scrum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful

Use of lung cancer nucleic acids

as vaccine targets, e.g., via CTL mechanisms.

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using tecluniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

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WO 02/086443 PCT/US02/12476 other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications.

Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

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particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for ndivitual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

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WO 02/086443 Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample 5 volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, vet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affvmetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

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reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a

template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a

quantitative amplification, the amount of amplification product will be proportional to the

amount of template in the original sample. Comparison to appropriate controls provides a

measure of the amount of lung cancer-associated RNA. Methods of quantitative

maplification are well known to those of skill in the art. Detailed protocols for quantitative

PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and

Applications.

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

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sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

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vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, supra).

In addition, in a preferred embodiment, the expression vector contains a selectable

marker gene to allow the selection of transformed host cells. Selection genes are well known
in the art and will vary with the host cell used.

The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

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The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microiniection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin. chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha,

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Kluyveromyces fragilis and K. lactis, Pichia guillerimondii, and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

25 Variants of lung cancer proteins

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer pentide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

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WO 02/086443 classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

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WO 02/086443 PCT/US02/12476 variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of 5 reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3.3'dithiobis(succinimidybropionate), bifunctional maleimides such as bis-N-maleimido-1,8-

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the y-amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

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Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981)

CRC Crit. Rev. Bjochem., pp. 259-306.

Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987)

<u>Arch. Biochem. Biophys.</u>, 259:52 and by Edge, et al. (1981) <u>Anal. Biochem.</u>, 118:131.

Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) <u>Meth.</u>

<u>Enzymol.</u>, 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fe region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

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thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes
Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein
Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science
255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:1516315166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l
Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to lung cancer proteins

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

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being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if nonhuman mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, hovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed, The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

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In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyelonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536). by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4.816.567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

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Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 5 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5.633,425; 5.661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

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WO 02/086443 PCT/US02/12476 antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

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afflicted area, but also serves to reduce deleterious side effects that may be associated with
the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

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WO 02/086443 PCT/US02/12476 normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that 5 expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby 10 expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

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Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled fiboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques. e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

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Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

imaging techniques are also provided by the invention.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, in situ hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

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WO 02/086443 genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in hung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

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cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

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In one aspect, a modulator will neutralize the effect of a lung cancer protein. By "neutralize" is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity.

Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (sec, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

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Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

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U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,

5 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman
Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems
typically automate procedures, including sample and reagent pipetting, liquid dispensing,
timed incubations, and final readings of the microplate in detector(s) appropriate for the
assay. These configurable systems provide high throughput and rapid start up as well as a
10 high degree of flexibility and customization. The manufacturers of such systems provide
detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides
technical bulletins describing screening systems for detecting the modulation of gene
transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

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In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

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5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,
5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697: Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

WO 02/086443 PCT/US02/12476 screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

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Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeuties to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019: Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

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Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

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genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein
may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the lisand binding site or activation

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sequence when the protein is bound to the support), direct binding to "sticky" or ionic
supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc.
Following binding of the protein or agent, excess unbound material is removed by washing.
The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

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WO 02/086443 between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of . competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

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Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

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A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art. as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells a Manual of Basic Technique</u> (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^3H) -thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^3H) -thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

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non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) <u>J. Natl. Cancer Insti.</u> 37:167-175; Eagle, et al. (1970) <u>J. Exp. Med.</u> 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer</u>, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in <u>Sem Cancer Biol.</u>).

Various techniques which measure the release of these factors are described in Freshney (1994), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

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Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) <u>Science</u> 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) <u>Manipulating the Mouse Embryo: A Laboratory Manual</u>, Cold Spring Harbor Laboratory and Robertson (ed. 1987) <u>Teratocarcinomas and Embryonic Stem Cells</u>: A Practical Approach, JRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Natl. Cancer Inst.</u> 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

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preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturallyoccurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
close homologs. Antisense polynucleotides may also have altered sugar moieties or intersugar linkages. Exemplary among these are the phosphorothicate and other sulfur containing
species which are known for use in the art. Analogs are comprehended by this invention so
long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g.,
Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.

Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

WO 02/086443 PCT/US02/12476 is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) <u>Sciencexpress</u> (21March2002); Sharp (1999)

5 <u>Genes Dev.</u> 13:139-141; and Cathew (2001) <u>Curr. Op. Cell Biol.</u> 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) <u>Nature</u> 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

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In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990)

Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No.
5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO
94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al.
(1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA
92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al.
(1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

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formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung 5 cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is downregulated in lung cancer, such state may be reversed by increasing the amount of lung cancer 10 gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. 15 Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

30 Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

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identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration.

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drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine,

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

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tose, corn and other starches; binding agents; sweeteners and other flavoring agents;

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacologial Basis of Therapeutics).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacologial Basis of Theraceutics, supra.

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The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo, or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

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Berger and Kimmel, <u>Guide to Molecular Cloning Techniques</u>, <u>Methods in Enzymology</u> volume 152 (Berger), Ausubel, et al. (eds. 1999) <u>Current Protocols</u> (supplemented through 1999), and Sambrook, et al. (1989) <u>Molecular Cloning - A Laboratory Manual</u> (2nd ed., Vol. 1-3).

In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), pentide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al. (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol, Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., v. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

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delivery technologies, also known as receptor mediated targeting, such as those of Avant
Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors. Salmonella publi vectors, detoxified anthrax toxin vectors, and the

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WO 02/086443 like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter 5 or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-10 associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular 15 epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

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WO 02/086443 Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of lung cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

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EXAMPLES

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Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and

analyzed using gene chips. RNA was isolated and gene chip analysis was performed as
described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981993).

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Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
	Pkey	ExAcon	UnigenelD	Unigene Title	70% chron/90% NL	70% SQAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		""Immunoglobulin Heavy Chain, Vdjrc Reg	2.68	3.28
10	100971	J02874	Hs.83213	fatly acid binding protein 4; adipocyte	1.96	0.14
10	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitte	0.79	0.07
	101102	L07594	Hs.79059	transforming growth factor; beta recepto	2.55	1
	101168	L15388	Hs.211559	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibritar-associated protein 4	0.89	0.26
15	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
13	101336	L49169 L76380	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15 0.81	0.31
	101345	M62505	Hs.152175 Hs.2161	calcitonin receptor-like complement component 5 receptor 1 (C5a I	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96	0.45
20	101842	M93221	Hs.75182	mannose receptor, C type 1	1.27	0.37
20	102283	U31384	Hs.83381	guarine nucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	arnine exidese; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2,81	3.45
	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
25	103025	X54131	Hs.123641	protein lyrosine phosphalase; receptor t	1.62	0.21
	103280	X79981	Hs.76206	cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697 ,	Hs.79197	CD83 antigen (activated B lymphocytes; I	1.86	1.
20	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
30	104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
	104691	AA011176	Hs.37744	ESTs	1.08 .	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27 3.3
	104857	AA043219	Hs.19058	ESTs	2.6 1.23	0.49
35	104865	AA045136 AA102098	Hs.22575 Hs.118615	ESTs ESTs	0.63	0.32
22	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398606	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
	106490	AA451861	Hs.115537	ESTs: Weakly similar to dipopticlase prec	1.2	0.47
40	106536	AA453997	Hs.23804	ESIs	0.82	0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99	0.07
	106667	AA461086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.46	0.43
	106797	AA478962	Hs.169943	ESTs	1.18	0.32
45	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphalidyl	1.05	0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative stress	1.07	2.58 0.21
30	107994 107997	AA036811	Hs.165030 Hs.82223	ESTs Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA037388 AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
	108382	AA074885	Hs.67726	macrophage receptor with collegenous str	1.52	0.72
55	108435	AA078787	Hs.194101	ESTs .	2.53	1.53
55	108480	AA061093	Hs.68055	ESTs	1.56	0.48
	109252	AA194830	Hs.85944	ESTS	2.69	3.18
	109660	F01534	Hs.26981	ESTs	1.19	0.66
	109613	F03031	Hs.27519	ESTs	1.01	0.29
60	109637	H00656	Hs.29792	ESTs	0.81	0.15
	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
	110837	N30796	Hs.17424	ESTs; Wealdy similar to semaphorin F (H.	1.1	0.22
65	111247	N69825	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26	0.26
	111341		Hs.22483	ESTs	1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
70	113195	T57112	11- 400010	""yc20g11.s1 Stratagene lung (#937210)	1.22 2.27	0.35
/0	113238		Hs.189813	ESTs	1.06	0.45
	113540	T90496 T90889	Hs.16757 Hs.16026	ESTs ESTs	1.16	0.42
	113552 113606	T93093	Hs.17125	ESTS	1.48	0.7
	113695	T96965	Hs.17948	ESTs	1.54	0.28
75	113946	W84753	Hs.37896	ESTs	1.79	0.72
	114251	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
	115279	AA279760	Hs.63671	ESTs	1.79	0.91
80	115566	AA398083	Hs.43977	ESTs	0.86	0.2
	115965	AA446661	Hs.173233	ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073	Hs.57352	ESTs	2.27	0.78
	117023	H88157	Hs.41105	ESTs	1.36	0.16

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	117209	H99959	Hs.42768	ESTs	1.46	0.4
	118901 118981	N90719 N93839	Hs.94445 Hs.39288	ESTs ESTs	1.51	6.4
	119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.0
5	119221	R96105	10110011	""vr30o11.s1 Soares felal liver spleen	1.32	0.5
	119824	W74536	Hs.184	advanced glycosylation end product-speci	1	0.1
	119861	W80715		ESTs; Moderately similar to IIII ALU SUB	1.83	0.4
	120041 120132	W92775 Z38839	Hs.59368 Hs.125019	ESTs ESTs; Highly similar to KIAA0886 protein	0.91	0.0
0	120132	AA261579	Hs.120019	ESTs Program and Reported Program	1.87	1.5
	121314	AA402799	Hs.182538	ESTs	1.3	0.2
	121643	AA417078	Hs.193767	ESTs	2.31	0.6
	121690	AA418074	Hs.110286	ESTs	1.47	0.5
5	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.6
١٥	123978 124214	C20653 HERROR	Hs.170278 Hs.151323	ESTs ESTs	1.52 0.93	0.3
	124214	N22401	PIS. 15 1323	"yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
	125167	W45560	Hs.102541	ESTs	1.46	0.6
20	125174	W51835	Hs.231082	EST	3.07	3.7
	125422	AA903229	Hs.153717	ESTs	1.34	0.2
	125561	Al417667	Hs.22978	ESTs	1.89	0.0
	125831 127002	D60968 R35380	Hs.24979	""HUM145B09B Clontech human fetal brain ESTs	3.02	4.0
25	127307	AA369367	Hs.126712	ESTs; Weakly similar to plL2 hypothelica	1.01	0.6
-5	127609	AA622559	Hs.150318	ESTs Westly similar to picz nypolitorca	1.21	0.2
	127959	Al302471	Hs.124292	ESTs	2.5	1
	128458	D52193	Hs.56340	ESTs	1.13	0.2
10	128624	AA479209	Hs.102647	ESTs	1,45	0.5
30	128789	AA486567	Hs.105695	ESTs	1.1	0.3
	128798 128952	AF014958 R51076	Hs.105938 Hs.107361	chemokine (C-C motif) receptor-like 2 ESTs; Highly similar to Rap2 interacting	1.16 2.04	0.5 2.4
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.7
	129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.3
35	129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.4
	129402	T63781		""yc21g01.s1 Stratagene lung (#937210)	1.36	0.4
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.0
	129593	AA487015	Hs.98314 Hs.11712	Homo sapiens mRNA; cDNA DKFZp586L0120 (f ESTs; Weekly similar to IIII ALU SUBFAMI	1.3	0.4
10	129626 129699	AA447410 AA458578	Hs.11/12 Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	1.58	4
10	129898	N48696	Hs.13256	ESTs	1.13	0.5
	129958	1,20591	Hs.1378	annexin A3	0.81	0.3
	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.2
	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinat)	1.44	0.7
15	130657	T94452	Hs.201591	ESTs	0.96	0.4
	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL ESTs	1.51 0.97	0.4
	131066 131263	F09006 R38334	Hs.22588 Hs.24950	regulator of G-protein signalling 5	2.34	2.6
	131589	US2100	Hs.29191	epithelial membrane protein 2	1.2	0.6
50	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.3
	131751	H18335	Hs.31562	ESTs	1.47	0.5
	132430	T23630	Hs.258675	EST	1.86	2.0
	132476	N67192	Hs.49476 Hs.57929	Homo sapiens clone TUAS Cri-du-chat regi	1.73 0.91	0.5
55	132836 133 12 0	P09657 X64559	Hs.65424	ski (Drosophila) homolog 3 tetranectin (plasminogen-binding protein	0.82	0.2
,,	133488	D45370	Hs.74120	adipose specific 2	1.29	0.4
	133565	H57056	Hs.204831	ESTs	2.25	0.5
	133651	U97106	Hs.173381	dihydropytimidinase-like 2	1.65	n.e
	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.3
50	133978	W73859	Hs.78061	transcription factor 21	0.79	0.2
	133985	L34657	Hs.78146	plateletiendothelial cell adhesion molec	0.99	0.0
	134299 134300	AA487558 U81984	Hs.8135 Hs.166082	ESTs endothelial PAS domain protein 1,	1.02 0.86	0.4
	134300	AA028976	Hs.166082 Hs.8175	enconnetta: PAS domain protein 1, Homo sapions mRNA; cDNA DKFZp564M0763 (f	1.19	0.5
55	134343	D50683	Hs.82028	trace forming growth factor; hata recents	1.21	0.0
-	134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci adenosine deaminase; RNA-specific; B1 (h	1.28	- 1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.8
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.
70	134696	H88354	Hs.8861	ESTs	1.35	0.3
70	134749	L10955	Hs.89485	carbonic anhydrase IV	0.89 0.48	0.3
	134786 134869	L06139 T35288	Hs.89640 Hs.90421	TEK tyrosine kinase; endothelial (venous ESTs; Moderately similar to IIII ALU SUB	2,14	2.0
	135346	M21056	Hs.90421	phospholipase A2; group IB (pancreas)	0.63	0.1
	100113	D00691	Hs.84746	Chromosome condensation 1	1	2.
75	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
	100280	D42065	Hs.155314	KIAA0095 gene product	1.02	1.3
	100335	D63391	Hs.6793	platelet-activating factor aonlythydrola	1	5.5
	100360	D78335	Hs.75939	Unidine monophosphale kinase	0.91	2.0
30	100372	D79997 HG1112-HT11	Hs.184339	KIAA0175 gene product	0.75	1.5
,,,	100486	HG1112-H111 HG2197-HT22		TIGR: ras-like protein TC4 collagen, type VII, alpha 1	0.97	3.6
	100576	HG2197-H122 HG2290-HT23	88 88	"calcitonin/alpha-CGRP, alt. transcript	1	1
	100668	HG2981-HT39	38	*TIGR: CD44 (epican, all. transcript 12	0.85	1.5
35	100906	HG4716-HT51	58	Guanceine 5'-Monophosphate Synthase	1.18	2.2
	100930	HG721-HT482	o .	"TIGR: placental protein 14, endometrial	1	1.4

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	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	"Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424 L10343	Hs.1619 Hs.112341	Achaete-scale complex (Drosophila) homol "Protease inhibitor 3, skin-derived (SKA	0.62	2.67
5	101175	L18920	Hs.36980	"Melanoma antigen, family A, 2"	1	1
	101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 1B (comifin)	0.85	2.51
	101448	M21389 M27826	Hs.195850 Hs.267319	keratin 5 (epidermolysis bullosa simplex Endogenous retroviral protease	. 0.61 1.03	8.83 1.13
10	101511	M29540	Hs.220529	Carcinosmisyonic antigen-related cell ad	1.07	4.61
10	101548	M31328	Hs.71642	"Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		"Human parathyroid hormono-related pepti	1	1_
	101649	M60047	Hs.1690	Heperin-binding growth factor binding pr bullous pemphigoid antigen 1 (230/240kD)	1	2.7 8.98
15	101724 101748	M69225 M76482	Hs.620 Hs.1925	Desmoglein 3 (pemphigus vulgeris antigen	- 1	2.78
13	101759	M80244	Hs.184601	"Solute carrier family 7 (calionic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psonas	0.74	1.76
20	101809 101845	M86849 M93426	Hs.78867	"Homo sapiens connexin 26 (GJB2) mRNA, c "Protein tyrosine phosphatase, receptor-	- 1	í
20	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1,13	2.6
	102083	U10323	Hs.75117	Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	Leminin, beta 3 (nicein (125kD), kalini	0.94 0.34	3.62 4.59
25	102193	U20758 U33286	Hs.313 Hs.90073	secreted phosphoprotein 1 (osteoponfin; chromosome segregation 1 (yeast homolog)	1.45	2.97
23	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed anlique in mola	1	3.88
30	102623	U66083	Hs.37110	"Me'anoma antigen, family A, 9 (MAGE-9)" Eyes ebseni (Drosophila) homolog 2	- 1	- 1
50	102669 102696	U71207 U74612	Hs-29279 Hs-239	Forkhead hox M1	1.06	2,77
	102829	U91618	Hs.80962	Neurolensin	1 .	1
	102888	X04741	Hs.76118	Ubiquitin cerboxyl-terminel esterase L1	1.13	2.59
35	102913	X07696	Hs.80342	keratin 15 Matrix Metalloproteinase 10 (Stromolysin	0.7 1.15	4.72 3.35
55	102915 102963	X07820 X15943	Hs.2258 Hs.37058	*Celcitonin/celcitonin-releted polypopti	1	1
	103021	X53587	Hs.85268	"Integrin, bela 4"	1.38	2.34
	103036	X54925	Hs.83169	Matrix metalloprolease 1 (interstitial c	1	14,93
40	103058	X57348	Hs.184510 Hs.155324	Stretifin matrix metalloproteinase 11 (stromelysin	1.25	4.17 1.72
70	103060	X57766 X63629	Hs,2877	"Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
	103242	X76342	Hs.389	Alcohol dehydrogenase 7 (class IV), mu	1	1
45	103312 103478	X82693 Y07755	Hs.3185 Hs.38991	*Lymphocyte antigen 6 complex, locus D; S100 calcium-binding protein A2	0.92 1.05	1.28 5.81
73	103558	Z19574	Hs.2785	keratin 17	0.65	6,68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083 .	Hs.82128	5T4 Oncofetal antilgen	1	3.93
50	103594	Z31560 AA089997	Hs.816	*SRY (sex determining region Y)-box 2, p *ESTs, Highly similar to integral membra	0.71 0.99	7.23 1.8
50	104158	AA454908	Hs,8127	KIAA0144 gene product	0.96	1,29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7,23
	104689	AA010665		ESTs	0.96	2.11
55	104733 104906	AA019498 AA055809	Hs.23071 Hs.26802	ESTs Protein kinase domains containing protei	1.18	1.88 3.15
55	104978	AA088458	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAMI	1.64	2,89
	105012	AA116036	Hs.9329	'Homo saplens mRNA for fis353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weekly similar to unknown [S.cerev ESTs	0.9	4.63
60	105263	AA227926 AA233459	Hs.6682 Hs.26369	ESTS ESTs	0.95	2.87 1.13
00	105312	AA233654	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1,28	2.31
	105743	AA293300	Hs.9598	ESTs	0.94	2.04
65	106012 106231	AA411621 AA429571	Hs.8895 Hs.38002	ESTs; same as BFH67 KIAA1355 protoin	1.04	1,5
05	106540	AA454607	Hs.38114	Hypothelical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
70	106727 106906	AA465342 AA490237	Hs.34045 Hs.222024	Hypothetical protein FLJ20764 Transcription factor BMAL2 (cycle-like f	0.87 0.61	1.59 1.6
70	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homotog (E coli Re	0.48	2.67
	107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs: proceltagen I-N proleinase	0.97	2.89
75	107284	S74039 AA026418	Hs.291904 Hs.91539	Accessory proteins BAP31/BAP29 ESTs	1.15 0.72	3,65 3,44
15	107922	AA028028	Hs.61460	to superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical profein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
80	108857	AA133250 AA133334	Hs.62180 Hs.129911	ESTs ESTs	0.73	7.3
00	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabkine	1	4.55
	109424	AA227919 F05012	Hs.85962 Hs.27027	Hyaturonan synthase 3 Hypothetical protein DKFZp762H1311	1.42	1.28
85	109665	H09281	Hs.27027 Hs.13234	FSTs	1.13	2,16
00	IVaalU		110.10234			

1905 1905		w	O 02/0864	43			
1695 16957					A disintennin and metallografeinase doma	0.84	1.95
110056 H086271 H3-5599 111023 M086271 H3-5599 111026 M086271 H3-5599 111027 M086272 H3-5599						0.94	1.41
5 11135 NSS20 H 1.14559 H		110561					
111076 Pol3239	-						3.13
1992 1998	5	111345	N89820	Hs.14559	Hypothetical protein FLJ10540		
100 110244 651300 18.70823 30.40177 pickish 30.40177 20.4017 2				HS.293240	VIAA1020 ordein		
10 17297 17217 17217 17218 125981 17219 17		112244		Hs.70823	KJAA1077 protein		
110007 125607 147.756 157.56		112973	T17271		"cDNA FLJ13308 fis, clone OVARC1001436,	1	
11931 1933 1934 1935	10	112989	T23482	Hs.89961	"Diacylglycerol kinase, zeta (104kD)"		
1533 193345 H. 1,15740 Psycholical protein FLH1095 0.42 1.44 1.44 1.45 1.45 1.45 1.45 1.45 1.45				Hs.7549			
15		113095					
15		113970			ESTs	1,17	1.73
14477 Au32077 H. 150413 Feb. markog 1.66 1.34 1.47	15	114346	Z41450	Hs.130489	"ATPase, aminophospholipid transporter-l		0.82
11009				Hs.103305		0.8	1.88
20 15999 A-X52014 in 15920 A-X		114471				1.06	1.34
20 115099 Aux35000 this 1.50223 (Aux3500s pooline to UPP I) to ow density 1 C59 1.502 (Aux3500s pooline to UPP I) to own density 1 C59 1.502 (Aux3500s pooline to UPP I) to own density 1 C59 1.502 (Aux3500s pooline to UPP I) to own density 1 C59 1.502 (Aux3500s poo		114509			*Con junction protein heta 5 (connevin		
1693	20						1,92
150006	20	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu law density I	0.59	
2.5 115022 A-3331932 Hs.47376 EST1		115291	AA279943	Hs.122579			1.25
1					Hypothetical protein KIAA1335		1.48
16987 Adv11902	25	115522	AA331393				
1 5.58 1 5.59	23	115030	AAA11502	Hs 63325			
1 16927 AA47252 H. 159517 C. 159517						i	6.98
16107			AA447522		Differentially expressed in Fenconi anom		
16/13	20					0.99	
196187	30	116107	AA456968	Hs.92030	ESTs		
161528		116134			Usedhelical protein		1.9
3.5 1603.5 A-68280 H.27013					Hypotricinal protein 2		0.86
35 16/88 C4/992 Hz/7816 Liberary (increase) Liberary ("Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
17937 103200 11,44520 10,44521 10,	35	116483	C14092	Hs.76118	Ubiquilin carboxyl-terminal esterase L1		
17768 180933 1.17110 1.07120 1.0814							0.64
40 11988 NS0073 H. 120022 Bely rise informed insucely 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					Distriction DITPOOR evaluation		
4.0 11988 NB4539 H.1.40956 Sept. 1 1.00 0.07 2.26 5 1.00		117093			Ruhrale-Induced transcript 1	1	
16956 16558 14.4224 hypothetical protein FL/10716 1.25 0.25 1.55	40	118368	N64339		ESTs		2.86
1995		118566	N68558	Hs.42824	Hypothetical protein FLJ10718		
45 19945 W9940 H.152961 C. Str. Abstraction of the Complete Comple			N71781	Hs.50081			
45 10102 W95426 H. 1010277 EST W95426 H. 1010277 EST W95426 H. 1010277 EST W95426 H. 101027 H.				Hs.191381	ESTs; Weakly similar to hypothetical pro		
120104 Weist177	45	119845			G protein-coupled receptor or "ECTs. Moderately similar to 653 receifed		
1,006	73			Hs.180479	ESTs	0.69	
1		120486	AA253400		Turnor protein 63 kDa with strong hornolog		
50 10686		120859	AA350158		Achaete-scute complex (Drosophila) homol	1	
10889	50	120660	AA360240		EST	101	246
1 12582 A465500 1457924 Condendation pecuaser 1 1 1 1 1 1 1 1 1	30	120948	AA397822	HS.104650	Hypothesical protein PLJ 10292		1
1,1269					Chondromodulin i precursor		
1			AA405657	Hs.128791	CGI-09 protein		1.8
12044 Aud 1969 11-30001 1-3000 1-300		121791	AA423978			1	1
12976	22	123005	AA479726	Hs.105577		1006	100
12477						159	
60 12227							1.64
0.0 12222 AbSOMPT H-11220 SAGE-EI proble 1.39 2.25 12400 D100000 H-110000 EE 1 12400 D10000 H-110000 H-1100000 H-110000 H-110000 H-110000 H-110000 H-110000 H-110000 H-1100000 H-110000 H-110000 H-1100000 H-11000000 H-1100000 H-1100000 H-1100000 H-1100000 H-1100000 H-1100000 H-1100000 H-11000000 H-11000000 H-11000000 H-11000000 H-11000000 H-11000000 H-11000000 H-11000000 H-110000000 H-110000000000		123571	AA608956	Hs.112619	ESTs, Weakly similar to PQ0109 Purkinje		1.14
1,465 1,573 1,499 748 1,499 748 1,499	60	123829	AA620697	Hs.112208	XAGE-1 protein	1.39	
12860 15356 15356 153576 1535						1 40	4.85
65 12528 W73981 Hs.11922 WALTH Staphenore colorenductions MRG cube 1.33 1.77 1.75		124069	F135/3	HS.99709			0.02
Act			W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu		1.77
12997	65	125453	R06041	Hs.18048	Melanoma antigen, family A, 10*		
1,2994 HS7512 H27079 EST 1,155					Glycoprolein (transmembrane) nmb		
70 12656 N70192 Hs.27898 Nypotheridar planeth FL19229 1 1.35 12721 ASSASS. Hs. 14784 Hs.1789 Hs. 1789							
70 19845 Altr5792 Hasf1535 STEAP (Februs appliess IM-Cook ROM0111 1 2.23 17721 Altr5718 Altr5						1	
172721 AUS4332	70	126390	N/0192 A1167942		STEAP1 /Home series BAC dose RG041D11	i	2.23
129/192	, ,						3.27
1,555.06 1,555.06				Hs.179729	collagen; type X; alpha 1 (Schmid metaph		
75 12777 185006 18-10326 29-1036 18-10326 29-1036 18-10326 29-1036 18-10326 29-1036 18-10326 29-1036 18-10326 29-1036 18-10326 29-1036 18-10326 29-1036 29-1					KIAA1085 protein		
12824 A225652	75	128610			Contains and abutes delt amesion motecu	1.89	1
12041 158573 1s. 15992 15086 center family 2 (brillated) 15094 150	13	128924			Pakonhiin 3	1.3	2.97
15999 H50598 H-1,10890 ATR-Hoding counted, sin the hamily C (CFT 0.87 1.54 1.2945 1.29				Hs.169902	"Solute carrier family 2 (facilitated of	0.84	
80 12866 A.17269 Hs.11118 ESTs 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 3 2 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 3 3 1 3 3 3 1 3 3 1 3 3		129099	H50398	Hs.108660	"ATP-binding casselle, sub-family C (CFT	0.87	
12969 5 572493 Hs.115947 Keralla 16 (foota non-egidemnélylic pallen 0.92 1.5 129626 UZ6727 hs.1174 Cycli-depondent Manas hilblar 24 (m. 0.85 1.93 130023 X13-61 Hs.23960 Calmodulla-Ris 3 — 0.44 1.22 130068 X14650 Hs.147097 *PLAN histon farally, number 2* 0.98 1.96	90			Hs.111128	ESTs	1 0.72	
129628 UZ9727 Hs.1174 Crycth-dependent Ninase inhibitor 2A (m 0.85 1.93 130023 X13651 Hs.239600 Calmodulin-like 3 0.84 1.22 130060 X14650 Hs.147097 *12A his know family , member X* 0.98 1.96	90			Lie 115047	Gendank riomo sapiens kerann o isciomi Keralin 16 ffocal neo-enidermolytic nalm		
130023 X13461 Hs.239600 Calmodulin-like 3 0.84 1.22 130080 X14850 Hs.147097 H2A histone family, momber X* 0.98 1.96					*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
130080 X14850 Hs.147097 "H2A histone family, member X" 0.98 1.96			X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
8D 130385 AA128474 Hs.155223 stanniocaton 2 1 1	0.5	130080		Hs.147097			
	63	130385	AA126474	Hs.155223	stanniocarcin 2	1	1

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	w	O 02/086-	143			
	130410	V01514	Hs.155421	A/pha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	"Human DNA-PK mRNA, partial cds"	1.15	3.65
	130482	L32866	Hs.1578	Baculoviral IAP repeal-containing 5 (sur	1	1.88
-	130553	AA430032	Hs.252587	Piluitary turnor-transforming 1	0.92	1.96
5	130577	M35410	Hs.162	Insufin-like growth factor binding prote	1.17	4.7
	130627 130600	L23808 AA223386	Hs.1695 Hs.19674	Matrix metalloproleinase 12 (macrophage ESTs; Weakly similar to katarin p80 subu	0,69 1,13	4.05 2.41
	130939	AA596669	Hs.19074 Hs.21400	ESTs; Weakly's imitar to kalairin pou subu	0.13	0.89
	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS		1.15
10	131244	D38076	Hs.24763	RAN hinding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
	131927	AA461549	Hs.34780	"Doublecortex; lissencephaly, X-linked (0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
1.5	131978	D80008	Hs.36232	KIAA0186 gene product	0.69	1,43
13	132354 132543	L05187 AA417152	Hs,211913 Hs,5101	Small proline-rich prolein 1A ESTs; Highly similar to prolein regulati	0.69	4.27
	132632	N59764	Hs.5398	guarine-monophosphale synthetase	1	1.08
	132653	U31201	Hs.54451	"laminin gamma2 chain gene (LAMC2), exon	i	1
	132659	Z75190	Hs.54481	*Low density lipoprotein receptor-relate	0.89	0.89
20	132710	W93726	Hs.55279	"Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.56105	*ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich prolein 2B	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.56
25	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (actival	1.16	3.53
43	133070 133282	U69611 U52960	Hs.64311 Hs.286145	*A disinfegrin end metalloproteinase dom	1.16	27
	133282	AA215299	Hs.280140 Hs.70830	"SRB7 (suppressor of RNA polymerase B, y U6 snRNA-associated Sm-like protein LSm7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp6641922	1,12	2.55
	133391	X57579	Hs.727	H.sapiers activin bela-A suburit (exon 2	1.65	1.76
30	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	"Serine (or cysleine) proteinase inhibit "Homo saciens cDNA; FLJ23602 fis, clone	1	1
	134168	AA398908	Hs.181634		0.95	1.53
	134218	AA227480	Hs.80205	Pirn-2 oncogene	1.36	2.48
35	134405	R67275	Hs.82772	""collagen, type XI, alphe 1""	0.76	2.86
23	134453 134470	X70683 X54942	Hs.83484 Hs.83758	SRY (sex determining region Y)-box 4	1.89	3.78 4.11
	134645	X54942 U87459	Hs.83758 Hs.167379	CDC28 protein kinase 2 *Cancer/lesils entigen (NY-ESO-1, CTAG1,	0.62	0.83
	134781	M17183	Hs.89626	Paralhyroid hormone-like hormone	1	1
	135002	U19147	Hs.272484	G anigen 6	i	i
40	100040	M97935	THE PERSON	AFFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family; member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
45	102031	U04898	Hs,2156	RAR-related orphan receptor A	1	1
43	102221	U24576	1) 75000	LIM domain only 4	1 1.08	1.43
	102270	U30255 U37022	Hs.75888 Hs.95577	phosphogluconete dehydrogenase cyclin-dependent kinase 4	0.88	1.32
	1023391	U41668	Hs.77494	decoygusnosine kinase	1.07	1.58
	103000	X51956	Hs.146590	enclase 2; (germma; neuronal)	0.91	1.49
50	103395	X94754	Hs.119503	methionine-IRNA synthelase	0.89	1.32
	105638	AA281599	Hs.20418	Homo saplens mRNA for for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
	114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.56
55	115206 115906	AA262491 AA436616	Hs.186572 Hs.82302	ESTs ESTs	0.74	2.52
55	119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
	124163	H30639	Hs.189838	FSTs	i"	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
	127141	AA307960	Hs.75478	KIAA0956 protein	0.85	1.4
60	128034	AA905754	Hs.75103	lyrosine 3-monockygenase/tryptophan 5-mo	1	1.18
	128609	AA234365	Hs.102456	survival of motor neuron protein interac	1_	1.5
	128895 130199	R37753 Z48579	Hs.106965	ESTs a disinform and metalloprotesse domain	1.7	2
	130199	U89995	Hs.172026 Hs.159234	a dismogni and metaloprotesse domain forkhead box E1	ł	1
65	133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	ł	i
05	133658	M25756	Hs.75426	secretogranin II (chromogranin C)	i	i
	135047	AA460466	Hs.93597	ESTs	i	1
	100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
	100114	D00696	Hs.82962	thymidylate synthelase	0.68	1.86
70	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
	100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.26
	100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.56
	100168	D14874 D17793	Hs.394 Hs.78183	adrenomedullin ardo-keto reductase family 1; member C3	0.46	1.17
75	100187	D21063	Hs.57101	minichromosome maintenance deficient (S.	0.97	1.4
,,,	100788	D26600	Hs.89545	professome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364	110.00040	"Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
	100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.92	1.78
80	100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
	100355	D78129		""Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154868	carbamoyl-phosphale synthetase 2; aspart	1.49 0.59	2.46
	100368	D79987 D84557	Hs.153479 Hs.155462	extra spindle poles; S. cerevisiae; homo minichomosome maintenance deficient (mi	1.08	1.32
85	100438	D89557	Hs.155462 Hs.91417	topoisomerase (CNA) Il binding protein	1.00	2.15
0.5	100100		.10.01.411			

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	100455	D87953	Hs,75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT11	53	Nucleoside Diphosphale Kinase Nm23-H2s	0.99	1.41
	100518	HG174HT174		Desmoplakin I	1.28	3.17
5	100528	HG1828-HT18 HG2874-HT30		""Nex.in, Glia-Derived"" Ribosomal Protein L39 Homolog	0.68	1.9 5.44
,	100667	HG2981-HT31	27	""Epigan, Alt. Spice 11""	0.8	1.97
	100830	HG4074-HT43	144	Rad2	1.01	2.12
	101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131	L10838 L14595	Hs.167460 Hs.174203	splicing factor; arginine/serine-rich 3 solute carrier family 1 (glutamate/neutr	1.23 1.35	1.87 2.73
10	101162	L14595 L19686	Hs.73798	macrophage migration inhibitory factor (1.03	1.78
	101183	L19779	Hs.795	H2A histone family: member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase Inhibitor 3 (CDK	0.7	2.2
15	101228	L27706 L29008	Hs.82916 Hs.878	chaperonin containing TCP1; subunit 6A (sorbitol dehydrogenase	0.99	1.99 2.11
13	101233	L29008 L33801	Hs.78802	giyoogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		""Homo sapiens (cell line HL-6) alpha t	0.69	2.78
	101342	L76191	Hs.182018	interleukin-1 receptor-associated kinase	1.04	1.84
20	101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55 1.5
20	101423 101445	M18391 M21259	Hs.89839 Hs.1066	EphA1 small nuclear ribonucleoprotein polypopt	1.21	1,96
	101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs.12163	enkaryotic translation initiation factor	1,19	1.93
25	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42 1.25
25	101607	M38690 M55998	Hs.1244	CD9 antigen (p24) ""Human alpha-1 collagen type I gene, 3	1.11	1.20
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
20	101853	M94362	Hs.76084	lamin B2	0.84	1.19
30	101977	S83364 U01038	Hs.77597	""putative Rab5-interacting protein (cl polo (Drosophia)-like kinase	0.89	1.9 1.46
	102009	U02680	Hs.82643	protein tyrosine Kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
25	102039	U05861	Hs.201967	aldo-kelo reductase family 1; member C1	0.93	2.32
35	102123	U14518	Hs.1594	centromere protein A (17kD)	0.89	4.28 1.42
	102130 102148	U15009 U16954	Hs.1575 Hs.75823	small nuclear ribonucleoprolein D3 polyp ALL1-fused gene from chromosome 1q	8.0	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
	102220	U24389	Hs.65436	lysyl axidase-like 1	1.15	2.34
40	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; Impor	1.14 1.05	2.69 1.7
	102330	U35451 U44754	Hs.77254 Hs.179312	chromobox homolog 1 (Drosophila HP1 beta smail nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discoidin domain receptor family; member	1.05	2.01
	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting, beta 3 poly	1.27	1.92
45	102522	U53347	Hs.183556	sciute camer family 1 (neutral amino a	0.84 1.11	1.31 1.6
	102590 102676	U62136 U72514	Hs.12045	"Homo sepiens enterocyte differentiali putative protein	1.04	2.17
	102687	U73379	Hs.93002	ublouifin carrier protein E2-C	0.86	2.28
=-	102704	U76638	Hs.54069	BRCA1 associated RING domain 1	1.12	1.63
50	102781	UE3843		""Human HIV-1 Nef interacting protein (0.9 0.98	1.39 2.16
	102784	U85658 U91327	Hs.61796 Hs.6456	transcription factor AP-2 gamma (actival chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
	102972	X16662	Hs.87268	annexin A8	1.25	2.32
55	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793 X54941	Hs.117950 Hs.77550	multifunctional polypeptide similar to S CDC28 protein kinase 1	1.58 1.32	5.44 3.79
	103035	X59543	Hs.2934	ribonucleoli de reductase M1 polypapilde	1.11	2.58
	103168	X68314	Hs.2704	dutathione peroxidase 2 (nastrointestin	0.75	3.05
60	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasml	1.01	1.97
	103212	X73874 X74801	Hs.2393 Hs.1708	phosphorylase kinase; elpha 1 (muscle) chaperonin containing TCP1; subunit 3 (g	0.97	1.72
	103223	X78416	Hs.3155	casein; alpha	1	1
	103262	X78565	Hs.204133	hexabraction (tenascin C; cytotactin)	1.23	3.09
65	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25 4.62
	103364	X90872 X91868	Hs.75854 Hs.54416	SULT1C sulfotransferase sine oculis homeobox (Drosophila) homolo	2.85	2.48
	103373	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (9kut	1	1.53
	103404	X95586	Hs.78596	orolegegee forosome: macropain) subunit	0.92	1.53
70	103437	X98260	Hs.82254	M-phase phosphoprotein 11 lipocalin 2 (oncogene 24p3)	0.92	1.54
	103448	X99133 Z35402	Hs.204238 Hs.194657	Ipocalin 2 (oncogene 24p3) cadhein 1; E-cadherin (epitheTal)	0.55 1.32	0.96 2.51
	103646	235902 768 22 6	Hs.194607 He 2340	junction plakoglobin	0.88	1.28
	103658	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
75	103774	AA092898	Hs.92918	FSTe: Weakly similar to R07G3.8 IC.cleon	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87 1.4	2.17 2.49
	104276 104289	C02193 C16281	Hs.85222 Hs.75478	ESTs; Weakly similar to R27090_2 [H.sapi KIAAQ956 protein	1.4	1.68
	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidenmolys	1.04	1.49
80	104453	M19169	Hs.123114	cystatin SN	0.38	0.76
	104611	R98280	Hs.125845	rbulose-5-phosphale-3-epimerase	1.08	2.25 1.65
	104758	AA024661 AA156532	Hs.7010 Hs.11801	ESTs; Weakly similar to ACYL-COA DEHYDRO adenosine A2b receptor pseudogene	1.14 0.91	1.65
	105114	AA156532 AA159501	Hs.11801 Hs.247280	HBV associated factor	1.08	1.7
85	105174	AA186613	Hs.34744	ESTs	0.95	2.05

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	105280	AA232215	Hs.14600	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516	AA257971	Hs.21214	ESTs	1.35	3.56
5	105621	AA280865 AA287393	Hs.6375 Hs.15202	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23 0.98	1.82 1.28
,	105698 105705	AA287393 AA290767	Hs.101282	ESTs; Weakly similar to oligodendrocyte- Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1,32
	105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
	105782	AA350215	Hs.21580	ESTs	1	1
	105799	AA372018	Hs.24743	ESTs	1.08	1.78
10	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95 0.87	1.34 2.25
	105891 105936	AA400768 AA404338	Hs.26662	ESTs; Weakly similar to tumor necrosls f ESTs	1.14	1.46
	106069	AA417741	He 20800	ESTs: Weakly similar to ZINC FINGER PROT	1	1.70
	106103	AA421104	Hs.12094	ESTs	1.04	1.44
15	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994 Hs.10862	ESTs ESTs	0,77 0.74	2.05 2.23
	106182 106220	AA426609 AA428582	Hs.10002 Hs.32196	ESTs: Moderately similar to metargidin p	0.97	1.99
20	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318	AA436570	Hs.9605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to plL2 hypothe	0.98	2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212 AA451676	Hs.42484 Hs.30299	Homo sapiens mRNA; cDNA DKFZp564C053 (fr IGF-II mRNA-blinding protein 2	14	2.29
23	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	i i	1.82
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
30	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.sa	1.11	1.49
30	107115	AA610108	Hs.27693 Hs.4756	ESTs; Highly similar to CGI-124 protein	1.13	3,63
	107129 107159	AA620553 AA621340	Hs.10600	flap structure-specific endonuclease 1 ESTs; Weakly similar to ORF YKR061c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
35	107516	X56597	Hs.99853	fibriliarin	0.94	1.77
	107529 107531	Y12065 Y13936	Hs.5092 Hs.17883	nucleolar protein (KKE/D repeat) protein phosphatase 1G (formerly 2C); ma	1.05 1.06	2.29 1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
	107957	AA031948	Hs.57548	ESTs	0.95	1.46
40	106565	AA085342	Hs.1526	ATPase: Ca++ transporting; card ac muscl	0.59	1.35
	108780	AA128561	Hs.117938	collager, type XVII; alpha 1	1,23	7.63 2.56
	108828 109060	AA180879	Hs.71435 Hs.241551	DKFZP564O0463 protein chloride channel: calcium activated; fam	0.67	1.42
	109112	AA169379	Hs.72865	ESTs	1.03	2.31
45	109344	AA213696	Hs.86559	poly(A) hinding protein.like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9 1.17	0.95 2.26
	110958 111018	N50550 N54067	Hs.24587 Hs.3628	signal transduction protein (SH3 contain mitogen-activated protein kinase kinase	1.17	1.85
50	111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56 1.03	1.96 1.57
55	112869 112992	T03313 T23513	Hs.4747 Hs.7147	dyskeratosis congenita 1; dyskerln ESTs	1.03	1.57
55	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
60	113573	T91166	Hs. 15990	ESTs	0.76 0.79	1.47 1.51
00	113811 114086	W44928 Z38266	Hs.4878 Hs.12770	ESTs Homo sapiers PAC clone DJ0777023 from 7p	0.9	1,34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32	2.36
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
65	115047	AA252627 AA258409	Hs.22554 Hs.198907	homeo box B5 myelin protein zero-like 1	1.01 1.06	2.36 2.31
	115166 115167	AA258403 AA258421	Hs.43728	hypothetical protein	1.52	2.52
	115239	AA278650	Hs.73291	ESTe: Weakly similar to similar to the b	0.7	2.57
	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
70	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs 43946	ESTs; Weakly similar to Weak similarity	1.2 0.96	1.98 1.31
	116004 116121	AA449122 AA459254	Hs.76086 Hs.48855	ESTs; Highly similar to small zinc finge ESTs	0.97	1.55
	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
75	116190	AA464963	Hs 67776	ESTs	8.0	1.57
	116312	AA490494	Hs.65403	ESTs	1.37	2.65
	116732	F13779	Hs.165909	ESTs	0.92 1.15	1.8 1.84
	117602 117950	N35020 N51394	Hs.44685 Hs.75478	ESTs; Weakly similar to GOLIATH PROTEIN KIAA0956 protein	1.04	2.36
80	117992	N52000	Hs.172069	Homo saplens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
	118785	N75386	Hs.111867	GLI-Kruppel family member GL12	1	1
	119717	W69134	Hs.57967	ESTs	1 0.78	1.4
	119814 120128	W74069 Z38499	Hs.58350 Hs.91448	ESTs MKP-1 like protein tyrosine phosphatase	0.78	1.77 1.46
85	120128	Z38499 Z98443	Hs.91448 Hs.86366	FSTs	0.83	2.01
95	120212	200110				201

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	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74
	121054	AA398604	Hs.97387	ESTs	1.05
	121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98
5	121376	AA405699 AA411448	Hs.166232 Hs.208985	ESTs; Moderately similar to SODIUM-AND	0.91 0.91
,	121457 121780	AA411448 AA422086	Hs.124660	ESTs ESTs	0.46
	121781	AA422150	Hs.98370	cylochrome P540 family member predicted	1,07
	121844	AA425732	Hs.98485	gap junction prolein; beta 2; 26kD (conn	0.94
	122059	AA431737	Hs.98749	EST	1.93
10	122338	AA443311	Hs.98998	ESTs	1
	122354	AA443772	Hs.186692	ESTs ESTs; Wealdy similar to MRJ [H.saplens]	0.88 2.28
	122591	AA453265 AA460156	Hs.99311 Hs.99556	FSTs	0.88
	123398	AA521265	Hs.105514	ESTs ·	1
15	123518	AA606531	Hs.170313	ESTs	i
	123673	AA609471	Hs.112712	ESTs	1
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74
	124367	N24006 N48000	Hs.99348 Hs.140945	distal-less homeo box 5 Homo sapiers mRNA; oDNA DKFZp586L141 (fr	0.67 1.19
20	125756	W25498	Hs.140945 Hs.81634	ATP synthase; H+ transporting; mitochond	0.93
20	125769	Al382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65
	125852	H09290	Hs.76550	Homo saplens mRNA; cDNA DKFZp56491264 (f	0.72
	125924	AA526849	Hs.82109	syndecan 1	1.22
0.5	126037	M85772	Hs.6066	KIAA1112 protein	1.36
25	126214	N29455 N78770	Hs.74316 Hs.223439	desmoplakin (DPI; DPII) FSTs	1.93 1.21
	126737	AA488132	Hs.62741	ESTs	1
	126743	AA179253	Hs.172182	ro/v/A\.hinding.omtein: cytoplasmic 1	1.3
	126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53
30	127432	AA501734	Hs.170311	helerogeneous nuclear ribonucleoprolein	1.57
	128218	H02682	Hs.99189	ESTs; Moderately similar to recombinatio	1.24
	128527 128568	M31523 X60673	Hs.101047 Hs.247568	transcription factor 3 (E2A Immunoglobul adenylate kinase 3	1.08 1.23
	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87
35	128628	C14037	Hs.251978	EST T. COLOR	1.22
	128891	W27939	Hs.103834	FSTs	1.1
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92
	128733	AA328993	Hs.104558	ESTs	1.34
40	128781 129052	X85372 AA496297	Hs.105465 Hs.182740	small nuclear ribonucleoprotein polypept ribosomal protein S11	2.59
40	129095	L12350	Hs.103623	thrombospondin 2	1.04
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 [M.muscu	0.95
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplesmic retic	1.28
	129703	AA401348	Hs.179999	ESTs	0.97
45	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09
	129850 129896	N20593 AA043021	Hs.56845 Hs.13225	GDP dissociation inhibitor 2 UDP-Gal betaGloNAc beta 1;4- galactosylt	0.74 1.43
	130069	AAQ55896	Hs.146428	collagen; type V; alpha 1	1.17
	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1,26
50	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1
	130699	M91670	Hs.174070	ubiquitin carrier protein	1.07
	130867	J04093 AA063596	Hs.2056 Hs.22142	UDP glycosyltransferase 1 ESTs; Weakly similar to NADH-CYTOCHROME	0.93
	131009 131028	U20240	Hs.2227	CCAAT ienhancer binding protein (C/EBP);	1
55	131083	U66861	Hs.22785	gamma-aminobulyric acid (GABA) A recepto	1.1
	131091	T35341	Hs.22880	ESTs; Highly similar to dipepticyl pepti	1.28
	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43
	131148	C00038	Hs.23579	ESTs	0.88
60	131164 131185	Y00503 M25753	Hs.182265 Hs.23960	keratin 19 cyclin B1	1.19 0.86
30	131219	C00476	Hs,24395	small Inducible cytokine subfamily B (Cy	0.66
	131454	AA455896	Hs.2699	alypican 1	0.99
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1
65	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1.55
03	131796	D50914 AA135554	Hs.30736 Hs.32125	KIAAD124 protein FSTs	1
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83
	131860	U02082	Hs.334	Oncogene TIM	1.08
	131884	H90124	Hs.3463	ribosomal protein \$23	1.23
70	131903	AA481723	Hs,3436	deleted in oral cancer (mouse; homolog)	0.91
	131945 131958	M87339 AA093998	Hs.35120 Hs.3566	replication factor C (activator 1) 4 (37 ESTs; Highly similar to phosphorylation	1 0.87
	131964	W42508	Hs.3593	ESTS, riiginy similar to priospitorysauor.	1
	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncoge	1.12
75	132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1
	132065	D82226	Hs.211594	profesisome (prosome; macropain) 26S subu	0.89
	132109	AA599801	Hs.40098	ESTs	0.99
	132112	AA150661 AA447123	Hs.40154 Hs.250705	jumonji (mouse) homolog ESTs	1.06
80	132123	H89551	Hs.41241	ESTS	1.08
00	132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02
	132309	AA460917	Hs.2780	jun D proto-oncogene	1.16
	132371	AA235448	Hs.46677	ESTS	0.8
85	132618 132736	AA253330 U68019	Hs.5344 Hs.211578	adaptor-related protein complex 1; gamma MAD (mothers against decapentaplegic; Dr	0.5 1.21
33	132130	200019	ris-2110/0	area (monas aganar accapenapeses) U	1.41

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	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3	
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43	
	132922	T23641	Hs.6066	IGNAT(12) parkin ETET, Weishy similar bestvoren (B. corov sostie currer family 2 (e-initiate) gli (i-initiate) gli (i	1.16	1.53	
_	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.corev	1.02	1.88	
5	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97	
	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34	
	133065	X62535	Hs.172690	diacytglycerol kinase; alpha (80kD)	0.93	1.23	
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2(b	1.14	1.76	
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43	
10	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8	
	133195	AA350744	Hs.181409	KJAA1007 protein	2.29	2.69	
	133313		Hs.70704	ESTs	1.07	1.68	
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18	
	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repair	0.91	1.45	
15	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68	
	133483	X52426	Hs.74070	keratin 13	0.85	1.14	
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69	
	133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	0.7	6.21	
	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3	
20	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25	
	133594	L07758	Hs,172589	nuclear phosphoprotein similar to S. car	0.84	1.29	
	133627	U09587	Hs.75280	glycyl-IRNA synthetase	1.09	1.99	
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5	
	133859	U66782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33	
25	133865	F09315	Hs.170290	descraptable (DPC DPP) ppi piention pueller diphi 1 4340 (con prolessore (grozone; macropori) 285 sebu nuclose phosphorosini milar la 5.0 con physi-(RRA) symbolase 285 prolessore-separation initiar la 5.0 con physi-(RRA) symbolase 285 prolessore-separation (and position formolog 285 prolessore-separation (and position formolog 285 prolessore-separation formolog 281 prolessore-separation formolog 281 prolessore-separation formolog 281 prolessore-separation formolog 281 prolessore-separation 281 prolessore-separation 281 prolessore-separation 282 prolessore-separation 283 prolessore-separation 283 prolessore-separation 283 prolessore-separation 283 prolessore-separation 284 prolessore-separation 284 prolessore-separation 285 prolessore-s	1.84	6.7	
	133913	W84712	Hs.7753	calumenin	1.15	1.86	
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91	
	133982	U47621	Hs.207251	nucleolar autoantinen (55kD) similar to	1.3	1.99	
	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65	
30	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated BCL2/adenovirus E1B 19k0-Interacting pro IGF-II mRNA-binding protein 3	1.04	1.62	
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55	
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95	
	134193	F09570	Hs.7980			1.48	
	134367	X54199	Hs.82285	phosphoribosyldycinamide formyltransfer	1	2.8	
35	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2	
	134457	D66963	Hs.174044	phosphonicoprighychnamide formyllremsfer fragle X mentil relatedation; autocomal dishovelide 3 (homologous to Diesophila smell mulear homologous to Diesophila smell mulear homologous to Diesophila homologous thronon, HENA symbolase collapside tradition initiation factor replication probin AT (7000) replication probin AT (7000) replication probin AT (7000) and the probin probin AT (7000) and the probin probin AT (7000) and the probin probin AT (7000) and dishippin and metalloproleinase doma ESTs	1	1.47	
	134469	X17567	Hs.83753	small nuclear n'bonucle corotein polypept	0.94	1.57	
	134496	M63180	Hs.84131	threonyl-IRNA synthetase	1.2	2.64	
	134501	WB4870	Hs.211568	eukaryolic translation initiation factor	0.84	1.36	
40	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93	
	134548	U41515	Hs.85215	Deleted in soil-hand/soil-foot 1 regio	1.46	2.73	
	134599	X99226	Hs.86297	Fanconi anemia: complementation group A	1.36	2.22	
	134692	R73567	Hs.8850	a distriction and metallogroleinase doma	0.77	1.64	
	134693	N70361	Hs.8854	ESTs	1.09	1.82	
45	134806	Z49099	Hs.89718			1.35	
	134821	Z34974	Hs.198382	spermine synfhase plakophilin 1 (etodermal dysplasia/skin actin related protein 2/3 complex; subun chibnase 1 (chilotnocidase)	0.99	1-4	
	134864		Hs.90370	actin related protein 2/3 complex: suburi	0.95	1.42	
		U29615	Hs.91093	chilinase 1 (chilotrios dase)	1.16	1.29	
		L10678	Hs.91747	nmilin 2		1.76	
50		AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73	
-0	135051		Hs,93668	ESTs	1.35	2.11	
		U51711		Human desmocollin-2 mRNA: 3' UTR	0.86	1,16	

Table 16 about the accords resolved for those plays in Table 14 backing impringeDis. For each problems the backing impringed for each problems will be appeared to the resolved for the plays of the plays and the plays of the pl

Pkey: Unique Eos probeset identifier number GAT number: Gene cluster number

	Accession:	Genbank a	ccession numbers
	Pkey	CAT	Accessions
55	100661 100667	23182_1 26401_3	BE623001 L050 L05424 X56794 AW606203 BE0

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85 101332 25130_1 JORGER NM_001057 AFG71747 AJ011741 M85/24 ALD42407 MA218572 BE295748 BE083981 AL040877 AW99918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA164024 AW71482 AI970337 AA737616 AI827444 AW003266 AV742333 AV344044 AV766634

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5			A ASSECT A ASSECTION ANNIQUASIS FINALLY RACGIVATA A ARREST HEISON A AMERICAN A MICROSINA ANNIQUATION ANNI IT TABLE ANNI ANNI ANNI ANNI ANNI ANNI ANNI ANN
10			AA11056 AV25191 AMB0272 AMB0202 AMB0202 ANT 1680 AA68972 AA239919 AA80949 AV27220 AV765294 A112007 AV788910 AA80579 AA27590 AA65029 AM50259 AW788911 TH 1879 ANDSOE AV35925 AV35920 AV
15	100780	458_127	BE551958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832 BE269596 BE559865 BE396861 BE560031 BE514199 BE560037 BE560454
13	100830	4002_1	ACCIDATO WIGGIOS ALGOSIOS ALGORIZOS HERIOSES TISATES INVESTIGIS 13,774 IESTIGAS ESTITAS ES EZVITOS ES EZGIZOS ESFORTATAZISCO BESABROS ANTATES ALTRICOR ESTIGAZ ALARGOS TISATINI TIDOSAO AMVISBOS ESCATOS ALGORIZOS AMBOSTOS ANTASTOS I MASSIOS ANTAS ANVISTAS DE EZPERT DE GAUGZOS ANVISBOS ESPESTIGOS ESTIGAS ESTIGAS ALGORIZOS ALGORIZOS ALGORIZOS DE EZBURTA ALGORIZOS ALGORIZOS ALGORIZOS DE EZBURTA ALGORIZOS A
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25	100906	4312_1	ALD/769 6 EZ298110 AVX25095 AWK97270 NAL 000575 U10860 AVX501755 EEZ2976S C03806 AT795975 AA64-165 T36030 AVX52852 AA48642 (AWR5166 AM64946 ESP-6410 T395206 FAR57 N7222 ASSE6404 AVX04964 AVX7022A AWK5746 AW70766 AA77464 A4305698 AA57123 AA53069A 1399371 AA528935 AXT9385 T HESTS A KSB6000 AWS 1285 T R 1090 AWK7465 T AWR57497 A AR37596 AWK574A AWAS 1485 AWK746A AWK746 AWK7
30	100930	16865_1	JUAI 28 NJ. (2002) 1 AG230280 AA17016 AA06451 172009 AA77050 AA35395 AA45395 AA45046 AA164507 NT6 1539 AA29 149 AA70816 AA29 14 AA29240 AA70862 AA42924 AA70869 AA06451 AA70869 AA7086 AA708 AA
35	102221	3861_1	NAL, 000759 (J2675 AMH1616) AMH60473 AMH160465 AMH60472 AMH161609 AB204831 AMH162835 AM960305 AMH60473 AMH161046 AB20485 AMH60282 AMH60724 AMH60476 AB20473 AMH60476
40			A 14.0026 A 1454-161 ANT 1912 ANTISHEM A 1227-18 ER 64055 ANKIDSOR DA 12221 A AMBIZZIS B 14.0023 B 14.003 B 15.00 B 15
40	101809	32963_1	A116EFS A1273TS B.A.610EFS A1787966 A4655003 A3600509 A3505675 A227894 AWKZ7958 A54064019 M66989 A3A15200 MLQ60004 A3455000 E112603 A34614040 AWKZ02405 B145003 AWKS2158 A4406068 AW117500 AWKS0458 AWKS2158 AWKS0456 AWKS0450 AWKS1450 AWKS0450 AWKS0
45	102590	15932_1	AMAZIONE A L'ITRESSE, ALESSINES,
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75	102781	20812_1	DECEMBER 2621 2020 ER-10004 T3327A WHITEVIEW ANN HOUSE AND CORRESPONDED THE SECTION OF THE SECTI
80			ASOLIT AL MANSTER, AMERI TAS SEGAT PETETINET URBAS CODER DE SE RESENTA ASSIGNA HASTO EL DESASTO ANA SEGAT PETETINET URBAS CODER DE SE RESENTA ASSIGNA HASTO EL DESASTO ANA SEGAT PARE ASSIGNA HASTO EL DESASTO ANA SEGAT PARE ASSIGNA PETETINET DE SEGATO EL DESASTE ANA SEGAT PARE ASSIGNATION ANA SEGAT PARE ASSIGNATION ANA SEGAT PARE ASSIGNATION ANA SEGAT PARE ASSIGNATION AND
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5			AGE TERM AMERICAN AME
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10			T35127 ARGAQUEZ NESSANET NASONERA MOTINARIA DEL REGISTO EL REGISTO
15			BE263903 BE514339 BE409073 BE281296 BE543396 BE395387 BE38390 BE546908 BE546570 BE390625 AA074638 AA301821 AW845230 AW882379 AB48222 AW029672 AA515843 AW272334 BE250234
20	119221	102947_1	C 14322 WT4GOS ADD74232 AASSSEAV BEEDBESS A HABIT AMSSEMS AMTAMON ABBIGS BANKTSTSSS ABSTAT I AKZSTAG AW4F9721 RBB105 AH4GSSS ABAPTES AMONES ON AMSSET AT STEED AMSSET HABIT AMSSESS ABSTAT BANKTSSS ABSTAT I AKZSTAG AW4F9721 RBB105 AADSSESS AATKSTSS AMONES ON BROSS AMSSET AMSSE
20	125831 128192 113195	1522905_1 45743_3 178688_1	HANAS DECORD DEBOST ACADICAS ADDICES ANTHORO HANDES ISSUE AND ASSES ANTRODOS INSPOSOS INSTRUTA AT PRINCE ACCEPTED AND THE ACCEPTED AND THE ASSES AND THE ASSES AND ASSES ANTRODOS AND ASSES AND ASSEST ASSEST AND ASSEST AND ASSEST ASSEST ASSEST AND ASSEST ASSEST ASSEST ASSEST ASSEST ASSEST ASSEST AND ASSEST ASSESTITUTE.
25	119861 112973	238266_1 4868_1	A-AS-6443 AAT/ANDA AAS/RFT 15/9751 WRB 16.AT/2006 AS/8006 AT 15/9751 WRB 16.AT/2006 AS/8006 AND AS/800
30			AIGS271 A 19 TR-IS A ASODO A WYE1969 AIBTREZ 177271 AIBDOSES A069533 TH6019 AVIS92439 ACK24535 ACK7552 DT 1149 AWI32033 AASSS614 AUSZG52 AW086155 171452 AA016160 AWIST DE SEDOZOH A ISKESSE DE 201916 TAW08167 HAASSS10 AWISTAHA AWISTOST AWISTASSE AWISTS64 AWRI75647 AW938037 AL138042 AW882619 BE243018 AW98544 BE246381 BE000062 BE278921 AW987642 AA282454 H30121
35	129402 105936	47367_1 260931_1	"M70004 A 766605" WIRESA AUSTIZIA HASHIGI ANAHGES ALSHGAT AB 19800 TSETZA AUSZOWA TSEGIST TRATFII AUSZEROSH HIZTO TRATFII AND THE AUSZOWA TSEGISTA AUSZOWA TSEGISTA AUGSTA AUSZOWA TSEGIST TRATFII AUGSTA AUG
40	129466	2094_50	LASSI NA. 105554. LEGAN DE SIRBATA ANI-122 DE CHARGA LASIS VANDES, ADDES ANI-1275TPZ ANISASSISSE ANISASIS I A, ASHT 102 EEGÎ 1266 ANI-124 ANISASSIS ANI-124 ANISASSIS ANISAS ANISASSIS ANI
45			A ASSISTA ASSISTA A ASSISTA ASSISTA A ASSISTA
50	100220 100355	45374_1 12538_1	AMY03599 WM2259 AM91653 AM91753 AM57259 ET 184/06 AM39953 WM512 WM5190 D05864 AM941111 D24445 D25553 AM25598 DD2229 AM2035863 AM1610 D02201 AM399595 D2441 AW961440 AM57810 B22023 AM258969 TERE (2823 BETE 2823 ET 18252 BETE 2824 AM701554 AM314596 AM250715 EESB6883 AW624944 D23545 AW965978 AM701714 AM35073 AM2144964 AM16154 AM16124 AM72154 DM210 AM. 00122 AM341650 TE4166 AF069865 AM160976 EE018953
55		H05719 F1344	T 1851 Z. AUTISSES FORJAL ATTEMP RICHON ALMOST AN AZZER DYST AN AZZEZ SINGHESO ANNEASTE ANAZZEK ANGHESO ANGHES
60	100491 BE277805	34803_1 AA147951 AA6I	De5168 MSS981 X59898 MBM, 002512 BE379177 A314836 BE259406 BE282016 AVX264934 AVX26934 AVX26971 BE380950 BE51972 AVX16401 AVX1640 AVX1
65			A 172527 ARESINA HUMEN HANDEN ARESINA HERBINA HERBINA TENENGA HANDEN HAN
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75	100518	13165_1	AND THE PROPERTY OF THE PROPER
80			AVERSIONE BEXIZETO PARTOSCEL ANGOTES ANGOTES ANGOTES CHITAR ANTOCAS DE ESONO ANGOSATO DE 100-023 ANCIT DE 00287 DE ESCRESA BEDIOLAT ANGOTES ANGOTES ANGOTES ANGOTES ANGOTES CHEROSCE BEZIEROS DE ESCRESA DE ANGOTES A
85			RS8704 AW395966 AW384859 AA028951 AA028952 AA465100 AA719968 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW809750 AW39 1912 AW645690 T87267 AW853812 AA852213 W74149 BE00509 AA056401 H91011 AW388523 AW397272 C18457

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10			AL-SHADOO BATTITIZE A HARDES A MERCORA
15	100528	45979_1	ELESBOOT MURTIPS ANALYSE ENEZZET MARSON BURIE EEZPENS ENEZTHO ENEZHIND ENEZHIND EZERTAR C1900 ANALYSE XIZOR AX3976
20	100559	2260_1	BE-88987 T RYS233 AM64 199 AM890N F AM6233 AM75370 AM65119 BE-88980 MA, 000064 LESPO T MEDIA BEST SERVICE MANGEO THE SERVICE AM6510 BE-88980 ANT SERVICE AM65150 AM65150 AM65150 AM7510 AM6510 AM651
25	100576 124357 101624 101625 135158	9986_1 genbank_N224 entrez_M5599 entrez_M57290 57963_1	XXXX356 NM_091741 M26095 XXX3662 M12667 XXX2330 XXXX330 AA716058 AWX36674 XXX4861 AX695720 AA719597 01 NX25401 01M55998

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Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A above 504 goest down-regulated in largy tumors relative to normal larg and drowloadly diseased largy. Classically diseased largy samples represent chronic normalignant turn gleaseses such as flowing, enabyeams, and borodriks. Those genes were solehead from 59000 produced on the ScatAffryminch in IATA Generality array. Gene expressed data for each probased clothed from this analysis was successed as better general conference as surveys intenting. As a normalized was including the relative cent of entitle operators.

	Pkey: ExAcon: Unigenel(Exemple		identifer number number, Genbank accession number								
10	Unigene 1 R1:	Filie: Unigene 90th per samples	gene title centile of Al fo	or normal lung samples divided by the 80th percent								
15	R2: R3:	median the 90th	of Al for norm percentile of	at lung samples divided by 90th percentite of Al for at lung samples minus the 15th percentite of Al for Al for adenocarcinoms and squamous cell carcino	all normal lun	a, chronic	aliv disea	sed lung a	nd turnor	samples di	vided by	
	R4: R5:	lung, ch average	ronically disea of Al for norm	sed lung and lumor samples. hallung samples divided by average Al for squamo of lung secondar divided by the Ofth percentile of A	us cell carcin	ome and a	denocaro	inoma lun	g tumors.			
20	R6:	percent	te of Al for ad-	al lung comples minus the 15th percentile of Al for encoardinomas minus the 15th percentile of Al for nat lung camples divided by the 90th percentile of A	eli normal lun _i Vi for squamo), chronica us cell can	illy diseas cinomas.	ed lung a	id tumor s	ampies.		
	R&	median	of Al for norm	al lung samples minus the 15th percentile of Al for usmous cell carcinomas minus the 15th percentile	all normal lun	a, chronic	aliv disca	lly disease	d lung an	lumor sa	mpies.	
25	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
	100095 100115 100138	Z97171 NM_002084 U83508	Hs.78454 Hs.336920 Hs.2463	myocilin; trobecutar meshwork inducible glutsthione peroxidase 3 (plasma) angiopoletin 1	40.20		2.30					3.46
30	100299	D49493 U86749	Hs.2171 Hs.80598	growth differentiation factor 10 transcription alongation factor A (SII);		11.00	2.00			3.06		
	100447 100458	NM_014767 874019	Hs.74583 Hs.247979	KIAA0275 gene product Vore-B	42.40							3.16
35	100862 100959	AA005247 AA359129	Hs.285754 Hs.118127	Hepatocyte Growth Factor Receptor actin; alpha; cardiac muscle	00.40			125.60		4.13		
	101032 101081 101088	BE206854 AF047347 X70697	Hs.46039 Hs.4880 Hs.553	phosphoglycerate mulase 2 (muscle) amylold beta (A4) precursor protein-bind solute carrier family 6 (neurotransmitte	36.40			34.60 193.20				
40	101125	AJ250562 U11874	Hs.82749 Hs.846	transmembrane 4 superfamily member 2 interleukin 8 receptor; beta				54.86		3.10		
	101308	L41390 L43821	Hs.80261	"Homo sapiens core 2 beta-1,6-N-acetylgl enhancer of filamentation 1 (cas-like do	33.20			36.40				
	101345 101346	NM_005795 AJ738616	Hs.152175 Hs.77348	Calcitonin receptor-like hydroxyprostaglandin dehydrogenase 15-(N			2.29	70.55				
45	101397 101414	M26380 NM_000066	Hs.180878 Hs.38069	lipoprotein lipase complement component 8; bela polypeptide				34.60			3.81	3.54
	101435 101507	NM_001100 X16896	Hs.1288 Hs.82112	actin; alpha 1; skeletal muscle Interleukin 1 receptor; type i cytochrome P450; subfamily IIB (phenobar				37.60				4.25
50	101530 101537 101542	M29874 AJ469059 NM.000102	Hs.1360 Hs.184915 He 1363	zinc finger protein; Y-finked cytochrome P450; subfamily XVII (steroid		5.50	2.54					7.20
	101545	BE246154 BE207611	Hs.154210 Hs.123078	EDG1; endothelial differentiation, sphin flyroid alimulating hormone receptor	39.40	13.00						
55	101560 101574	AW958272 M34182	Hs.83733 Hs.158029	Intercellular adhesion molecule 2, exon protein kinase; cAMP-dependent, catalyli						4.37		3.38
	101605 101621	M37984 BE391804	Hs.62661	troponin C; slow guanylate binding protein 1; interferon-	30.20						2.75	3.80
60	101680 101829 101842	AA299330 AW452398 M93221	Hs.1042 Hs.129763 Hs.75182	Sjogren syndrome antigen A1 (52kD; ribon sotute carrier femily 8 (sodium/celcium mannose receptor; C type 1				38.20		3.37	2.10	
00	101961	AW004056 T92248	Hs.168357 Hs.2240	"Hs-TBX2=T-box gene (T-box region) [huma uleroslobin			2.32					6.85
	102020 102091	AU077315 BE280901	Hs.154970 Hs.83155	transcription factor CP2 aldehyde dehydrogenase 7			2.45					6.75
65	102112 102190	AW025430 AA723157	Hs.155591 Hs.73769	forkhead box F1 fotate receptor 1 (adult)	54.60							3.98 3.62
	102202 102241 102310	NM_000507 NM_007351 U33839		fructose-bisphosphatase 1 Multimerin Accession not listed in Genbank		7.00	2.32					J.U.
70	102397	U41898 U60115	Hs.239069	"Human sodium cotransporter RKST1 mRNA, "Homo sapiens skeletal musclo LIM-protei	29.40							3.75
	102620 102636	AA976427 U67092	Hs.121513	Human clone W2-6 mRNA from chromosome X "Human etaxia-telangiectasia locus prote			2.40			3.07		
75	102667 102675	U70867 U72512	Hs.83974 Hs.7771	solute carrier family 21 (prostaglandin "Human B-cell receptor associated protei			3.15			3.56		4.51
	102698	M18667 U79251 V00571	Hs.1867 Hs.99902 Hs.75294	progastricsin (pepsinogen C) opicid-binding protein/cell adhesion mol corticotropin releasing hormone	37 40			•	12.00			4.01
80	102852 103026 103028	X54162 X54380	Hs.75294 Hs.79386 Hs.74094	thyroid and eye muscle outportigen D1 (6 pregnancy-zone protein	28.80				13.00			
30	103098	MB6361 X63578	Hs.295449	Human mRNA for T cell receptor; clone IG parvalbumin		6.00			10.00			
0.5	103241 103280	X76223 U84722	Hs.76206	H.saplens MAL gene exon 4 Cadherin 5, VE-cadherin (vascular epithe			2.47 2.69				0.40	
85	103360	Y16791	Hs.73082	keratin; hair; acidic; 5							2.16	

	**	O 02/086	(442							DCT/	LICOST	2476
	103496	Y09267	Hs.132821	flavir containing monopygenase 2						PC I/	US02/1	5.97
	103508	Y10141	110.102021	"H.sapiens DAT1 gene, partial, VNTR"						3.27		
	103561	NM_001843		contactin 1			2.40					
5	103569	NM_005512	Hs.151641	glycoprolein A repetitions predominant			2.99			4.18		
J	103575 103627	Z26256 Z48513		"H. sapiens isoform 1 gene for L-type cal H. sapiens XG mRNA (clone PEP6)						3.44		
	103767	BE244667	Hs.296155	CGI-100 protein							2.25	
	103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR				46.55				
10	104078	AA402801	Hs.303276	ESTs						3.05		
10	104326 104352	AW732858 BE219898	Hs.143067 Hs.173135	ESTs dual-specificity tyrosine-(Y)-phosphoryl						3.16		
	104398	AJ423930	Hs.36790	ESTs; Weakly similar to putative p150 [H	64.80					0110		
	104473	A1904823	Hs.31297	ESTs								3.38
1.5	104493	AW960427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC			2.47					
15	104495	AW975687 A1799603	Hs.292979 Hs.271568	ESTs ESTs	28.60					3.42		
	104595	A1799503 A1364504	Hs.93967	ESTs; Weakly similar to Siil-1 protein [6.00				3.76		
	104659	AW969769	Hs. 105201	ESTs	34.00							
00	104686	AA010539	Hs.18912	ESTs		11.00						
20	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor ESTs	56.80			60.40				
	104764 104776	AJ039243 AA026349	Hs.278585	ESTS ESTS	34.20			00.40				
	104825	AA035613	Hs.141883	ESTs			3.03					
0.5	104865	T79340	Hs.22575	Homo sepiens cDNA: FLJ21042 fis, clone C	41.20							
25	104942	NM_016348	Hs.10235	ESTs				40.00				3.27
	104989	R65998 AW954365	Hs.285243 Hs.36529	ESTs ESTs				40.00				3.20
	105101	H63202	Hs.38163	ESTs	34.20							
••	105173	U54617	Hs 8364	ESTs								4.17
30	105194	R06780	Hs.19800	ESTs		16.00	2.34					
	105226	R58958 AA430650	Hs.26608 Hs.16529	ESTs transmembrane 4 superfamily member (telf			2.72					
	105236	BE245812	Hs.8941	ESTs			2.61					
	106647	Y09308	Hs.30148	homeodomain-interacting protein kinase 3	33.60							
35	105789	AF106941	Hs.18142	arrestin; bela 2						4.46		3.59
	105817	AA397825 AW964490	Hs.32241	synaptopodin ESTs				35.40		4.40		
	105894	A1904740	Hs.25691	calcitonin receptor-like receptor activi			3.43	00.40				
	105999	BE268786	Hs.21543	ESTs		7.00						
40	106075	AA045290	Hs.25930	ESTs				42.60				
	106178	AL049935 AB040916	Hs.301763 Hs.24106	KIAA0554 protein ESTs	34.80				12.00			
	106381 106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2					12100	3.69		
	106536	AA329648	Hs.23804	ESTs				98.40				
45	108569	R20909	Hs.300741	sorcin				47.20				
	106905	AW772298	Hs.21103	Homo saplens mRNA; cDNA DKFZp664B076 (fr			2.55	220.40				
	106842	AF124251 AA485055	Hs.26054 Hs.158213	novel SH2-containing protein 3 sperm associated antigen 6	39.20		2.00					
	106870	AI983730	Hs.26530	serum deprivation response (phosphalidy)			2.28					
50	106943	AW888222	Hs.9973	ESTs								4.28 4.32
	108954	AF128847	Hs.204038	ESTs					10.45			4.32
	107106	AA862496 AF233588	Hs.28482 Hs.27018	ESTs ESTs			2.57		10,40			
	107201	D20378	Hs.30731	EST						3.84		
55	107238	D59362	Hs.330777	EST		8.00						
	107376	U90545	Hs.327179	solute cerrier femily 17 (sodium phospha talent transforming growth factor beta b		10.67	2.32					
	107530	Y13622 AW082221	Hs.60636	ESTs			2.32	34 60				
	107706	AA015579	Hs.29276	ESTS	28.40							
60	107723	AA015967		EST				80.80		3.29		
	107727	AA149707	Hs.173091 Hs.60781	DKFZP434K151 protein ESTs				51.40				
	107750 107751	AA017291 AA017301	Hs.235390	ESTs				31.40		3.14		
	107873	AK000520	He.143811	ESTa		9.00						
65	107899	BE019261	Hs.83869	ESTs; Weakly similar to IIII ALU SUBFAMI						3.65		
	107994	AA036811	Hs.48469	ESTs				44.60 32.00				
	107997 108041	AL049176 AW204712	Hs.82223 Hs.61957	Human DNA sequence from clone 141H5 on c ESTs				30.80				
	108048	A1797341	Hs.165195	ESTs							4.75	
70	108338	AA070773		"zm53g11.s1 Stratagene fibroblast (#9372			2.33					
	108434	AA078899		"zm94b1.s1 Stratagene colon HT29 (#93722						3.06	2.92	
	108447 108480	AA079126 AL133092	Hs.68055	"zm92a11.s1 Stratagene ovarian cancer (# ESTs				34.00		3.00		
	108499	AA083103	na.00000	*zn1b12.s1 Strategene hNT neuron (#93723				01.00				3.36
75	108535	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence					19.00			
	108550	AA084867		zn11f6.s1 Stratagene hNT neuron (#93723			2.33		12.00			
	108604	AA934589 AW972330	Hs.49696 Hs.283022	ESTS ESTS			233					5.82
	108625 108629	AA102425	110.463044	*zn24c6.s1 Stratagene neuroepithelium NT							3.42	
80	108655	AA099980		zm65c6 s1 Stratagene fibroblast (#93721		7.00						
	108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f		6.05						
	108864	Al733852 AL138272	Hs.199957 Hs.62713	ESTs FSTs	28.80 32.80							
	108921	AL136272 Al568801	Hs.71721	ESTs	36.00			57.80				
85	108967	AA142989	Hs.71730	ESTs	28.80							

		O 02/086		Feb. 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			2.57			PCT/U	JS02/1	2476
	109001 109003	AI066548 AA147497	Hs.72116 Hs.71825	ESTs, Moderately similar to hedgehog-int ESTs			2.5/				2.11	
	109004	AA156235	Hs.139077	EST		5.60						
5	109065	AA161125	Hs.252739	EST					10.00		3.44	
J	109250 109490	H83784 AA233416	Hs.62113 Hs.139202	ESTs; Weakly similar to PHOSPHATIDYLETHA ESTs							2.92	
	109510	Al798863	Hs.87191	ESTs			2.40					
	109578	F02208	Hs.27214	ESTs		10.00		40.80				
10	109601 109613	F02695 H47315	Hs.311662 Hs.27519	EST ESTs				54.40				
10	109650	R31770	Hs.23540	ESTs	31.20							
	109682	H18017	Hs.22869	ESTs		8.40		29.40				
	109724 109782	D59899 AB020644	Hs.127842 Hs.14945	ESTs long fatty acyl-CoA synthetase 2 gene				29.40	8.00			
15	109833	R79864	Hs.29889	ESTs		10.00			0.00			
	109837	H00656	Hs.29792	ESTa			6.49				2.75	
	109977 109984	T64183 Al796320	Hs.282982 Hs.10299	ESTs				107.00			2./5	
	110146	H41324	Hs.31581	ESTs, Moderately similar to SYNTAXIN 1B				101.00			2.22	
20	110271	H28985	Hs.31330	ESTs						3.48		
	110280	AW874263 R93141	Hs.32468 Hs.184261	ESTs	44.20			32.00				
	110578	T62507	Hs.11038	ESTa	28.40			32.00				
	110634	R98905	Hs.35992	ESTS					20.00			
25	110726	AW961818 H03109	Hs.24379 Hs.108920	potassium voltage-galed channel; shaker- ESTs; Weakly similar to semaphorin F (H.				56.80				4.15
	110837 110875	N35070	Hs.26401	turnor necrosis factor (Igend) superfami			3.13	30.60				
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic		5.33						
20	110971	Al760098	Hs.21411	ESTs	32.40			44.60				
30	111023	AV655386 T79639	Hs.7645 Hs.14629	ESTs ESTs	32.40				17.14			
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f							4.58	
	111330	BE247767	Hs.18166	KIAA0870 protein								3.42
35	111374	BE250726 AW449573	Hs.283724 Hs.181003	ESTs; Moderalely similar to HYA22 (H.sap ESTs				33.20				3,91
55	111442	H04607	Hs.9218	ESTs				53.00				
	111747	AI741471	Hs.23866	ESTS	46.20							
	111807 111882	R33508 R37472	Hs.18827 Hs.21559	ESTs EST		16.00				3.91		
40	112045	Al372588	Ha.8022	TU3A protein						0.01	2.74	
	112057	R43713	Hs.22945	EST							4.92	
	112214	AW148652	Hs.187398	ESTs ESTs			2.43		13.00			
	112263 112314	R52393 AW206093	Ha.25917 Ha.748	ESTs		9.00	240					
45 ·	112324	R55965	Hs.28479	limbic system-associated membrane protei					14.00			
	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H			2.49					
	112380	H63010 AA324998	Hs.5740 Hs.321877	ESTs: Weakly similar to !!!! ALU SUBFAM!		8.00	2.54					
	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9						4.53		
50	112492	N51620	Hs.28694	ESTs				29.80		3.62		
	112541 112620	AF038392 R80652	Hs.118874 Hs.29040	ESTs ESTs			2.37			3.02		
	112623	AW373104	Hs.25094	ESTs			2.26					
55	112867	T03254	Hs.187393	ESTs		6.50			12.00			
33	112894 112954	T08188 AA928953	Hs.3770 Hs.6655	ESTs ESTs		7.00						
	113029	AW081710	Hs.7369	ESTs; Weakly similar to III1 ALU SUBFAMI								4,39
	113086	AA346839	Hs.209100	DKFZP434C171 protein					10.00			4,47
60	113140 113252	T50405 NM_004469	Hs.175967 Hs.11392	ESTs c-fos induced growth factor (vascular en		14.00			10,00			
00	113257	AJ821378	Ha.159367	ESTa						3.72		
	113394	T81473	Hs.177894	ESTs						3.60		
	113437 113454	T85349 Al022166	Hs.15923 Hs.16188	EST ESTs	35.00	6.00						
65	113502	T89130	na.10100	ESTs	39.60	0.00						
	113552	AI654223	Hs.16026	ESTS							2.58	3.88
	113645 113691	T95358 T96935	Hs.333181 Hs.17932	ESTs EST				38.20			2.58	
	113706	AA004693	Hs.269192	ESTs .				30.20		3.09		
70	113883	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro			2.31					
	113924	BE178285	Hs.170056	Homo saplens mRNA; cDNA DKFZp586B0220 (f	30.40				13.00			
	114035	W92798 AK002016	Hs.269181 Hs.114727	ESTs ESTs					13.00			5.00
	114084	AA708035	Hs.12248	ESTs				40.60				
75	114121	H06785	Hs.25425	ESTs			2.31					
	114124	W57554 AW515443	Hs.125019	Human lymphoid nuclear protein (LAF-4)		7.00 6.00						
	114275 114297	AN515443 AA149707	Hs.306117 Hs.173091	Interleukin 13 receptor; alpha 1 DKFZP434K151 protein		0.00		48.80				
	114427	AA017176	Hs.33532	FSTs: Highly similar to Miz-1 protein IH						3.45		
80	114449	AA020736		ze63b11.s1 Soares refina N2b4HR Homo sa		14.00			10.00			
	114452	AJ369275 AA079505	Hs.243010	ESTs, Moderately similar to RTC0_HUMAN G "zm97a5.s1 Stratagene colon HT29 (#93722		14.00				3.13		
	114648	AA101056		*zn25b3.s1 Stratagene neuroepithelium NT				35.40				
85	114731	BE094291	Hs.155651 Hs.288464	Homo sapiens HNF-3beta mRNA for hepatocy ESTs	33.00							3.42
0.5	114762	AA146979	na.466464	E019	30,00							

	w	O 02/08	5443							PCT/	US02/1	2476
	114776	AA151719	Hs.95834	ESTS	34.40							
	115009	AA251561	Hs.48689	ESTs .	30.20							
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60	6.00						
5	115279 115302	AW964897 AL109719	Hs.290825 Hs.47578	ESTs ESTs		0.00			12.00			
_	115365	AW976252	Hs.268391	ESTs						3.32		
	115559	AL079707	Hs.207443	ESTs				48.00				
	115566	Al142336	Hs.43977	ESTs	31.40			56.20				
10	115683 115744	AF255910 AA418538	Hs.54650 Hs.43945	ESTs, Weakly similar to (defiline not ava ESTs; Highly similar to dJ1178H5.3 (iLsa	31.40			33,60				
10	115819	AA486620	Hs.41135	Endomucin 2				74.40				
	115949	AJ478427	Hs.43125	ESTs			3.18					
	115965 116035	AA621405	Hs.173233 Hs.184664	ESTs ESTs				388.80 33.20				
15	116049	AA454033	Hs.41644	ESTs .				45.80				
	116081	Al190071	Hs.55278	ESTs						3.57		
	116082	AB029496	Hs.59729	ESTs	50.60		3.06					
	116213 116228	AA292105 AJ767947	Hs.326740 Hs.50841	leucine rich repeat (in FLII) interactin ESTs; Weakly similar to tuffelin (M.musc	50.60		3.85					
20	116250	N76712	Hs.44829	ESTs		6.00	5.00					
	116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular tekti				30.00				
	116617	D80761 AB007979	Hs.45220 Hs.301281	EST tenascin R (restrictin; janusin)	47.20		2.27					
	116784 116835	N39230	Hs.38218	ESTs	47.20			41.20				
25	116970	AB023179	Hs 9059	KIAA0962 protein					11.00			
	117023	AW070211	Hs.102415	ESTs	49.40			91.00				
	117027 117036	AW085208 H88908	Hs.130093 Hs.41192	ESTs EST	40.40			32.60				
	117110	AA160079	Hs.172932	ESTs		8.67						
30	117209	W03011	Hs.306881	ESTs				30.60	9.29			
	117325	N23599 N29569	Hs.43396 Hs.44055	ESTs ESTs					9.29	3.19		
	117454	N30205	Hs.93740	ESTS	44.00					0.10		
	117543	BE219453	Hs.42722	ESTs		16.00						
35	117567	AW444761	Hs.44565	ESTs					12.00 11.00			
	117570 117600	N48649 N34963	Hs.44583 Hs.44676	ESTs EST					11.00	3.74		
	117730	N45513	Hs.46608	EST ₅		6.00						
40	117791	N48325	Hs.93956	EST		9.00		00.00				
40	117929 117990	N51075 AA446167	Hs.47191 Hs.47385	ESTs ESTs		8.00		29.20				
	118224	N62275	Hs.48503	EST	31.40	0.00						
	118244	N62516	Hs.48556	ESTS	32.80							
45	118357 118446	AL109667 N66361	Hs.124154 Hs.269121	Homo sepions mRNA full length insert cDN ESTs			2.40					
73	118447	N66399	Hs.49193	EST	30.80		220					
	118530	N67900	Hs.118446	ESTs						3.10		
	118549	N68163	Hs.322954	EST			3.94			3.41		
50	118823 118882	W03754 W17085	Hs.50813 Hs.54522	ESTs; Weakly similar to long chain fatty ESTs			3.34			3.58		
20	118935	A1979247	Hs.247043	KIAA0525 protein				33.00				
	118944	Al734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAMI		14.00			11.43			
	118995 119073	N94591 BE245360	Hs.323058 Hs.279477	ESTs ERG-2/ERG-1; V-ets avian erythroblasiosi		14.00		52.60				
55	119268	T16335	Hs.65325	EST	31.40			52.00				
	119514	W37937		Accession not listed in Genbank						3.50		
	119824 119831	W74536 AL117664	Hs.184 Hs.58419	advanced glycosylation end product-speci DKFZP586L2024 protein			2.75					3.21
	119881	W78818	Hs.49943	ESTs; Moderately similar to Itti ALU SUB				33.80				0181
60	119889	W84346	Hs.58671	ESTs				30.03				
	119921	W86192 H80286	Hs.58815 Hs.40111	ESTs ESTs	29.00					3.80		
	120082	AA811339	Hs.40111 Hs.124049	ESTS ESTS		6.00				0.00		
	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)				36.60				
65	120378	AA223249	Hs.285728	ESTs	39.40	12.00						
	120404 120504	AB023230- AA256837	Hs.96427	KIAA1013 protein ESTs	39.40				8.00			
	120504	N55761	Hs.194718	ESTS	33.00							
70	120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa								4.18
70	120777 121082	AA287702 AA396722	Hs.10031	KIAA0955 protein ESTs				46.60 39.00				
	121191	AA400205	Hs.104447	ESTS	41.60			00.44				
	121248	AA400914	Hs.97827	EST							5.08	
75	121363 121366	AJ287280 AJ743515	Hs.97933	ESTs ESTs					12.00			
13	121483	A/660332	Hs.25274	ESTs; Moderately similar to putative sev					20.00	3.32		
	121518	AA412155		ESTs				30.20				
	121545	AA412442	Hs.98132	ESTs		9.00	2.29					
80	121622 121665	AA416931 AA416556	Hs.126065 Hs.96234	ESTs ESTs		9.00		34.80				
00	121709	Al338247	Hs.98314	Homo sapiena mRNA; cDNA DKFZp586L0120 (f	34.80							
	121730	A/140683	Hs.96328	ESTs	38.80							
	121740 121772	AA421138 Al590770	Hs.98334 Hs.110347	EST Homo sapiens mRNA for alpha integrin bin	36.20	7.00						
85	1217/2	AL040235	Hs.3346	ESTs	30.20							3.61

	w	O 02/080	5443							PCT/	US02/1	2476
	121835	AB033030	Hs.300670	ESTs			2.34			101/	0.5027	2410
	121841	AA427794	Hs.104864	ESTs			2.61					
	121885	AA934883	Hs.98467	ESTs ESTs							2.25	
5	121888 121938	AA426429 AA428659	Hs.98463 Hs.98610	ESTS				46,80			2.52	
,	121950	AA429515	16.50010	EST				31.40				
	122030	AA431310	Hs.98724	ESTs	34.40							
	122054	AA431725	Hs.98746	EST	49.40						3.58	
10	122211	AA300900 AA436455	Hs.98849 Hs.98872	ESTs; Moderately similar to bithoraxoid- EST	29.80							
	122247	AA436676	Hs.98890	EST				39.80				
	122253	AA436703	Hs.104936	ESTs; Weakly similar to hypothetical pro		9.00				3.60		
	122266	AA436840 AA436981	Hs.98907 Hs.121602	EST EST						3.14		
15	122409	AA446B30	Hs.99081	ESTs	30.80					0		
	122485	AA524547	Hs.160318	nhosobolemman			2.65					
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA		15.00 6.67						
	122772	AW117452 A8857570	Hs.99489 Hs.5120	ESTs ESTs		0.07				3.37		
20	122913	Al638774	Hs.105328	ESTs				32.20				
	123049	BE047680	Hs.211869	ESTs	AF 00			41.80				
	123076 123136	AJ345569 AW451999	Hs.190046 Hs.194024	ESTs ESTs	35.80						2.58	
	123309	N52937	Hs.102679	ESTs					19.00		2.00	
25	123455	AA353113	Hs.112497	ESTS				82.80				
	123691 123756	AA609579 AA609971	Hs.112724	ESTs EST	35.40					3.96		
	1237802	AA620448	Hs.112795	Homo saplens clone 24760 mRNA sequence	58.00							
••	123837	AI807243	Hs.112893	ESTs				32.40				
30	123844 123936	AA938905 NM_004673	Hs.120017 Hs.241519	olfactory receptor, family 7; subfamily ESTs	29.00		2.63					
	123936	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR				70.60				
	124013	AJ521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40							
35	124160 124205	R40290 H77570	Hs.124686 Hs.108136	ESTs ESTs					13.00	4.74		
33	124205	AA618527	Hs.190266	ESTS			2.35			4.14		
	124246	H67680	Hs 270962	ESTs				29.40				
	124348 124358	AJ796320 AW070211	Hs.10299 Hs.102415	ESTs "wx35g11.s1 Morion Fetal Cochlea Homo sa		17.00	3.07					
40	124409	Al814166	Hs.107197	FSTs						3.14		
	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate			2.48					
	124468 124479	N51413 AB011130	Hs.109284 Hs.127436	ESTs calcium channel; voltage-dependent; alph				30.80				8.03
	124479	AB011130 AI670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO			2.50					0.00
45	124711	NM_004657	Hs.26530	serum deprivation response (phosphalidy)	59.20	8.00						
	124866 124874	A/768289 BE550182	Hs.304389 Hs.127826	ESTs ESTs		8.00		37.60				
	125097	AW576389	Hs.335774	ESTs				01.00	10.00			
50	125179	AW206468	Ha.103118	ESTs						3.12	0.70	
30	125200 125299	AW836591 T32982	Hs.103156 Hs.102720	ESTs ESTs				34.20			2.79	
	125400	AL110151	Ha.128797	DKFZP586D0824 protein	29.00			01120				
	125810	H00083		aryl hydrocarbon receptor-interacting pr	32.20	12.00						
55	126176 126303	BE242256 D78841	Hs.2441	KIAA0022 gene product HUM525A05B Human placenta polyA+ (TFuji		12.00		33.60				
-	128403	AW829054	Hs.125976	ESTs: Weakly similar to metalloprotessel	35.80							
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu	39.60			29.80				
	126773 127307	AA648284 AW962712	Hs.187584 Hs.126712	ESTs ESTs; Weakly similar to p/L2 hypothetica	28.80							
60	127462	AA760776	Ha.293977	aa59b04.s1 NCI_CGAP_GCB1 Homo sapiens c				34.40				
	127486	AW002846	Hs.105468	ESTs		9.00	2.36					
	127572 127609	AA594027 X80031	Hs.191788 Hs.530	ESTs ESTs			2.00	29.40				
	127832	AW976035	Hs.292396	ESTs				37.20				
65	127898	AA774725	Hs.128970	ESTs				38.40			4.42	
	128073 128101	AW340720 AA905730	Hs.125983 Hs.128254	ESTs ESTs		7.33		30.40				
	128149	NM_012214	Hs.177576	mannosyl (alpha-1;3-)-glycoprotein beta-							2.58	
70	128212 128333	W27411 W68800	Hs.336920 Hs.12126	glutathione peroxidase 3 (plasma) ESTs; Weakly similar to LR8 [H.saplens]			3.09	34.40				
70	128333	N76462	Hs.12125 Hs.269152	ESTs; Weakly similar to Live (rusapiens) ESTs; Weakly similar to ZINC FINGER PROT		10.00		34.40				
	128426	Al265784	Hs.145197	ESTs							4.31	
	128598 128634	AA305407 AA464918	Hs.102308	potassium inwardly-rectifying channel; s ESTs: Moderately slmitar to IIII ALU SUB	31.20			41.60				
75	128687	AW271273	Hs.23767	ESTs				87.00				
	128726	Al311238	Hs.104476	ESTs								4.02
	128773 128833	NM_004131 W26667	Hs.1051 Hs.184581	granzyme B (granzyme 2; cytotoxic T-lymp ESTs					9.00			3.76
	128870	W26667 H39537	Hs.75309	eukaryofic translation elongation factor			2.66					3.10
80	128878	R25513	Hs.10683	ESTs					11,00	3.10		
	128885 128998	AF134803 W04245	Hs.180141 Hs.107761	coffin 2 (muscle) ESTs; Weakly similar to PUTATIVE RHORAC					11.00		3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-Kill inhi								3.68
85	129038	AW156903 AW580945	Hs.108124	ribosomal protein L41 ESTs	34.60					3.17		
05	129098	AN080945	Hs.330466	EOID	34.00							

	w	O 02/080	6443							PCT/	US02/1	12476
	129210 129240	AL039940 AA361258	Hs.202949 Hs.237868	KIAA1102 protein Interleukin 7 receptor			2.29					4.09
	129262	BE222198	Hs.109843	FSTs			6.23			3.30		
5	129301	AF182277 AW167668	Hs.330780 Hs.279772	Human cylochrome P450-IIB (hIB3) mRNA;								4.05
,	129381	AW245805	Hs.110903	ESTs; Highly similar to CGI-38 protein [claudin 5 (transmembrane protein deleted			2.93					4.05
	129565 129595	X77777 U09550	Hs.198726 Hs.1154	vasoactive intestinal populae receptor 1				160.80	10.00			
	129695	AW978517	Hs.172847	oviductal glycoprotein 1; 120kD ESTs; Weakly similar to collegen alpha 1					10.00	3.40		
10	129782	AW016932	Hs.104105	EST		9.00						
	129950 129958	F07783 R27496	Hs.1369 Hs.1378	decay accelerating factor for complement annexin A3				87,80 44,60				
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque			2.72					
15	130160 130259	AA305688 NM_000328	Hs.267696 Hs.153614	UDP-Gal:betaGlcNAc beta 1;3-galactosyltr retinitis pigmentosa GTPase regulator			2.54	42.20				
13	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr			24.	51.60				
	130312 130436	AF056195 NM_001928	Hs.15430 Hs.155597	DKF2P586G1219 protein D component of complement (adipsin)						3.16		4.11
	130523	AA999702	Hs.214507	ESTs						4.77		
20	130799 130885	ABC28945 NM_005883	Hs.12696 Hs.20912	ESTs adenomalous polyposis coli fike		6.00				3.54		
	131002	AL050295	Hs.22039	KJAA0758 protein								3.50
	131012 131031	AL039940 NM 001650	Hs.202949 Hs.288650	KIAA1102 protein aquaporin 4	41.20	20.00						
25	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.	41.20			31.40				
	131066	AW169287	Hs.22588 Hs.246218	ESTs ESTs; Weakly similar to zinc finger prot				29.60	9.00			
	131082	AI091121 AF147709	Hs.22824	ESTs: Weakly similar to p160 myb-binding					5.00			3.86
30	131161	AF033382	Hs.23735	potessium voltage-gated channel; subfami						3.14		
50	131179	AA171388 AI824144	Hs.184482 Hs.23912	DKFZP586D0624 protein ESTs						0.00		3.87
	131205	NM_003102	Hs.2420	superoxide dismutese 3; extracellular			2.98 3.15					
	131277 131281	AA131466 AA251716	Hs.23767 Hs.25227	ESTs ESTs			3.10	32.20				
35	131282	X03350	Hs.4	elcohol dehydrogenase 3 (class I); gamma								3.44
	131285 131355	AI567943 R62804	Hs.25274 Hs.25966	ESTs; Moderately similar to putative sev DKFZP564D206 protein		8.00				6.40		
	131391	AW085781	Hs.26270	ESTs		10.00						
40	131461 131487	AA992841 F13036	Hs.27263 Hs.27373	butyrate response factor 2 (EGF-response Homo sapiens mRNA; cDNA DKFZp564O1763 (f	28.80						4.03	
	131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin VIa [39.00				11.00			
	131545 131583	AL137432 AK000383	Hs.28564 Hs.323092	ESTs Weakly similar to dual specificity					10.00			
45	131647	AA359615	Hs.30089	ESTs ESTs			2.47			3.06		
43	131675 131676	H15205 Al126821	Hs.30509 Hs.30514	ESTs	45.80					3.00		
	131708	S80415	Hs.30941	calcium channel; vollage-dependent; beta			2.28					3.78
	131717 131756	X94630 AA443966	Hs.3107 Hs.31595	CD97 antigen ESTs				40.60				
50	131782 131821	AA744902 AA017247	Hs.107767 Hs.164577	ESTs; Moderately similar to CaM-KII inhi ESTs			2.87					3.67
	131839	AB014533	Hs.33010	KIAA0633 protein			201				3.48	
	131881 132015	AL098858 Al418006	Hs.184245	KIAA0929 protein Msx2 interacting nuclea ESTs	54.00			49.20				
55	132070	BE622641	Hs.3731 Hs.38489	ESTS				34.80				
	132242	AA332897 AW080704	Hs.42721 Hs.45033	ESTs lacrimal proline rich protein			2.68 4.66					
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20							
60	132490	NM_001290 Al922988	Hs.4980 Hs.172510	LIM binding domain 2 ESTs		13.00	2.66					
00	132598	X80031	Hs.530	collanen; type IV; alpha 3 (Goodpasture		10.00		30.60				
	132619	H28855 N41739	Hs.53447 Hs.61260	ESTs; Moderately similar to kinesin ligh ESTs						4.02 3.18		
	132652 132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1					11.43	2.10		
65	133028	R51604 BE384932	Hs.300842 Hs.64313	ESTs ESTs			2.37 2.27					
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein			2.63					
	133129 133147	AA428580 AA026533	Hs.65551 Hs.66	ESTs interleukin 1 receptor-like 1			6.20					5.49
70	133151	NM_014051	Hs.94896	ESTs			0.20			3.69		
	133213	AA903424 AW978439	Hs 6786 Hs 69504	ESTs ESTs				31.40	9.00			
	133377	AJ131245	Hs.7239	SEC24 (S. corevisiae) related gene famil	41.20				****			
75	133407	AF017987 AL134030	Hs.7306 Hs.284180	secreted frizzled-related protein 1 protocodherin 2 (cadherin-like 2)	50.20					3,72		
15	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr								3.35
	133656 133689	BE149455 NM_001872	Hs.75415 Hs.75572	Accession not listed in Genbenk carboxypeptidase B2 (plasma)			2.65	90.80				
0.0	133779	T58486	Hs.222566	ESTs						3.05		
80	133978 133985	AF035718 L34657	Hs.78061 Hs.78146	transcription factor 21 plateletiendotheliel cell adhesion molec			2.92					3,45
	134000	AW175787	Hs.334841	selenium binding protein 1								4.05
	134111 134185	A1372588 AA285136	Hs.8022 Hs.301914	TU3A protein: Homo sapiens mRNA; cDNA DKFZp586K1220 (f			4.49				3.27	
85	134204	A1873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein [40.80				

	134641 134677	O 02/086 A/092634 AA251363	Hs.156114 Hs.177711	protein tyrosine phosphetase; non-recept ESTs				32.20	PCT/U 3.76	S02/12476
5	134745 134749 134786 134825	NM_000685 T28499 T29618 U33749	Hs.89472 Hs.89485 Hs.89640 Hs.197764	angiolensin receptor 1B carbonic anhydrase IV angiopoietin 1 receptor; TEK tyrosine ki Ihyroid transcription factor 1		15.00	3.05	57.80		3.73
4.0	134978 135010 135053	A'829008 N50465 AW796190	Hs.333383 Hs.92927 Hs.93678	ficolin (collagen/fibrinogen domain-cont ESTs ESTs			2.52	31.60	3.21	0.0
10	135081 135091 135135	AF069517 AA493650 AA775910	Hs.173993 Hs.94367 Hs.95011	RNA binding molif protein 6 ESTs synfrophin; beta 1 (dystrophin-associate	28.80	8.00				4.24
15	135203 135236 135266 135346	C15737 Al636208 R41179 NM 000928	Hs.269386 Hs.96901 Hs.97393 Hs.992	ESTs ESTs Human mRNA for K/AA0328 gene; partial od phospholipase A2; group IB (pancreas)	43.00		3.82		4.31	6.42
	135378 135387 135388	AW961818 NM_001972 W27965	Hs.24379 Hs.99863 Hs.99865	potassium voltage-galed channel; shaker- elestase 2; neutrophil EST	37.20 38.80		4.15			
20	135402	L12398	Hs.99922	doparrine receptor D4					4.21	

TABLE 28 shows the accession numbers for those primetrys tacking unigonal Ofs for Table 24. For each probeset we have fisted the gene dissent number from which the oligonacidoties were designed. Gene clusters were compiled using sequences defined from Centerin ESTS and nRTMA. These sequences were clustered blased on sequence interest to be a compiled using sequences and primetry large clustering and Alighment Into Chockle Hast, Calder distinuis. The destrukant accession unmented for sequences comprising exchanged are falsed in the 25 "Accession" column.

30 Accession: Genbenk accession numbers Pkey CAT number Accessions 108447 43452_-7 120073_1 127522_1 AA079126 AA084867 AA084996 35 108550 108655 AA099960 AA113013 102397 44371_-1 U41898 126303 1525933_1 D78841 D78880 1526933_1 1554054_1 2615_2 280401_1 116777_1 172113_1 112186_1 125810 H00083 R81062 40 103627 Z48513 Z48512 121366 AI743515 AA405617 AW276706 114609 AA079505 AA079537 115272 AW015947 AA211890 AA279425 108338 AA070773 AA070774 45 108434 114012_1 AA078899 AA078782 AA075788 123802 genbank_AA620448 A NOT_FOUND_entrez_U33839 entrez_U67092 U67092 AA620448 102310 102838 104776 genbank_AA026349 AA026349 50 120504 genbank_AA256837 AA256837 113502 genbank_T89130T89130 genbank_AA083103 entrez_L41390 L41390

AA083103

AA102425

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number

221_215 M86591 Z26593 X028 entrez_X76223 X76223 entrez_Y10141 Y10141 entrez_226256 Z26256 NOT_FOUND_entrez_W37937 W37937 genbank_AA395722 AA396722 AA464918_a1 AA464918 genbank_AA397825 AA397825 103508 103575 119514 60 121082 AA398722 128634 121518 genbank_AA412155 AA412156

genbank_AA 102425

108499

101308 108629

103241

55 103098 221_215

114449 genbank_AA020736 AA020736 65 114648 genbank_AA101056 genbank_AA429515 AA101056 121950 AA429515 genbenk_AA015967 AA015967

M86361 Z26593 X02850 D13070 AE000659 M17649 M67869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169

WO 02/086443

PCT/US02/12476 Table 34 shows 450 genes up-regulated in chronically diseased larg studies to normal larg. Chronically diseased larg samples represent chronic nor malagratic large such as fibrosis, emplyacems, and branchilis. These genes were selected from 19900 probeseds on the ISEA/Rymerk Hald Connachy array. Gene expression data for each proceed chlorated from this analysis was expressed as across principle (A)p. normalisated vision prices and charge interpretable proposed collected from this analysis was expressed as across principle (A)p. normalisated vision prices and procedure of procedure of

,	Pixey:			KOERTINET DURDER						
	ExApone	Exemp	ilar Accession	number, Genbank accession	rumber					
	UnigenelD:	Uniger	e number							
	Unigene Title	: Uniger	e gene title							
4.5	R1:	80th pe	ercentile of All 1	or chronically diseased lung	samples divided by the 90	th percentile o	of Al for norn	nel lung samples		
10	R2:	80th p	ercentile of Al 1	or chronicelly diseased lung	samples divided by the 90	th percentile	of normal lun	g samples, squa	mous cell carcinomas and	
			cardnomas							
	R3:	70th p	ercentile of All	for chronically diseased lung	samples minus the 15th pe	ercentile of Al	for all norm:	al lung, chronical	ly diseased lung and tumor sar	mples
		divided	by the 90th p	ercentile of normal lung sam	pies, squamous cell carcini	omas and ado	enocardinom	as minus the 15	h percentile of Al for all normal	lung,
		chronic	celly diseased	lung and tumor samples						
15										
	Pixey Ex	Acon	UnigenelD	Unigene Title		R1	R2	R3		

	Pixey	ExAcon	UnigeneiD	Unigene Title	R1	R2	R3
	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
20	135378	AW961818	Hs.24379	MUM2 protein			2.13
	135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
	135235	AW298244	Hs.293507	ESTs	12.40		
	135057 134951	U90268 BE305081	Hs.93810 Hs.169358	cerebral cavernous malformations 1 hypothetical protein	11.67	8.00	
25	134799	M36821	Hs.89690	GRO3 oncouene		8.20	
20	134786	T29618	Hs.89640	TEK tyrosine kinase, endotheliai (venous		****	
	134772	NM_000829	Hs.163697	glutemate receptor, ionotrophic, AMPA 4	29.80		
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
30	134749	T28499	Hs.89485	carbonic anhydrase IV ESTs			2.07
30	134696 134636	BE326276 NM_005582	Hs.8861 Hs.87205	lymphocyte anligen 64 (mouse) homolog, r	13.60		
	134627	Al018768	Hs.12482	glyceronephosphale O-acytransferase	10.00		1.92
	134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 faciogeni			1.92
	134570	U66615	Hs.172280	SWVSNF related, matrix associated, acti	13.20		
35	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h			1.78
	134468	NM_001772	Hs.83731	CD33 antigen (gp67)		6.20	
	134417 134343	NM_006416 D50683	Hs.82921 Hs.82028	solute carrier family 35 (CMP-sialic act bransforming growth factor, beta recepto			
	134323	BE170651	Hs.8700	deleted in liver cancer 1			
40	134300	NM_001430	Hs.8136	endolhelial PAS domain protein 1			
	134299	AW680939	Hs.97199	complement component C1q receptor			
	134253	X52075	Hs.80738	sialophonin (gpl.115, leukosialin, CD43)	20.60		
	134182	D52059	Hs.7972	KIAA0871 protein	12.20		
45	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec			
43	133978 133835	AF035718 Al677897	Hs.78061 Hs.76640	transcription factor 21 RGC32 protein			
	133651	Al301740	Hs.173381	ditydropyrimidinase-like 2			
	133833	D21282	Hs.75337	nucleolar and coiled-body phosphprotein	15.20		
	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7, HUMAN A			
50	133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAUL			1.77
	133488	AA335295	Hs.74120	adipose specific 2			
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein		9.60	2.08
	133337	AF085983 AB037715	Hs.293676 Hs.183839	ESTs hypothetical protein FLJ10210		9.00	1.77
55	133153	AF070592	Hs.66170	HSKM-B protein	30.60		1,11
-	133130	Al128606	Hs.6557	zinc finger protein 161	22.60		
	133120	NM_003278	Hs.85424	tetranectin (plasminogen-binding protein			
	132928	AW168082	Hs.169449	protein kinaso C, alpha	13.80		
60	132836	AB023177	Hs.29900	KIAA0960 protein			
00	132799	W73311 AA025480	Hs.169407 Hs.292812	SAC2 (suppressor of actin mutations 2, ESTs, Weakly similar to T33468 hypotheti	41.60 40.40		
	132548	X12830	Hs.193400	interleukin 6 receptor	40.40	7.20	
	132476	AL119844	Hs.49476	Homo sapiens done TUA8 Cri-du-chat regi		4.76	
	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
65	132240	AB018324	Hs.42676	KIAA0781 protein	21.20		
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
	132199	AL041299	Hs.165084	ESTs ESTs	15.20		1.76
	131751	T96555 AJ828559	Hs.31562 Hs.31447	ESTs, Moderately similar to A46010 X-li	27.80		1.70
70	131694	NM_000246	Hs.3076	MHC class II transactivator	67.00	4.00	
	131686	NM 012296	Hs.30687	GRB2-associated binding protein 2			
	131676	Al126821	Hs.30514	ESTs		6.20	
	131629	Z45794	Hs.238809	ESTs	21.40		
75	131589	C18825	Hs.29191	epithelial membrane protein 2		9.40	
13	131536	AA019201	Hs.269210	ESTs		9.40 3.59	
	131517	AB037789 R52804	Hs.263395 Hs.25956	sema domain, transmembrane domain (TM), DKFZP564D206 protein		4.48	
	131253	R71802	Hs.24853	ESTs	15.00		
	131207	AF104266	Hs.24212	latrophilin			1.75
80	131156	AI472209	Hs.323117	ESTs			1.84
	131066	AW169287	Hs.22588	ESTs		3.54	
	131061	N64328	Hs.268744	KIAA1796 protein			4.02
	131053	AA348541	Hs.296261 Hs.21015	guanine nucleotide binding protein (G pr hypothetical protein DKFZp564L0864 slmll	16.60		1.93
85	130895	AA641767 D84371	Hs.1898	peracoonase 1	12.00		
00	130102	DUNTI	110.1400	poromoneo r	12.00		

126816 44248234

126666 AA648886 Hs.151999 ESTs

126645 AA316181 Hs.61635

126592 Al611153 Hs.6093

126556 AF255303

126299 AW979155 Hs.298275

126218 AL049801

126182 AA721331 Hs.293771 ESTs

126177 AW752782 Hs.129750

126077 M78772

125994 A1990529

125934 AA193325 Hs.32646

125847 AW161885 Hs,249034 ESTs

125731 R61771

125676 RF612918

125561 F18572

125552 H09701

65 126812 AB037860 Hs.173933

70 126433 AA325606

75 126142 H86261

80 125831 H04043

85 125489 H49193

PCT/US02/12476

WO 02/086443 130657 AW337575 Hs.201591 EST: 130655 AI831962 Hs.17409 cysteine-rich protein 1 (intestinal) Hs.16441 130589 AL110226 DKFZP434H204 protein 2.08 130562 D50402 Hs.182611 solute carrier family 11 (proton-coupled 1.91 5 130555 R69743 Hs.116774 integrin, alpha 1 9 60 eukaryotic translation initiation factor MAD (mothers against decapentaplegic, Dr retinitis pigmentosa GTPase regulator 130365 W56119 He 155103 11.60 130273 AW972422 He 153963 6.60 130259 NM 000328 Hs.153614 1.91 zinc finger protein 36 (KOX 18) annexin A3 130090 H97878 Hs.132390 21 20 10 129958 R27496 Hs. 1378 5.05 129898 AI672731 He 13256 ESTs hypothetical protein FLJ13920 homolog of yeast ubiquifin-protein ligas 129875 44181018 Hs 13056 18.60 120600 4B007899 He 12017 ferritin, light polypeptide 129626 F13272 He 111334 15 Homo sapiens cDNA FLJ12566 fis, clone NT Homo sapiens mRNA; cDNA DKFZp586L0120 (f 129596 N30436 Hs.11556 129593 41338247 Hs.98314 129565 X77777 Hs. 198726 vasoactive Intestinal peptide receptor 1 253 129527 AA769221 Hs.270847 delta-tubulin 39,20 120402 W72062 No 11112 EST 2 11 20 120385 AA172106 He 110950 Rag C protein spondyloepiphyseal dysplasia, late 15.20 129315 NM 014563 Hs.174038 12.40 129312 T97579 Hs.110334 ESTs, Wealdy similar to 178885 serine/th 20.83 129240 AA361258 Hs.237868 interleukin 7 receptor 1.95 129210 41 039940 He 202949 KIAA1102 protein KMA1102 proton

CDW52 antigen (CAMPATH-1 antigen)
kynurerine 3-monooxygenase (kynurenine 3
chemokine (C-C molif) receptor-like 2 25 129122 AW958473 Ht 301957 4.20 129057 NORRER Hs 276770 128946 Y13153 Hs 107318 5.20 128798 AF015525 Hs.302043 128789 AW368576 Hs.139851 2.24 30 ESTs, Weakly similar to 138022 hypothet 128778 AA504776 Hs.186709 12.20 128766 AW160432 Hs.296460 craniofacial development protein 1 KIAA1060 protein; Golgi-associated, gamm 26.40 128631 PA4238 Hs.155546 1.78 ESTs, Weekly similer to TRHY_HUMAN TRICH 128624 BE154765 Hs.102647 2.51 survival of motor neuron protein interac ATP-binding cassette, sub-family G (WHIT 128609 NM_003616 NM_004915 AA305407 Hs.102456 16.00 35 128603 He 10237 1280 126598 Hs.102308 potassium inwardly-rectifying channel, a 4.00 128458 H55864 Hs.56340 **ESTs** 128061 AE150882 He 186877 sodium channel, voltage-gated, type XII, 17.20 127968 AA830201 Hs 124347 ESTa 21.30 40 127959 AI302471 Hs.124292 Homo saplens cDNA: FLJ23123 fis, clone L 127944 AI557061 Hs.262476 S-adencevimethionine decarboxylase 1 127925 AA805151 Hs.3628 mitogen-activated protein kinase kinase 13.40 127896 A1669586 Hs.222194 FSTe 7.00 127850 44761802 Hs 291550 ESTe 14.00 45 127817 44838641 Hs 163085 FST: 14.00 127742 AW203406 Hs.180138 ESTS 11.00 127628 A1240102 Hs.322430 NDRG family, member 4 11.10 collagen, type IV, alpha 3 (Goodpasture X80031 Hs.530 127582 AAGREGEA Hs.130644 FSTe 19 60 50 Home seplens cDNA FLJ20780 fis, clone CO 127543 AK000787 Hs.157392 15.40 ESTs 17.50 127535 0.4588424 Hs 184450 127404 AJ379920 Hs.270224 ESTs 14.60 127396 L31968 Hs.187991 DKFZP564A122 protein DR:-279844122 protein ESTs, Weakly similar to 138022 hypothet DnaJ (Hsp40) homolog, subfamily B, membe ESTs, Weakly similar to ZN91_HUMAN ZINC ESTs, Weakly shallar to AF191020 1 E2IGS 127374 AA442797 Hs.312110 14.60 55 127346 AA203616 Hs.44896 21.00 127340 RE047653 Hs.119183 15.80 127307 AW982712 Hs 128712 127242 AW390395 Hs 181301 colhensin S 22.60 127167 AA625690 Hs.190272 ESTa 21.40 60 127048 AA321948 Hs.293968 ESTs 126928 AA480902 Hs.137401 ESTS 11.00 128000 AF137386 Hs.12701 plasmolipin 1.78

gb:zu68c01.r1 Soares_lestis_NHT Homo sao

gb:csg2228.seq.F Human fetal heart, Lamb

six transmembrane epithelial antigen of Home septens cDNA: FLJ22783 fis, clone K

membrane-associated nucleic acid binding gb:EST28707 Cerebellum II Homo sapiens c

Novel human gene mapping to chomosome 13

gb:yj45c03.r1 Soares placenta Nb2HP Homo ESTs

ESTS, Weekly similar to ALU4_HUMAN ALU S ESTS, Weekly similar to ALU4_HUMAN ALU S ESTS, Weekly similar to 138022 hypotheti ESTS, Moderately similar to ALU7_HUMAN A

nuclear factor I/A

amino acid transporter 2

hypothetical protein FLJ10546 ESTs

hypothetical protein FLJ21901

Hs.112227

Hs.13649

Hs 40568

Hs.210636 ESTs

Hs.270799 ESTs

Hs.26912

Hs.151973

Hs 22978

Hs.278366

Hs.124984

103

5.60

4.67

3.50

12.20

17.19

13.57

15,40

18 00

16.77

14,60

13.40

18.20

14 00

16.59

17.40

49.57

13.20

11.20

33.40

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	w	O 02/086	443				
	125422	AA903229	Hs.153717	ESTs			1.80
	125331	Al422996	Hs.161378	ESTs	38.00		
	125309	T12411	Hs.183745	hypothetical prolein FLJ13456	18.20		
5	125167	AL137540	Hs.102541	netrin 4			1.95
3	125139 125042	AW194933 T78906	Hs.9788 Hs.269432	hypothetical protein MGC10924 similar to ESTs, Moderately similar to ALU1_HUMAN	21.80		1.04
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidy)	11.00	10.60	
	124631	NM_014053	Hs.270594	FLVCR protein	23.20		
	124578	N68321	Hs.231500	EST	21.43		
10	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	37.20		1.77
	124472 124438	N52517 BE178536	Hs.102670 Hs.11090	EST membrane-spanning 4-domains, subfamily A	37.20		
	124357	N22401	ns.11090	gb:yw37g07.s1 Morton Fetal Cochiea Homo	14.64		
	124306	AW973078	Hs.293039	ESTs		4.00	
15	124214	H58608	Hs.151323	ESTs			
	124097	AW298235	Hs.101689	ESTs		27.20	
	123978 123972	T89832 T46848	Hs.170278 Hs.70337	ESTs immunoglobulin superfamily, member 4		6.00	2.03
	123972	AL050184	Hs.21610	DKFZP4348203 prolein		0.00	1.79
20	123936	NM .004673	Hs.241519	angiopoletin-like 1		15.80	,
	123802	AA620448		gb:ac58c09.s1 Stratagene lung carcinoma		4.23	
	123734	AA609861	Hs.312447	ESTs		4.20	
	123619 123596	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens EST	33.60 10.93		
25	123596	AA421130 AA384564	Hs.112640 Hs.108829	EST E	10.93		2.18
23	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20		
	123190	AA489212	Hs.105228	EST	14.20		
	123136	AW451999	Hs.194024	ESTs		7.00	
30	123073	AA485061	Hs.105652	ESTs	31.20	4.80	
30	123055 122699	AA482005 AA456130	Hs.105102 Hs.301721	ESTs, Weekly similar to reverse transcri KIAA1255 protein		5.00	
	122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40		
	122633	NM 001546	Hs.34853	inhibitor of DNA binding 4, dominant neg			
20	122553	AA451884	Hs.190121	ESTs	40.00		
35	122544	AW973253	Hs.292689	ESTs FXYD domain-containing ion transport reg	15.40		1.81
	122485 122211	AA524547 AA300900	Hs.160318 Hs.98849	ESTs, Moderately similar to AF161511 1 H		12.10	1-01
	122127	AW207175	Hs.106771	ESTs			1.95
	122011	AA431082		gb.zw78a10.s1 Soares_testis_NHT Homo sap			1.89
40	121992	Al860775	Hs.98506	ESTs		3.60	2.01
	121989 121835	W56487 AB033030	Hs.193784 Hs.300670	Homo sepiens mRNA; cDNA DKFZp585K1922 (f K/AA1204 protein			1.85
	121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	12.43		
	121690	AV660305	Hs.110286	ESTs			1.82
45	121843	AA840987	Hs.193767	ESTs			
	121633	AA417011	Hs.98175	EST	14.00	16.40	
	121622 121497	AA416931 AA412031	Hs.126065 Hs.97901	ESTs EST	11.20	10.40	
	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20		
50	121314	W07343	Hs.182538	phospholipid scramblase 4			1.83
	121242	AA400857	Hs.97509	ESTs	22.40		
	121059 120934	AA393283 AA226198		gb:zt74e03.r1 Soares_testis_NHT Homo sap gb:nc26e07.s1 NCI_CGAP_Pr1 Homo sapiens	14.80 21.20		
	120755	AA312934	Hs.190745	Homo sepiens cDNA: FLJ21326 fis, clone	21.20		1.79
55	120637	AA811804	110.130140	gbxbb39a05.s1 NCI_CGAP_GCB1 Homo sapiens	20.00		
	120484	AA253170	Hs.96473	EST	40.20		
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60	
	120266 120132	Al807264 W57554	Hs.205442 Hs.125019	ESTs, Weakly similar to T34036 hypotheti ESTs	16.80	4.73	
60	120041	AA830882	Hs.59368	ESTs		4.10	1.75
•••	119996	W88996	Hs.59134	EST		7.20	
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20		
	119861 119824	W78816 W74536	Hs.49943 Hs.184	ESTs, Weakly similar to \$65657 alpha-1C-		3.78	
65	119824	W/4535 AW021407	Hs.184 Hs.21068	advanced glycosytation and product-speci hypothetical protein	20.20		
05	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20		
	119221	C14322	Hs.250700	tryptase beta 1			
	119126	R45175	Hs.117183	ESTs	12.60		
70	119073	BE245360	Hs,279477	ESTs activator of CREM in testis		10.00	
70	118928 118901	AA312799 AW292577	Hs.283689 Hs.94445	ESTs CREM IN (estas		3.96	
	118661	AL137554	Hs.49927	nrotein binaso NYD-SP15		9.60	
	118607	A1377444	Hs.54245	ESTs, Weakly similar to \$65824 reverse t	10.40		
	118449	AI813865	Hs,164478	hypothetical protein FLJ21939 similar to			1.90
75	118416	N66028	Hs.49105	FKBP-associated protein	16.20	4.00	
	118379 118329	N64491 N63520	Hs.48990	ESTs gb:yy62f01.s1 Soares_multiple_sclerosis_		6.60	
	118329	N63451	Hs.141600	ESTs, Weakly similar to alternatively s		3,80	
	118253	AA497044	Hs.20887	hypothetical protein F1.110392	17.60		
80	118124	N56968	Hs.46707	chromosome 21 open reading frame 37	14.00		
	118056	AB037746	Hs.42768	hypothetical protein DKFZp761O0113		5.00	1.86
	118032 117840	N52802 T26379	Hs,47544 Hs,48802	EST Homo sapiens clone 23632 mRNA sequence		4.00	
	117404	N39725	Hs,15220	zinc finger protein 106			1,90
85	117314	N32498	Hs,42829	ESTs	14.20		

	w	O 02/086	443				
	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f			2.31
	116814 116784	H50834 AB007979	Hs,301281	gb:yp86a10.s1 Soares fetal liver spleen Home sapiens mRNA, chromosome 1 specific	20.20	3.51	
5	116766	A1608657	Hs.95097	FSTs	16.20	0,01	
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Weekly similar to A Chain A, Human	18.60		
	116351 116279	AL133623 AW971248	Hs.82501 Hs.291289	similar to mouse Xm1 / Dhm2 protein ESTs, Weakly similar to ALU1_HUMAN ALU S	19.40		
10	116166	AL039940	Hs.202949	KIAA1102 protein			2.13
	116152	AL040521	Hs.15220	zinc finger protein 106			1.75
	116117	BE613410	Hs.31575	SEC63, endoplasmic reliculum translocon	13.20		
	116107 115965	AL133916 AA001732	Hs.172572 Hs.173233	hypothetical protein FLJ20093 hypothetical protein FLJ10970	30.11		2.36
15	115955	AF263613	Hs.44198	intracellular membrane-associated calciu	18.20		2.00
	115844	Al373062	Hs.332938	hypolhetical protein MGC5370	18,57		
	115683	AF255910	Hs.54650	junctional adhesion molecule 2		23.00	
	115673 115672	AA406341 AI889110	Hs.269908 Hs.73251	Homo sapiens cDNA FLJ11991 fis, clone HE ESTs	11.82 10.60		
20	115566	Al142336	Hs.43977	Human DNA sequence from clone RP11-196N1	10.00		1.76
	115313	AA808001	Hs.184411	a'bumin	25.20		
	115279	AW964897	Hs.290825	ESTs		8.00	
	115230 115110	AA278300 AK001671	Hs.124292 Hs.11387	Homo sapiens cDNA: FLJ23123 fis, clone L KIAA1453 protein	14.20		1.80
25	114999	BE246481	Hs.87856	ESTs	19.20		
20	114930	AA237022	Hs.188717	ESTs		5.60	
	114922	AA235672	Hs.87491	ESTs		3.60	
	114837	BE244930 AA149060	Hs.166895 Hs.296100	ESTs ESTs	43.70 11.00		
30	114769	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
-	114736	AI610347	Hs.103812	ESTs, Moderalely similar to ALU1_HUMAN A	11.00	4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevislae) 3-like	20.40		
35	114455	H37908 Al369275	Hs.271616 Hs.243010	ESTs, Weakly similar to ALUS_HUMAN ALU S Homo sepiens cDNA FLJ14445 fis, clone HE	20.40	17.20	
-	114359	NM_016929	Hs.283021	chloride infracellular channel 5		17.20	2.09
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	12.40		
	114251	H15261	Hs.21948	ESTs			2.00
40	114138 114124	AW384793 W57554	Hs.15740 Hs.125019	Homo sepiens mRNA; cDNA DKFZp434E033 (fr ESTs		11.40 6.04	
	113946	AW083883	Hs.37896	Homo sepiens cDNA PLJ13510 fis, clone PL		5101	1.82
	113695	T96965	Hs.17948	ESTs, Weakly similar to Al.UB_HUMAN !!!			
	113606	NM_013343	Hs. 278951	NAG-7 prolein			2.15
45	113590 113560	R49642 T91015	Hs.142447 Hs.268628	ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs	32.00	3.60	
43	113552	A)654223	Hs.16026	hypothetical protein FLJ23191	02.00		
	113540	AW152618	Hs.16757	ESTs			
	113502	T89130		gb:ye12d01.s1 Stratagene lung (937210) H	12.40	8.35	
50	113288 113252	A1076838 NM 004469	Hs.12967 Hs.11392	eSTs e-fos Induced growth factor (vascular en	12.40	4.27	
50	113238	R45467	Hs.189813	ESTs		7-67	
	113203	AA743563	Hs-10305	ESTs	21.20		
	113195	H83265 T40707	Hs.8881 Hs.270862	ESTs, Weakly similar to S41044 chromosom ESTs	14.33		1.92
55	113089 113076	AF033199	Hs.8198	zinc finger protein 204	14.33	6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	Al694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti		12.20	
	112891	T03927	Hs.293147	ESTs, Moderetely similar to A46010 X-li	10.57 26.60		
60	112794 112691	R97018 R88708	Hs.220647	gb:yq74b08.s1 Soares fetal liver spleen ESTs	15.33		
	112602	AW004045	Hs.203365	ESTs	15.60		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequance	15.40		
	112210 112064	R49645 AL049390	Hs.7004 Hs.22689	ESTs	14.00 13.00		
65	111998	R42379	Hs.138283	Homo sapiens mRNA; oDNA DKFZp586O1318 (f ESTs	11.00		
	111987	NM 015310	Hs.6763	KIAA0942 protein	22.40		
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A			1.77
	111737 111605	H04607 T91061	Hs.9218 Hs.194178	ESTs	23.00		1.86
70	111510	F07856	Hs.194178 Hs.16355	ESTs, Moderately similar to PC4259 ferri ESTs	11.02		
, 0	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr	11.02		1,88
	111280	AA373527	Hs.19385	CGI-58 protein	18.40		
	111247	AW058350 Al247763	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	27.60		
75	111232 110942	R63503	Hs.16928 Hs.28419	ESTs ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HT018 protein			2.18
	110824	AI767183 AB032417	Hs.26942	ESTs	12.20		1.75
80	110776 110576	ABU32417 H60869	Hs.19545 Hs.37889	frizzled (Drosophila) homolog 4 ESTs	13.00		1./5
	110369	AK000768	Hs.107872	hypothetical protein FLJ20761		5.60	
	110099	R44557	Hs.23748	ESTs			2.31
	109984	AI796320 AA001266	Hs.10299 Hs.133521	Homo sapiens cDNA FLJ13545 ffs, clone PL ESTs	11.25		
85	109958	AA884208	Hs.133521 Hs.30484	ESTs	11.20		2.68
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	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83			
	109837	H00656	Hs.29792	ESTs, Weakly similar to 138022 hypotheti ESTs		17.20	3.91	
	109796 109688	AI800515 R41900	Hs.12024 Hs.22245	ESTs		9.60		
5	109648	H17800	Hs.7154	ESTs	22.80	0100		
-	109613	H47315	Hs.27519	ESTs				
	109550	AW021488	Hs,26981	ESTs				
	109523	AW193342	Hs.24144	ESTs		6.00	1.89	
10	109472 109355	AK001989 AA524525	Hs.91165 Hs.48297	hypothetical protein DKFZP586C1620 protein	15.00	0.00		
10	109355	AW978515	Hs.131915	KAA0863 protein	25.60			
	108781	AA128654		obczn98o07.s1 Stratagene fetal retina 93	14,20			
	108663	BE219231	Hs.292653	ESTs, Weskly similar to T26845 hypotheti	11.00			
15	108573	AA086005		gb:zl84c04.s1 Stratagene colon (937204)	26.00			
13	108480 108382	AL133092 NM_006770	Hs.68055 Hs.67726	hypothetical protein: DKFZp434l0428 macrophage receptor with collagenous sir			1.83	
	108174	AA055632	Hs.303070	ESTs	15.20		1.00	
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr		3.60		
20	108087	AA045708	Hs.40545	ESTs	15.44			
20	108048	AI797341	Hs.165195	Homo sepiens cDNA FLJ14237 fis, clone NT ESTs		11.40		
	108041	AW204712 AL049176	Hs.61957 Hs.82223	chordin-like		4.76		
	107994	AA036811	Hs.48469	LIM domains containing 1				
	107922	BE153855	Hs.61460	lg superfamily receptor LNIR	14.20			
25	107681	EE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80			
	107666 107332	AA010611 T87750	Hs.60418 Hs.183297	EST DKFZP566F2124 protein	29.20 10.73			
	107332	RF166479	Hs.4789	Homo sepiens serologically defined breas	32.00			
	107230	AJ034467	Hs.34650	ESTs	17.40			
30	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43			
	107160 107054	AA314490 Al076459	Hs.27669 Hs.15978	KIAA1563 protein KIAA1272 protein	11.40			
	107029	AF264750	Hs.288971	myeiold/lymphold or mixed-lineage teukem	21.40			
	106999	H93281	Hs.10710	hypothetical prolein FLJ20417	35.80			
35	106954	AF128847	Hs.204038	indolelhylamine N-melityltransferase			1.76	
	106870	Al983730	Hs.26530	serum deprivation response (phosphalidy)	13.40			
	106865 106844	AW192535 AA485055	Hs.19479 Hs.158213	ESTs sperm associated antigen 6	13.40	7.13		
	106820	NM_016831	Hs.12592	period (Drosophile) homolog 3		7.00		
40	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00			
	106797	Al768801	Hs.169943	Homo seplens cDNA FLJ13569 fis, clone PL			2.05	
	106773	AA478109 NM_007118	Hs.188833 Hs.171957	ESTs triple functional domain (PTPRF interact	12.60			
	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60			
45	106687	AW380847	Hs.18578	ESTs				
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr chromosome 9 open reading frame 5			2.40 1.78	
	106567 106562	AW450408 AL031846	Hs.86412 Hs.152151	plakophilin 4			1.76	
	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prof			2.19	
50	106533	AL134708	Hs.145998	ESTs	23.20			
	106507 106490	AA259068 AA404265	Hs.287819	protein phosphatase 1, regulatory (inhib putative dipeptidase	15.20			
	106490	BE383668	Hs.115537 Hs.42484	hypothetical prolein FLJ10618	10.44			
	106211	AA428240	Hs.126083	ESTs		29.80		
55	105986	AB037722	Hs.8707	K/AA1301 protein		3.70		
	105894	Al904740	Hs.25691	receptor (calcitorin) activity modifying			1.94	
	105847 105803	AW964490 AW747996	Hs.32241 Hs.160999	ESTs, Weakly similar to S65657 alpha-1C- ESTs, Moderately similar to A56194 throm			2.47	
	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71			
60	105729	H46612	Hs.293815	Homo saplens HSPC285 mRNA, partial cds				
	105688	Al299139	Hs.17517	ESTs	23.40 37.20			
	105510 105101	Z42047 H63202	Hs.283978 Hs.38163	Homo sepiens PRO2751 mRNA, complete cds ESTs	31.20	8.30		
	104989	R65998	Hs.285243	hypothetical prolein FLJ22029		8.09		
65	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92	
	104969	A)670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40 7.60		
	104903 104896	Al436323 AW015318	Hs.31141 Hs.23165	Home sapiens mRNA for KIAA 1568 protein, ESTs	13.80	7.60		
	104865	T79340	Hs.22575	Homo saplens cDNA; FLJ21042 ffs, clone C	10.00			
70	104825	AAC35613	Hs.141883	ESTs			1.87	
	104781	AA099904	Hs.21610	DKFZP434E203 protein		10.20	1.93	
	104776 104691	AA026349 U29690	Hs.37744	gb:zi99f01.s1 Soares_pregnant_uterus_NbH Homo sepiens beta-1 adrenergic receptor		5.69		
	104691	A1239923	Hs.30098	ESTs		3.82		
75	104404	H58762		gb:EST00057 HE6W Home sapiens cDNA clone		4.20		
	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		404	
	104212	AB002298	Hs.173035	KIAA0300 protein Homo saplens mRNA; cDNA DKFZp434M229 (fr	11.20		1.91	
	104074	AL162039 AL135301	Hs.31422 Hs.8768	hypothetical protein FLJ 10849	10.86			
80	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00			
	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22MD			1.80	
	103541	AI815601 Y09267	Hs.79197 Hs.132821	CD83 antigen (activated B lymphocytes, i flavin containing monooxygenase 2				
	103496	RE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20			
85	103353	XB9399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80			

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	103295	X81479	Hs.2375	egf-like module containing, mucin-like,		3.60		
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula				
	103100	NM 005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)			1.78	
_	103025	NM 002837	Hs.123641	protein tyrosine phosphalase, receptor t			2.15	
5	102598	M18667	Hs 1867	progestricsin (pepsinogen C)				
	102659	BE245169	Hs.211610	CUG iriplet repeat, RNA-binding protein	11.00			
	102580	U60808	Hs.152981	CDP-discylglycerol synthese (phosphatida	25.40			
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00			
	102353	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc				
10	102302	A4306342	Hs.69171	protein kinase C-like 2	10,86			
		AW161552	Hs.83381	guarine nucleotide binding protein 11				
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1		7.40		
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40			
	101957	L28824	Hs.74101	spieen tyrosine kinase	15.40			
15		M93221	Hs.75182	mannose receptor, C type 1				
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant				
		A1198550	Hs.81256	S100 cslclum-binding protein A4 (calcium			1.78	
		AF050658	Hs.2563	tochykinin, precursor 1 (substance K, su	18.80			
		M62505	Hs.2161	complement component 5 receptor 1 (C5a)			2.22	
20	101447	M21305		gb:Human alpha satatite and satellite 3	504.80			
	101383	NM_000132	Hs.79345	cosgulation factor VIII, procoeguiant co		31.00		
	101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N			1.75	
	101345	NM_005795	Hs.152175	calcitonin receptor-like				
~ ~	101336	NM_006732	Hs.75678	FBJ murine ostposarcoma viral oncogene h			2.24	
25		L43821	Hs.80251	enhancer of filamentation 1 (cas-like do				
	101277		Hs.296049	microfibrillar-associated protein 4				
		L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00			
	101168		Hs.211569	G protein-coupled receptor kinase 5			2.01	
• •	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto				
30	101088		Hs.553	solute carrier family 6 (neurotransmitte		7.52		
		AW970254	Hs.889	Charot-Leydan crystal protein	19.38			
	100971		Hs.83213	fatty ecid binding protein 4, adipocyle			1.91	
		BE245294	Hs.180789	S164 protein	15.40			
25	100770			emyloid beta (A4) precursor protein (pro	11.20			
35		X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80			
	100555			gb:Humen nonmuscle myosin heavy chain-B	33.00			
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20			
	100408		Hs.56045	are homology three (SH3) and cysteine n		4.00 4.24		
40	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik		6.20		
40	100351	D64158				21.20		
	100299	D49493	Hs.2171	growth differentiation factor 10		21.20		
		AA305746	Hs.49	mecrophage scavenger receptor 1			1.79	
	100108	U09577	Hs.76873	hyeluronoglucosaminidase 2		5.40	111.0	
45	100095	297171	Hs.78454	myodlin, trabecular meshwork inducible	11,29	3.40		
43	100066				11.20			

TAILS 50 shows the source or the base of privacy to below up showed. Yet might 30. For make hydroxing to been liked for speed cubic varieties from which the showed common recognition of the speed cubic varieties from which the showed common recognition of the speed common for common from the speed common for the speed common from the speed common fro

55 Pkey: Unique Eos probesel (denlifier number CAT number: Gene cluster number Accession: Genbank accession numbers

60	Pkey	CAT number	Accessions		
00	123619	371681_1	AA602964	AA609200	
	126433	127143_1		AA099517 N89423	
	125831	1522905_1		0988 D60337	
	126816	122973_1	AA248234		
65	126852	136135 1	AA399961		
-	121059	273450 1	AA393283		
	120637	200885 1		AA809404 AA286907 AW9	77624
	122011	76172	AA431082		
		177521 1		AA226513 AA383773	
70	123802	ganbank AA62		AA620448	
, ,	116814	genbank_H508	34	H50834	
		genbank N635	20	N6352D	
	104404		H58762		
	104776	genbank AA02		AA026349	
75	113502				
	101262	entrez L35854			
	108573	genbank AA06		AA086005	
	101447				
		oenbank N224		N22401	
80	108781	genbank AA12		AA128654	
	112794	ganbank R970		R97018	
	100351	entrez D64158			
	100555	llgr_HT2245		81105 U51039	
85					

WO 02/086443 PCT/US02/12476 Table 4A shows 202 genes up-regulated in samples from patients inseted with chemotherapy or radiothorapy. These genes were selected from 1998 protesses on the Exal/stymetrix Hud3 Centechip array. Gene expression data for each protest obtained from this analysis was expressed as arrange intensity (AI), a normalized value reflecting

the relative level of mRNA expression. Pkey: Unique Ecs probeset identifier number

ExAcon: Exemplar Accession number, Genbank accession number UnigenelD: Unigene number Urigene Title: Unigene gene title
R1: everage of Al for samples from patients treated with chemotherapy or radiotherapy divided by the average of Al for normal lung samples.

R1: 10 Pkey ExAcon UnigenetD Unigene Title 100113 NM_001269 Hs 84746 chromosome condensation 1 aldo-kelo reductase family 1, member C3 27.20 100187 D17793 Hs.78183 20.60 KIAA0042 gene product 15 20.40 100210 D26361 Hs.3104 D28539 Hs.167185 olulamale receptor, metabotropic 5 20.60 100225 NM_001949 Hs.1189 E2F transcription factor 3 29.40 100269 lopoisomerasa (DNA) Il binding protein 100438 AA013051 Hs.91417 23.50 100877 X80821 Hs.27973 KIAA0874 protein 35.56 20 100893 BF245294 Hs.180789 S164 protein POU domein, class 3, transcription facto 43.40 101273 711933 Hs 182505 21,80 gb:Human alpha satellite and satellite 3 M21305 193,60 101447 101649 AW959908 Hs.1690 heparin-binding growth factor binding pr bullous pemphigoid antigen 1 (230/240kD) 38.40 101724 L11690 Hs.620 198.80 bellous permphipoid entipen 1 (2002/4062) genephigos vulgadas entipen gap junction protein, beta 2, 26KC (coon nuclear autosetigents perm protein), beta 2, 26KC (coon nuclear autosetigents perm protein) plas cytocofic ovarien carcinoma entipen 1 UDP-N-acety-baiha D-gladotosemirispolyp mut8 (E. colf) homolog 2 (colon cancer, RAR-related ophigan receptor A. ISLI i ranacription facior, LIMhomeodoma detoxyvulanosiate bisase 25 NM_001944 Hs.1925 78 60 101809 M86849 Hs.323733 162 20 101879 AA176374 Hs.243886 50.00 Hs.155185 101915 AF207881 101973 1141514 Hs.80120 37.20 30 102025 U04045 Hs.78934 102031 U04898 Hs.2156 32.00 102052 NM_002202 Hs.505 Hs.77494 51 20 102391 AA296874 deoxyguanosine kinase Homo saylens cDNA: FLJ21800 fis, clone H preferentietly expressed antigen in meta 13,90 Hs.14427 28,80 102420 144060 35 1165011 Hs.30743 110.60 102610 102829 NM_006183 Hs.80962 116.80 neurotensin neurotensin
enolsse 2, (gamma, neuronal)
malitz metalloproteinase 1 (intersitial
serum/hucocorticold regulated kinase
574 onorbiela hophotetas (gkycorpolan
Homo sapiena mRNA; cDNA DKF2p684D016 (fr 103000 NM_001975 Hs.146580 2 30 103036 M13509 Hs.83169 181 40 103507 A.1000512 Hs.296323 49.20 40 103587 BE270288 Hs.82128 86,60 Hs.14846 42.60 104660 BE298665 104896 AW015318 Hs.23185 ESTs 29,40 ESTs.
KIAA1488 protein
hypothetical protein FLJ20287
Horno sapitiens PROZ751 mRNA, complete cds
paired box gene 5 (B-cell lineage specif
downsinear neighbor of SON
ESTs, Weakly similar to 138022 hypotheti 105038 AW503733 Hs.9414 21 50 105298 BE387790 Hs.26369 32.80 45 105510 742047 Hs.283978 20.20 105667 AA767536 Hs.22030 28.40 Al.157441 Hs.17834 25,40 106073 AW965058 Hs.111583 32.00 106205 106516 AL137311 Hs.234074 Homo sapiens mRNA; cDNA DKFZp761G02121 (40.60 50 106533 AL134708 Hs.145998 ESTs 59.80 106575 AW970602 Hs.105421 ESTs 43.40 106654 AW075485 Hs.286049 phosphoserine aminotransferase 50.80 gb:lk04g09.x1 NCI_CGAP_Lu24 Homo sapiens 53.40 106851 AM58823 AB023139 Hs.37892 KIAA0922 protein 20.68 106995 DKFZP56F2124 protein Homo sapiens mRNA; cDNA DKFZp762G207 (fr Ig superfamily receptor LNIR 55 107332 T87750 Hs.183297 23.60 107532 AA443473 Hs.173684 57.20 107922 BE153855 Hs.61460 49.00 108609 BE409857 Hs.69499 hypothetical protein collagen, type XVII, alpha 1 RAB6 interacting, kinesin-like (rabkines 19.67 Hs.117938 48.17 108780 AU078442 60 AA219691 Hs.73625 59.20 109166 109260 AW978515 Hs.131915 KIAA0863 protein 20 00 hypothetical protein FLJ10493 KIAA1702 protein 109280 AK001356 Hs.279610 22.80 109292 AW975746 Hs.188662 109384 AA219172 He SERIO ESTs 21,00 65 109415 U80738 Hs.110826 trinucleofide repeat containing 9 31.60 109445 AA232103 Hs.189915 ESTs 109502 AW967069 Hs.211556 hypothetical protein MGC5487 21.40 109633 AW003785 Hs.170267 ESTs 20 40 109786 A1989482 Hs.146286 kinesin family member 13A 19.60 70 109958 AA001266 Hs.133521 **ESTs** 24.00 110920 N47224 Hs.20521 HMT1 (bnRNP methyltransferase, S. cerevi 28.40 zinc-fingers and homeoboxes 1 AW058463 Hs.12940 36.00 110924 H44186 Hs.15456 PDZ domain containing 1 61.20 111084 111132 AB037807 Hs.83293 hypothetical proteir 24.60 75 111229 AW389845 Hs.110855 27.20 LIS1-interacting protein NUDE1, rat homo 111337 AA837396 Hs.263925 48.00 111087 NM 015310 He 6763 KIAA0942 protein CDC14 (cell division cycle 14, S. cerevi 37.80 AA383343 Hs.22116 112046 112268 W39609 Hs.22003 solute carrier family 6 (neurotransmitte ESTs, Weakly similar to ALU1_HUMAN ALU 63,80 80 112685 R87650 Hs.33439 20.40 112871 AL110216 Hs.12285 ESTs, Weakly similar to 155214 salivary 47.64 112897 AW206453 He 3782 **ESTs** 22.00 hypothetical protein FLJ10201 112973 AB033023 Hs.318127 65.00 Hs.133315 Homo saplens mRNA; cDNA DKFZp761J1324 (f Hs.103042 microtubule-associated protein 1B 112992 AL157425 85 N30342 113073

	W	O 02/086	443		
	113494	T91451	Hs.86538	ESTs	22.80
	113560 113849	T91015 AA457211	Hs.268626 Hs.8858	ESTs bromodomein adjacent to zinc finger doma	22.80 51.80
	113950	AI267652	Hs.30504	Homo sepiens mRNA; cDNA DKFZp434E082 (fr	28.20
5	114339	AA782845	Hs.22790	ESTs	20.20
	114365	H42169 H37908	Hs.18653 Hs.271616	hypothetical protein FLJ14627 ESTs, Weakly similar to ALU8_HUMAN ALU S	21.00 25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
10	114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
10	114837	BE244930 AW966931	Hs.166895 Hs.179662	ESTs nucleosome assembly protein 1-like 1	30.20 20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
15	115291 115313	BE545072 AA808001	Hs.122579 Hs.184411	hypothetical protein FLJ10461 albumin	38.00 22.60
10	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
	116090	Al591147 AL133916	Hs.61232 Hs.172572	ESTs hypothetical protein FLJ20093	164.20
20	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699 AF161470	Hs.260622	gb:yv16a11.s1 Soares fetal liver spleen butyrate-induced transcript 1	21.60 49.40
	118091	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22,40
0.5	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein.	22.00
25	118720	N73515 Al824009	Hs.44577	gb:za49d07.s1 Soares fetal liver spicen ESTs	20.00 19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
30	119940 120268	AL050097 Al807264	Hs.272531 Hs.205442	DKFZP586B0319 protein ESTs, Weakly similar to T34036 hypotheti	31.00 20.20
-0	120515	AA258356		gb;zr59c10.s1 Soares_NhHMPu_S1 Homo sapl	25.00
	120859	AA826434	Hs.1619	achaete-scute complex (Drosophile) homol EST	95.40 105.20
	120983	AA398209 AW976570	Hs.97587 Hs.97387	ESTs	38.80
35	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335 122612	AA443258 AA974832	Hs.241551 Hs.128708	chloride channel, calcium activated, fam ESTs	30.80 19.60
	123130	AA487200	H8-120/U0	gb;ab19f02.s1 Stratagane lung (937210) H	33.20
40	123440	A1733592	Hs.112488	ESTs	23.17
40	123596 123619	AA421130 AA602964	Hs.112640	EST gb:nc97c02.s1 NCL_CGAP_Pr2 Homo sepiens	23.00
	124006	Al147155	Hs.270018	ESTs	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
45	124281	Al333756 N52517	Hs.111801 Hs.102670	arsanate resistance protein ARS2 EST	42.20 32.60
-13	124617	AW628168	Hs.152684	ESTs	21.80
	124831	NM_014053	Hs.270594	FLVCR protein	30.40 21.20
	124839 125186	R55784 AA610620	Hs.140942 Hs.181244	ESTs major histocompatibility complex, class	42.80
50	125321	T86652	Hs.178294	ESTs	27.00
	125535 125646	NM_013243 AA628962	Hs.22215 Hs.75209	secretogranin III protein kinasa (cAMP-dependent, catalyti	23.80 23.20
	125884	AW589427	Hs.158849	Homo sapiens cDNA: FL/21663 fis, clone C	21.20
55	125724	AL360190	Hs.295978	Homo sapiens mRNA full length Insert cDN	48.80
33	125847 125934	AW161885 AA183325	Hs.249034 * Hs.32646	ESTs hyposhetical protein FLJ21901	31.00 21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299 128395	AW979155 AJ468004	Hs,298275 Hs,278958	amino acid transporter 2 hypothetical protein FLJ12929	21.80 71.00
60	126433	AA325606	na.2/6800	gb:EST28707 Cerebellum II Homo sapiens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80
	126538 126666	AB030656 AA648886	Hs,17377 Hs,151999	coronin, actin-blinding prolein, 1C ESTs	23.10 36.00
	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
65	126872 127046	AW450979 AA321948	Hs,293968	gb:UI-H-Bi3-ala-a-12-0-ULs1 NCL_CGAP_Su ESTs	46.29 22.80
	127431	AW771958	Hs.293968 Hs.175437	ESTs, Moderately similar to PC4259 fami	30.00
	127489	AA650250	Hs.272076	ESTs	20.80
70	127521	AW297206 AW293496	Hs.164018 Hs.180138	ESTs ESTs	25.20 28.00
, 0	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672 AA830201	Hs.123304	ESTs	20.54 28.20
	127988	AA63U2U1 AI022103	Hs.124347 Hs.124511	ESTs ESTs	19.60
75	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609	NM_003616 AI878918	Hs.102456 Hs.10526	survival of motor neuron protein interac cysteine and glycine-rich protein 2	34.40 53.80
	128777	A/878918 AA009647	Hs.10526 Hs.8850	a disintegrin and metalloproteinase doma	23.00
00	129168	AJ132988	Hs.109052	chromosome 14 open reading frame 2	37.60
80	129404 129527	A1267700 AA769221	Hs.317584 Hs.270847	ESTs delta-lubulin	28.60 40.80
	129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT FSTs	29.60
85	129785	H19006 AV655806	Hs.184780 Hs.296198	LISTS chromosome 12 open reading frame 4	72.20 22.20

	W	O 02/086	443		
	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase doma	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
	130466	W19744	Hs. 180059	Homo segiens cDNA FLJ20653 fis, clone KA	20.20
5	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine fructose 6 phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs ·	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
	130867	NM 001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
10	131028	AJ879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM 001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KtAA0648 protein	21.00
	131860	BE383676	Hs.334	Rho guarine nucleotide exchange factor (33,40
15	131945	NM 002916	Hs.35120	regilication factor C (activator 1) 4 (37	60.80
	132040	NM 001196	Hs.315689	Homo seplens cDNA: FLJ22373 fis, clone H	20.40
	132084	NM_002267	Hs.3886	karvopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32,40
	132437	AA152106	Hs.4859	cyclin L ania-6a	27.40
20	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
200	132617	AF037335	Hs.5338	carbonic anhydrase XIII	31.36
	132632	AU076916	Hs.5398	quanine monohosphete synthetase	32,40
	132672	W27721	Hs.54697	Cdc42 quarine exchange factor (GEF) 9	23,40
	132742	AA025480	Hs.292812	ESTs. Weakly similar to T33468 hypotheti	61,20
25	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	1192649	Hs.64311	e disintonin end motallogroteinase doma	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (Droscobila) homolog (acrocephalos	23.80
	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51,60
30	133350	Al499220	Hs.71573	hypolitetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor thA	82.00
	133658	AA319146	Hs.75426	secretogranin tt (chromogranin C)	
	133865	AB011155	Hs.170290	discs, large (Drosophile) homolog 5	69.33
	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase Intibilo	33.20
35	134125	NM 014781	Hs.50421	KIAAC203 gene product	31.60
55	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs. Moderately similar to A46010 X-lin	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
40	134753	NM 006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryt	20.80
-10	135002	AA448542	Hs.251677	G antigen 7B	37.60
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53,40
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
	135345	X53655	Hs.99171	neurotrophin 3	28.80
45	130040		110.00171	nouvelen. •	

TABLE 48 shows the accession numbers for those primetays tacking uniquentIV's for Table 4A. For each probaset we have listed the gase cluster number from which the objounces deemed from Genthark ESTs and mRVMs. These sequences were distincted based on sequence manner of the company of the c 50 "Accession" column.

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

55 Pkay CAT number Accessions 123819 371881_1 AA602964 AA609200

AABSCEAA AABSCE200 AAASSSEA AAASSEST 7189423 AAASSSEA AAASSEST AATSSESS AATSSESS AAASSA AAASSA SAAASSA BEEGISA AAASSA AAASSA BEEGIT 212 BEDIT389 BEDIT387 BEDIT388 BEDIT382 BEDIT382 BEDIT385 EEDIT385 AAASSA AAASSA AAASSA AAASSA BEDIT382 BEDIT385 EEDIT385 AAASSA AAASSA AAASSA AAASSA BEDIT382 BEDIT385 AAASSA TO 126433 126872 142696_1

106851 322947_1 118720 genbark_N73515 N73515 AA258356 120515

genbark_N73515 N73515 genbark_AA258356 AA258356 321671_1 H93699 H97976 H80036 entrez_M21305 M21305 117099 101447 123130 genbank_AA487200 AA487200

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60

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PCT/USI2/2476
Table 8.4 shades 859 group spegulided in opumnous cell cardiones or obtrocardiones lung binner relative to normal lung and chronically deseased to the cardiology deseased to the facility flower services of the problement of the facility flower services of the problement of the market flower services of the problement of the market flower services of

	attornon)	, 0,, 0		9					
5	Pkey:	Unique	Eos probasati	denlifer number					
-	ExAcen:	Exame	ler Appassion n	umber, Genbank accession number					
	Unigenell		e number						
	Unigene '	Tito: Uniner	o gone title						
	R1:	70th pe	proentile of All fo	r squarnous cell carcinoma and adenocarcinoma lu	ng tumor sar	nples divi	ded by the	90th percent	lie of Al for normal and chronically
10		diseas	ed lung sample:						
	R2:	80th or	proportio of Al a	tenocardnoma lung hungr samples divided by the !	90th percenti	le of At fo	r normal ar	nd chronically	diseased lung samples.
	R3:	80th pa	proentile of All st	quarnous cell carcinoma lung turnor samples divide	d by the 90th	percentil	of Al for n	normal and ch	ronically diseased lung samples.
	R4:	80th no	ercentile of Al a	denocarcinoma lung tumor samples divided by the	80th percenti	e of Al fo	r squamou	s cell carano	malung tumor samples.
	R5:	70th pe	ercentile of All fo	r squamous cell carcinoma and adenocarcinoma le	ng tumor sar	nples mir	us the 15th	i percentile o	f Al for all normal lung, chronically
15		diseas	nul bne grul be	or samples divided by 90th percentile of Al for nor	nal and chror	rically dis	eased lung	samples mi	rius the 15th percentile of Al for all
		norma	lung, chronical	ly diseased lung and tumor samples					
						-	-	-	R5
20	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R3
20									6.76
	100035			AFFX controt GAPDH					5.77
	100036			AFFX control: GAPDH AFFX control: GAPDH					5.75
	100037	100100		Human GABAs receptor sloha-3 subunit		8.00			0.70
25	100114	A28102 X02308	Hs.82962	thymidylate synthetase		0.00			5.71
23	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				•
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs-57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, ptatelet					5.49
30	100216	AA489908	Hs.1390	proleasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.88
	100297	AU077258	Hs.182429	protein disuffice isomerase-related prot					3.81
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	plotelet-ectivating factor acetylhydrole	5.07				
	100380	W70171	Hs.75939	uridine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product				15.65	3.79
	100474	NM_000699	Hs.300280	emylase, siphe 2A; pancreatic RAN, member RAS oncogene family				10.00	5.49 .
40	100486	T19008 D56165	Hs.10842 Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
+0	100491	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs-99949	protactin-induced protein				14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
	100576	X00356	Hs.37058	celcilonin/calcitonin-related polypopiid				9.30	
45	100629	AA015693	Hs-21291	milogen-activated protein kinase kinase				20.60	
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100596	D14887	Hs.121688	general transcription factor IIA, 1 (37k				10.00	
60	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem		7.60	24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			7.99
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1 gb:Human transketotase-like protein gene		10.20			7.00
	100867	U14622 M18029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
	100902	AU076916	Hs.5398	guanine monphosphate synthetase		0.00			5.16
55	100960	J00124	Hs.117729	keratin 14 (epidermolysis buttosa simple	2.57				
00	101045	J05614		gb:Human proliferating cell nucleor anti					4,69
	101061	NM_000175	Hs.180532	glucos e phosphate Isomerase					4.19
	101071	L02840	Hs.84244	potassium voltage-gated channet, Shab-re		12.91			
	101124	L10343	Hs.112341	prolease inhibitor 3, skin-derived (SKAL	3.12				
60	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (5.69
	101204	L24203	Hs.82237	ataxia telangiectasia group D-associated	4.08		6.40		
	101210	L29301	Hs.2353	opioid receptor, mu 1	2.53		0.40		
65	101216	AA284166	Hs.84113	cyclin-dependent kinese inhibitor 3 (CDK chaperonin containing TCP1, subunit 6A (2,55				7.90
03	101228	AA333387 AL135173	Hs.82916 Hs.878	sorbital dehydrogenese					4.45
			Hs.182505	POU domain, class 3, transcription facto	8.50				
	101273 101342	Z11933 U52112	Hs.182018	interleukin-1 receptor-associated kinase	0.00				4.17
	101342	A1738616	Hs.77348	hydroxyprostaglandin dahydrogenase 15-(N				21.89	
70	101369	NM_000892	Hs.1901	kelikroin B, plesma (Flotcher factor) 1				12.80	
	101396	BE267931	Hs.78996	profiferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)					7.90
	101448	NM_000424	Hs.195850	keretin 5 (epidermolysis bullosa simplex	8.31				
70	101462	AL035668	Hs.73853	bone morphogenatic protein 2				38.80	4.01
75	101466	BE262660	Hs.170197	glutamic oxaloacetic transaminase 2, mit				40.00	4.01
	101484	AA053486	Hs.20315	interferon-induced protein with tetratri	10.50			12.00	
	101502	M26958	11- 25000	gb:Human parathyroid hormone-related pro	10.50				4.46
	101505 101526	AA307680 NM_002197	Hs.75692 Hs.154721	asperagine synthetase aconitase 1, soluble	4.02				
80	101526	X57152	Hs.99853	Springer I, Solution	-				4.65
00	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
0.5	101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
85	101669	L24498	Hs.80409	growth arrest and DNA-demage-inducible,		7.60			

	W	O 02/086	443						PCT/US02/12476
	101695	M69136	Hs.135626	chymase 1, mast cell	4,79				
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21				
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	55,50				
5	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino					4,10
)	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	4.00			18.57	
	101804	M86699	Hs.169840	TTK prolein kinase	4.50 140.00				
	101809 101833	M86849 AU076442	Hs.323733 Hs.117938	gep junction protein, bets 2, 26kD (conn collegen, type XVII, alpha 1	2,56				
	101842	M93221	Hs.75182	mennose recepior, Citype 1	2.00			12.80	
10	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor				12.00	5,88
10	102002	NM_002484	Hs.81469	nucleolide binding prolein 1 (E.coli Min		7,80			5.00
	102039	AL134223	Hs,306098	aldo-kelo reductase family 1, member C1					4.35
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)			7,40		
	102083	T35901	Hs.75117	Interleukin enhancer binding factor 2, 4					5,12
15	102111	L36196	Hs.81884	sulfotransferase family, cylosofic, 2A,				12.00	
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20				
	102154	U17760	Hs.75517	taminin, beta 3 (niceln (125kD), kalinin	2.62				
	102193	AL036335	Hs.313	secreted phosphoprotein 1 (asleopontin,	5.85				
20	102217	AA829978	Hs.301613	JTV1 gene					6.18
20	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu					4.49
	102234	AW163390 NM_004398	Hs.278554 Hs.41706	heterochromatin-like protoin 1 DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50				5.80
	102251 102305	AL043202	Hs,90073	chromosome segregation 1 (yeast homolog)	4.30				5.15
	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 bola					4.17
25	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro				9.33	****
20	102348	U37519	Hs.87539	eldehydie dehydrogenase 3 family, member	8,87			0100	
	102368	U39817	Hs.36820	Eloom syndrome	15.91				
	102394	NM_003816	Hs.2442	a dishtegrin end metalloproteinase doma			19.20		
	102404	NM_005429	Hs.79141	vascular endothelial growth factor C				14.00	
30	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family				12.00	
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophile) homolog 2					4.57
	102605	AJ435128	Hs.181369	ublgulin fusion degradation 1-like					3.98
	102610	U65011	Hs.30743	preferentially expressed entigen in mela	77.50				
35	102623	AW249285	Hs.37110	melanoma enligen, family A, 9	12.50		00.00		
22	102642 102654	AA205847 AV649989	Hs.23016 Hs.24385	G protein-coupled receptor Human hipo647 mRNA sequence		12.00	22.00		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein		12.00		12.80	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50			16.00	
	102672	U72066	Hs.29287	refinoblestome-binding protein 8	8.50				
40	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	****				9.24
	102696	BE540274	Hs.239	forkhead box M1					5.54
	102768	U82321		gb:Homo sapiens clone 14.98 mRNA sequenc		6.60			
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunil 7 (e					3,78
	102784	U85658	Hs.61796	transcription fector AP-2 gamma (actival					4.26
45	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H			14.40		
	102829	NM_006183	Hs.80962	neurolensin	8.00				
	102888	Al346201	Hs.76118	ubiquifin carboxyl-lerminal esterase L1			6.70		5.50
	102892 102913	BE440042 NM_002275	Hs.83326 Hs.80342	matrix metalloproleinase 3 (stromelysin keratin 15	4.64		6.70		
50	102913	BE561850	Hs.80506	smell nuclear ribonucleoprotein polypept	2.93				
50	102951	X15218	Hs.2989	v-ski avian sarcoma viral oncogene homol	2.30			11.40	
	102983	BE387202	Hs.118638	non-melastatic cells 1, protein (NM23A)				11140	7.26
	103023	AW500470	Hs.117950	multifunctional polypoptide similer to S	3.01				
	103036	M13509	Hs.83189	matrix metalloproteinase 1 (interstitial	27.90				
55	103038	AA926960	Hs.334883	CDC28 protein kinase 1					8.79
	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin					4.27
	103099	A1893251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro		9,80			
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05				
60	103168	X53463	Hs.2704	glutathione percoidase 2 (gastrointestin	3.07				- 00
60	103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmi					5.62
	103192	M22440 BE275607	Hs.170009	transforming growth factor, alpha chaperonin containing TCP1, subunil 3 (g		7.40			4.70
	103223	X76342	Hs.1708 Hs.389	alcohol dehydrogenase 7 (class IV), mu o			100.00		4.70
	103242 103316	X83301	Hs.324728	SMA5			100.00	9.80	
65	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71			5.00	
05	103376	AL036166	Hs.323378	costed vesicle membrane protein	14.00				
	103385	NM.007069	Ha,37189	similar to rat HREV107				11.00	
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthelase (glut	2.93				
	103404	BE394784	Hs.78596	proleasome (prosome, macropain) subunit,					5.15
70	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr					3.98
	103446	X98834	Hs.79971	sal (Drosophila)-like 2				21,40	
	103476	Y07701	Hs.293007	arninopopiidase puromycin sensifive		13,00			
	103477	AJ011812	Hs.119018	transcription factor NRF			6.40		
75	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02				
13	103515	Y10275	Hs.56407 Hs.2785	phosphoserine phosphatase keratin 17	10.50 6.41				
	103558 103580	BE616547 AA328046	Hs.2785 Hs.46405	polymerase (RNA) il (DNA directed) polyp	0.41				3.84
	103580	PA328096 BE270266	Hs.40405 Hs.82128	5T4 oncofetal trophoblasi glycoprotein	78.50				UNU-T
	103594	A1368680	Hs.816	SRY (sex determining region Y)-box 2	6.51				
80	103636	NM 006235	Hs.2407	POU domain, class 2, associating factor	3.50				
	103768	AF086009		POU domain, class 2, associating factor gbd-tomo sapiens full length insert cDNA					4,48
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468		8.00			
	103847	AF219946	Hs.102237	lubby super-family protein		10.40			
0.5	103913	AW967500	Hs.133543	ESTs				15.60	
85	104094	AA418187	Hs.330515	ESTs			6.60		

	W 104150	O 02/086	443 Hs 331633	hypothetical protein DKFZp566N034				25.00	PC	T/US02/12476
	104257	BE560621	Hs.9222	estrogen receptor binding site associate		6.80		20,00		
	104261	AW248364	Hs.5409	RNA polymerase I subunit					3.98	
5	104331 104415	AB040450 BE410992	Hs.279862 Hs.258730	cdk inhibitor p21 binding protein heme-regulated initiation factor 2-alpha		6.80				
,	104558	R56678	Hs.88959	hypolhetical protein MGC4816	4.21	10.29				
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	-			15.79		
	104658	AA360954	Hs.27268	Homo sapiens cONA: FLJ21933 fis, clone H				17.40		
10	104660 104689	BE298665 AA420450	Hs.14846 Hs.292911	Homo sepiens mRNA; cDNA DKFZp564D016 (ir ESTs, Highly similar to S60712 band-6-pr	6.40				6.55	
10	104754	AJ206234	Hs.155924	cAMP responsive element modulator				10.00	0.33	
	104758	BE560269	Hs.7010	NPD002 protein					4.47	
	104971	BE311926	Hs.15830	hypothetical protein FLJ 12691	2.87					
15	105011 105012	BE091926 AF098158	Hs.16244 Hs.9329	mitotic spindle colled-coil related prot chromosome 20 open reading frame 1	3.83 2.86					
13	105026	AA809485	Hs.124219	hypothetical protein FLJ 12934	2.00	11.00				
	105076	AI598252	Hs.37810	hypothetical protein MGC14833					5.01	
	105132	AA148164	Hs.247280	HBV associated factor					3.99	
20	105143 105158	A/368836 AW976357	Hs.24808 Hs.234545	ESTs, Weakly similar to 138022 hypotheti hypothetical protein NUF2R		16.00	11.00			
~0	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32	10.00				
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00					
	105264	AA227934		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi				10.00		
25	105298 105409	BE387790 AW505076	Hs.26369 Hs.301855	hypothetical protein FLJ20287 DiGeorge syndrome critical region gene 8	3.69			9.20		
20	105460	AW296078	Hs.271721	Homo seziens, clone IMAGE:4179986, mRNA.			7.80	5.40		
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12					
	105743	BE246502	Hs.9598	seme domain, immunoglobulin domain (lg),	3.82					
30	105782 105848	H09748 AW954064	Hs.57987 Hs.24951	B-coil CLL/lymphome 11B (zinc finger pro ESTs			27.00 7.60			
50	105891	U55984	Hs.289088	heat shock 90kD prolein 1, alpha			7.00		4.14	
	106019	AF221993	Hs.46743	McKusick-Keufmen syndromo			16.80			
	106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip			23.40			
35	106073 106126	AL157441 AA576953	Hs.17834 Hs.22972	downstreem neighbor of SON hypothetical protein FLJ13352	9.50 6.00					
55	108159	AK001301	Hs.3487	hypothetical protein FLJ 13332	0.00				3.95	
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36					6.04	
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S			13.20			
40	106300 106307	Y10043 AA436174	Hs.19114 Hs.37751	high-mobility group (nontristone chromoso		6.60			5.02	
70	106307	AA025610	Hs.9605	ESTs, Weakly similar to putative p150 (cleavage and polyadenylation specific fa		6.00			5.04	
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced					7.25	
	106440	AA449563	Hs.151393	glutamate cysteine ligase, catalytic sub			13.80			
45	106481 106588	D61594 AA243837	Hs.17279 Hs.57787	tyrosylprotein sulfotransferase 1 ESTs	4.75			10.84		
73	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr				45.60		
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00					
	108785	Y15227	Hs. 20149	deleted in lymphocytic leukemia, 1	3.00					
50	106813 106895	C05766 AK001826	Hs.181022 Hs.25245	CGI-07 protein hypothetical protein FLJ11269			11.40			
	106913	AJ219346	Hs.86178	M-phase phosphoprotein 9		6.56	0.00			
	108919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S					4.27	
	107054	A1076459	Hs.15978	KIAA1272 protein				34.80		
55	107059 107098	BE614410 AI823593	Hs 23044 Hs 27688	RAD51 (S. cerevisiae) homolog (E coli Re ESTs	4.71			24.80		
	107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)					7.05	
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60					
	107198	AV657225 D20426	Hs.9846	K/AA1040 protein		19.20				
60	107203 107217	AL080235	Hs.41639 Hs.35861	programmed cell death 2 DKFZP586E1621 protein	9.50	7.60				
	107284	MM_005629	Ha. 187958	solute carrier family 6 (neurotransmitte	2.71					
	107318	T74445	Hs.5957	Horno sapiens clone 24418 mRNA sequence			8.71			
	107516 107529	X57152 BE515065	Hs.99853 Hs.296585	fibrillarin nucleolar protein (KKE/D repeat)					4.33 4.00	,
65	107728	AA019551	Hs.294151	Homo saplens, clone IMAGE:3603838, mRNA,		10.80			4.00	•
	107851	AA022953	Hs.61172	EST		14.00	8.00			
	107901	L42612	Hs.335952	keratin 6B	3.40					
	107922 107932	BE153855 AW392555	Hs.61460 Hs.18878	lg superfamily receptor LNIR hypothetical protein FLJ21620	2.88 7.50					
70	108015	AW298357	Hs.49927	prolein kinase NYD-SP15	1.50			23,40		
	108056	AA043675	Hs.62633	ESTs				12.80		
	108075	Al867370	Hs.139709	hypothetical protein FLJ 12572				12.80		
	108187 108296	BE245374 N31256	Hs.27842 Hs.161623	hypolhetical protein FLJ11210 ESTs		7.00 6.60				
75	108305	AA071391	115.101023	9b:zm61e06.r1 Stralagene fibroblast (937		6.00		11.80		
	108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer				11.80		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428				20.80		
	108554	AA084948 AA086005		gb:zn13b09.s1 Stratagene hNT neuron (937 gb:zl84c04.s1 Stratagene colon (937204)		6.40		25.40		
80	108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE		9.60		20.40		
	108597	AK000292	Hs. 278732	hypothetical protein FLJ 20285				14.60		
	109695	AB029000	Hs.70823	KIAA1077 protein	3.00			40.00		
	108699 108700	AA121514 AA121518	Hs.70832 Hs.193540	ESTs ESTs, Moderately similar to 2109260A B c			11.00	10.00		
85	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.21					

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	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50				
	108816 108857	AA130884 AK001468	Hs,270501 Hs,62180	ESTs, Moderately similar to ALU2_HUMAN anilin (Drosophila Scraps homolog), act	4.00	7.49			
	108860	AA133334	Hs.129911	ESTs	6.09				
5	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.00				
	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69				4.00
	109121 109166	BE389387 AA219591	Hs.49767 Hs.73625	NADH dehydrogenase (ubiquinone) Fe-S pro RABS interacting, kinesin-like (rabkines	10.58				4.53
	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21	10.30	9.00			
10	109415	U80736	Hs.110826	trinucleofide repeat containing 9		51.40			
	109418	Al866946	Hs.161707	ESTs				11.00	
	109454	AA232255 AW967069	Hs.295232 Hs.211556	ESTs, Moderately similar to A46010 X-II hypothetical protein MGC5487			17.60 9.49		
	109543	AA584994	Hs.222851	ESTs .		12.67	0.40		
15	109648	H17800	Hs.7154	ESTs				10.40	
	109680	AB037734	Hs.4993	KIAA1313 protein			33.20	16.00	
	109700 109704	F09609 AI743880	Hs.12876	gb:HSC33H092 normalized Infant brain cDN ESTs			11.00	15.00	
	109792	R49525	na.12070	gb:yg61f03.s1 Soares infant brain 1NtB H			11.00	12.60	
20	109981	BE546208	Hs.26090	hypothetical protein FLJ20272	4,00				
	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80			
	110039	H11938 AA581322	Hs.21907 Hs.4213	histone acelytransferase hypothetical protein MGC16207		7.00			4.24
	110500	AA907723	Hs.36962	ESTs	4.50				4.24
25	110551	AW450381	Hs.14529	ESTs		8.60			
	110561 110854	AA379597 BE612992	Hs.5199 Hs.27931	HSPC150 protein similar to ublquitin-con	3.06	6.80			
	110886	AW274992	Hs.72249	hypothetical protein FLJ 10607 similar to three-PDZ containing protein similar to		0.00	8.80		
	110916	BE178102	Hs-24349	ESTs		6.80			
30	111003	N52980	Hs.83765	dihydrofolate reductase				16.80	
	111337	AA837396	Hs.263925	LIST-interacting protein NUDE1, rat homo	2.54			9.80	
	111434	R01608 Al476429	Hs.142736 Hs.19238	ESTs ESTs				10.40	
	111540	U82670	Hs.9786	zinc finger protein 275			15.40		
35	111597	R11499	Hs.189716	ESTs				9.20	
	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence		6,80		14,87	
	111929	AF027208 R43590	Hs.112360	prominin (mouse)-like 1 gb:yc85g02.s1 Soares infant brain 1NIB H		10.80		14,07	
	112210	R49845	Hs.7004	ESTs				10.20	
40	112244	AB029000	Hs.70823	KIAA1077 protein	2.99				
	112382	R59904 R80763	Hs.193274	gb:yh07g12.s1 Soares infant brein 1NIB H ESTs, Moderately similar to 157588 HSrel		6.60	7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00		7.10		
	112539	R70318	Hs.339730	ESTs				37.20	
45	112772	AJ992283	Hs.35437	ESTs, Moderately similar to 138026 MLN 6				14.60	
	112869 112935	BE261750 R71449	Hs.4747 Hs.268760	dyskeratosis congenita 1, dyskerin ESTs	2.73				4.83
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence				12.00	
50	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50				
50	112992 113063	AL157425 W15573	Hs.133315 Hs.5027	Homo sapiens mRNA; cDNA DKFZp761J1324 (f ESTs, Weakly similar to A47582 B-cell gr	15.00		10.89		
	113003	N39342	Hs.103042	microtubule-associated protein 1B	15.00		15.31		
	113078	T40444	Hs.118354	CAT56 protein		7.00			
55	113238	R45467	Hs.189813	ESTs				41.20	
33	113591 113702	T91881 T97307	Hs.200597	KIAA0563 gene product gb;ye53h05.s1 Soares felel liver spleen	25.00			9.40	
	113844	Al369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	20.00			13.91	
	113984	R96696	Hs.35598	ESTs		7.80			
60	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f	3.42	7.20			
00	114162 114208	AF155661 AL049466	Hs.22265 Hs.7859	pyruvate dehydrogenase phosphatase ESTs	3.42		6.74		
	114251	H15261	Hs,21948	ESTs			01.14	33.20	
	114285	R44338	Hs.22974	ESTs				13.20	
65	114313	H18456 AA782845	Hs.27946 Hs.22790	ESTs ESTs		7.80		10.00	
05	114407	BE539976	Hs.103305	Homo sapiens mRtNA; cDNA DKFZp434B0425 (f		7.00			4.14
	114560	AI452469	Hs.165221	ESTs				9.80	
	114699	AA127385		gb:zn90d09:r1 Strategene lung carcinoma		7.60			
70	114767 114793	AI859865 AA158245	Hs.154443	minichromosome maintenance deficient (S gb:ze76c03.s1 Strategene pancress (93720	3.21		6.00		
,,	114833	A)417215	Hs.87159	hypothetical protein FLJ12577			0.00	11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3				35.40	4.03
75	115097 115113	AA256213 AA256460	Hs,72010	ESTs obzz81a04.s1 Soares_NhHMPu_S1 Homo sapi				15.20	
,,,	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m					4.19
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol				12.40	
	115291 115347	BE545072 AA356792	Hs.122579 Hs.334824	hypothetical protein FLJ10461 hypothetical protein FLJ14325	25.00	7.00			
80	115414	AA662240	Hs.283099	AF15q14 protein	3.25	1.00			
	115522	BE614387	Hs.333893	o-Myc target JPO1	3.68				
	115536	AK001468	Hs.62180	arilin (Drosophila Scraps homolog), act	10.50			04.40	
	115566 115645	Al142336 Al207410	Hs.43977 Hs.69280	Human DNA sequence from clone RP11-196N1 Homo saniens, clone IMAGE:3636299, mRNA,	4.17			24.40	
85	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22548 fls, clone H			6.00		

	w	O 02/086	443						PCT/US02/12476
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81				101,0002,121,10
	115697	D31382	Hs.63325	transmembrane protesse, serine 4	62.14				
	115793	AA424883	Hs.70333	hypothetical protein MGC10753				11.80	
-	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL				9.71	
5	115892	AA291377	Hs.50831	ESTs	2.53		27.40		
	115906 115909	Al767756 AW872527	Hs.82302 Hs.59761	Homo sapiens cDNA FLJ14814 fis, clone NT ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82				
	115965	A4V072527 AA001732	Hs.173233	hypothetical prokin FLJ10970	11.02			34.29	
	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 9					8.23
10	115985	AA447709	Hs.268115	ESTs, Wealdy similar to T06599 probable	3.00				
	116090	AI591147	Hs.61232	ESTs	5.17				
	116096	AA682382	Hs.59982	ESTs		10.60	8.20		
	116127 116157	AF126743 BE439838	Hs.279884 Hs.44298	DNAJ domein-containing mijochondrial ribosomal protein S17		10.00			5.82
15	116190	A1949095	Hs.67776	ESTs, Weakly similar to T22341 hypotheti					4.06
15	116278	NM_003686	Hs.47504	exoruclesse 1	9.50				
	116335	AK001100	Hs.41690	desmocotin 3	3.67				
	116496	AW450694	Hs.21433	hypotheEcal protein DKFZp547J036		7.00			
20	116503	AI925316	Hs.212617	ESTs			32.00	12.60	
20	116674 116929	A1768015 AA586922	Hs.92127 Hs.80475	ESTs polymerase (RNA) II (DNA directed) polyp		7.60	32.00		
	116929	AR300922 AI702054	Hs.166982	phosphalidylinostiol glycan, class F		9.80			
	116993	AI417023	Hs.40478	ESTs		0.00		10.20	
	117079	H92325		gb:ys85f05,s1 Soares retina N2b4HR Homo				15.20	
25	117317	AI263517	Hs.43322	ESTs				13.40	
	117326	N23629	Hs.241420	Home saplens mRNA for KIAA1756 protein,				20.60	
	117396	W20128	Hs.296039	ESTs				10.60 16.00	
	117412	N32536 N32528	Hs.42645 Hs.146286	ESTs kinesin femily member 13A				9.11	
30	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42					4.01
-	117721	N46100	Hs.93939	EST				19.80	
	117881	AF161470	Hs.260622	butyrate-Induced transcript 1	2.71				
	117903	AA768283	Hs.47111	ESTs				17.80	4.17
35	117992	AI015709	Hs.172089	Homo saplens mRNA; cDNA DKFZp586I2022 (f				10.60	4.17
33	118013 118017	Al674126 Al813444	Hs.94031 Hs.42197	ESTs ESTs			8.82	10.00	
	118186	N22886	Hs.42380	ESTS		7.00			
	118325	AI868065	Hs.166184	Intersectin 2				13.80	
40	118367	N64269	Hs.48946	EST			6.14		
40	118368	N64339	Hs.48956	gap Junction protein, bela 6 (connexin 3	3.14		12.40		
	118472 118709	AL157545 AA232970	Hs.42179 Hs.293774	bromodomein and PHD finger containing, 3 ESTs			12.40	12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50			in the	
	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22				
45	119052	R10889		gtcyf38d02.s1 Soares fetal liver spleen		9.60			
	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome			6.60		
	119188	AI979147	Hs.101265	hypothetical protein FLJ22593				10.80 9.44	
	119243 119490	T12603 AA195276	Hs.263858	gb:CHR90123 Chromosome 9 exon II Homo sa ESTs, Moderately similar to B34087 hypot				11.80	
50	119490	AA190276 AI918908	Hs.55080	ESTs			14.80	11.00	
50	119599	W45552	112.55560	gbzc26d03.s1 Soares_senescent_fibroblas		12.60			
	119780	NM_016625	Hs.191381	hypothetical protein	17.00				
	119845	W79123	Hs,58561	G protein-coupled receptor 87	13.50				
55	119941	AA699485	Hs.58896	ESTs	7.73	8.00			
33	119994 120102	AA642402 W67353	Hs.59142 Hs.170218	ESTs K(AA0251 protein	1.10		39.60		
	120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91				•
	120294	AK000059	Hs.153881	Homo saciens NY-REN-62 antigen mRNA, par			8.20		
	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73				
60	120599	AA804448	Hs.104463	ESTs		7.00		10.00	
	120699	Al683243 AA292700	Hs.97258	ESTs, Moderately similar to \$29539 ribos ab:zs59a06.s1 NCL_CGAP_GCB1 Homos aplens		9.40		10.00	
	120715 120821	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein		5.40		13.80	
	120859	AA826434	Hs.1619	achacle-scule complex (Drosophila) homol		9.00			
65	120880	AA360240	Hs.97019	EST		15.60			
	120983	AA398209	Hs.97587	EST			27.66		
	121034	AL389951	Hs.271623	nucleoporin 50kD		22.80	20.80		
	121121 121313	AA399371 AA402713	Hs.189095 Hs.97872	similar to SALL1 (sal (Drosophila)-like ESTs		22,00		10.00	
70	121369	AW450737	Hs 128791	CGI-09 protein	25.71			10100	
, ,	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte					5.42
	121476	AA412311	Hs.97903	ESTs		8.30			
	121509	AA868939	Hs.97888	ESTs	18.50	8.59			
75	121553	AA412488 AK000552	Hs.48820 Hs.323518	TATA box binding protein (TBP)-associal	7.00				
13	121753 121838	AK000552 AA425680	Hs.323518 Hs.98441	WD repeat domain 5	7.00			10.40	
	121857	BE387162	H\$.280858	ESTs, Highly similar to A35661 DNA excis	6,00				
	121991	AA430058	Hs.98649	EST				12.20	
00	122089	AW016543	Hs.98682	hypothetical protein FKSG32			8.60		
80	122105	AW241685	Hs.98699	ESTs			6.14	10.40	
	122163	AA435702	Hs.98829	EST gb:zv60b05.r1 Soares_lestis_NHT Homo sap				10.40 18.20	
	122318	AA429743 AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50			10.00	
	122338	AA443311	Hs.98998	ESTs	4.80				
85	122414	A/313473	Hs.99087	ESTs, Wealdy similar to \$47073 finger pr		8.00			

	w	O 02/086	6443						PCT/US02/12476
	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1			8.80		
	122516	AA449352	Hs.99217	ESTs				9.40	
	122702	AI220089	Hs.99439	ESTs		9.20		10.40	
5	122852 122925	AI580056 AW268962	Hs.98992 Hs.111335	ESTs ESTs		6.80		10.40	
,	123005	AW309771	Hs.52620	integrin, bete 8		0.00	12.60		
	123044	AK001035	Hs.130881	B-cell CLL Aymphorna 11A (zinc finger pro					5.35
	123160	AA488687	Hs.284235	ESTs, Weakly similar to 138022 hypotheri			6,06		
10	123315	AA496369		gb:zy37d10.s1 Soares overy tumor NbHOT H			12.40 11.80		
10	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po ESTs, Weakly similar to unnamed protein		12.00	11.00		
	123497 123518	AA765256 AL035414	Hs.135191 Hs.21068	hypothetical protein		12300	13.00		
	123519	AW015887	Hs.112574	ESTs		12.20			
	123614	AK000492	Hs.98806	hypothetical protein			7.80		
15	123616	AA680003	Hs.109363 Hs.158549	Homo sapiens cDNA: FLJ23603 fs, clone L	03.00			10.60	
	123673 123727	EE550112 Al083986	Hs. 158549 Hs. 282977	ESTs, Weakly similar to T2D3_HUMAN TRANS hypothetical protein FLJ13490	23.00	7.00			
	123731	AA609839	10-202511	gbae62/01.s1 Stratageno lung carcinoma		1.00	9.80		
	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50				
20	123900	AA621223	Hs.112953	EST				12.80	
	124006	Al147155	Hs.270016	ESTs	97,00 3.02				
	124059 124069	BE387335 AF134160	Hs.283713 Hs.7327	ESTs, Weakly similar to S64054 hypotheti claudin 1	3.02		27.80		
	124069	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha			21.00	35.80	
25	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma		7.20			
	124297	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f				11.00	
	124305	AW963221		gb:EST375294 MAGE resequences, MAGH Homo				16.00	6.08
	124676 124874	AI360119.co BE550182	mpHs.181013 Hs.127826	phosphoglycerate mutase 1 (brain) RelGEF-like protein 3, mouse homolog				21.00	0.00
30	124904	AK000483	Hs.127020 Hs.93872	KIAA1682 protein		9,40		21.00	
50	124969	A1650360	Hs.100256	ESTs				10.80	
	125000	T58615	Hs.110640	ESTs				9.80	
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypotholi		7.60			
35	125266	W90022 T32982	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO ESTs		8.59		9.57	
33	125299 125356	AI057052	Hs.102720 Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC				14.00	
	125370	AA256743	Hs.134158	Homo sapiens, Similar to KIAA0092 gene p			8.20		
	125418	AA777690	Hs.188501	ESTs				13.20	
40	125433	AL162066	Hs.54320	hypothetical prolein DKFZp762D096		21.40 6.96			
40	125437 125446	Al909449 BE219987	Hs.140197 Hs.166982	ESTs phosphalidylinositol glycen, class F		8.80			
	125711	AA305800	Hs.5672	hypothetical protein AF140225				11.20	
	125756	BE174587	Hs.289721	growth arrest specific transcript 5					4.31
40	125757	Al274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass				15.60	
45	125769	BE270266	Hs.82128	5T4 oncoletal trophoblast glycoprolein ESTs	3.20	8.20			
	125839 125850	AW836261 W85858	Hs.337717 Hs.99804	ESTs	2.65	0.20			
	125875	H14480		gb:ym18b09.r1 Soares Infant brain 1NIB H		7.40			
	125924	BE272506	Hs.82109	syndecan 1					4.23 3.98
50	125972	A/927475 H60340	Hs.35406	ESTs, Highly similar to unnamed protein gb:yr39b04.r1 Soares fetal liver spleen				10.60	3.96
	126034 126327	AA432266	Hs.44648	ESTs		11.60		10.00	
	126345	N49713	110.71010	gb:yv23f06.s1 Soares fetal liver spicen		6.67			
	126435	AW614529	Hs.285847	CGI-19 protein				10.60	
55	126487	AA283809	Hs.184601	solute carrier family 7 (calionic amino					4.38
	128521	AJ475110 W31912	Hs.203933	ESTs gb:zc76d03.s1 Pancreatic tslet Homo sapt		6.60		14.80	
	126522 126543	AL035864	Hs.69517	cDNA for differentially expressed CO16g				14.00	4.01
	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein			7.80		
60	126605	AA676910		gb:zj65h07.s1 Soares_fetal_liver_spleen_				11.60	
	126627	AA497044	Hs.20887	hypothetical protein FLJ 10392	8.00			14.60	
	126628 126737	N49776 AW976516	Hs.170994 Hs.283707	hypothetical protein MGC10946 Homo sapiens cDNA: FLJ21354 fis, clone C	2.92				
	126795	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cor	7.50				
65	126802	AW805510	Hs.97056	hypothetical protein FLJ21634		11.60			
	126892	AF121856	Hs.284291	sorting nextn 6	3.50				
	126928	AA480902	Hs.137401	ESTs gb:zg89h10.r1 Stratagene hNT neuron (937				22.83 11.80	
	126979 126986	AA210954 AI279892	Hs.46801	sorting nexin 14				11.60	
70	126992	Al809521	113,40001	gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s				20.80	
	127066	R25066		gb:yg42c07.r1 Soares infant brain 1NtB H				27.60	
	127099	AA347668		gb:EST54026 Fetal heart II Homo saplens				21.60 11.20	
	127139 127209	AA830233 AA305023	Hs.293585 Hs.81964	ESTs SEC24 (S. cerevisiae) related gene famil	3.10			11.20	
75	127229	BE062109	Hs.241551	chloride chennel, calcium activated, fam	2.76				
	127225	AA315933	Hs.120879	ESTs				16.80	
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00				
	127444	AW978474	Hs.7560	Homo sepiens mRNA for KIAA1729 protein,		11.20		13.60	
80	127500 127524	AW971353 Al243596	Hs.162115 Hs.94830	ESTs ESTs, Moderately similar to T03094 A-kin		11.20	7.80		
50	127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53				
	127599	AA613204	Hs.150399	ESTs				13.80	
	127609	X80031	Hs.530	collagen, type tV, alpha 3 (Goodpasture				28.00	
85	127662	W80755 Al343257	Hs.8294 Hs.139993	KIAAD196 gene product ESTs				19.80	
0.5	127668	M34323/	178.139990	Loria					

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	127746	At239495	Hs.120189	ESTs				14.18	
	127812	AA741368 AA836641	Hs.291434 Hs.163085	ESTs ESTs	4.50			24.60	
	127959	AJ302471	Hs.124292	Homo sapiens cDNA: FLJ23123 ffs, clone L				9.20	
5	127960	Al613226	Hs.41569	phosphalidic acid phosphalase type 2A				16.83	
	127969	F06498	Hs,93748	Homo sapiens cDNA FLJ14676 fis, clone NT		13.60			
	128015	Z21169	Hs.334659	hypothetical protein MGC14139		7.00			
	128027	AI433721	Hs.164153	ESTs				37.40 9.60	
10	128077 128166	Al310330 NM 006147	Hs.128720 Hs.11801	ESTs interferon regulatory factor 6				9.24	
10	128226	A1284940	Hs.289082	GM2 ganglioside activator protein	19.00			0121	
	128305	Al954968	Hs.279009	matrix Gla protein				10.40	
	128341	AA191420	Hs.185030	ESTs		9.00			
1.5	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul					4,30
15	128539 128568	R46163	Hs.258618 Hs.274691	ESTs		12.60			4.56
	128568	H12912 AA933022	Hs.256583	adenylate kinase 3 Interteukin enhancer binding factor 3, 9				10.00	4.36
	128777	Al878918	Hs.10526	cysleine and glycine-rich protein 2			16.80		
	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept					4.48
20	128796	AJ000152	Hs.105924	defensin, beta 2		8.12			
	128920	AA622037	Hs.166468	programmed cell death 5					4.62 4.04
	128924 128971	BE279383 H05132	Hs.26557 Hs.107510	plakophilin 3 ESTs		12.60			4.04
	129008	AL079648	Hs.301088	ESTS		8.80			
25	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu					6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59				
	129105	Al769160	Hs.108681	Home sapiens brain tumor associated prof		8.00	6.67		
	129189	AB023179	Hs.9059 Hs.109643	KIAA0952 protein	4.00	8.00			
30	129229 129241	AF013758 A)878857	Hs.109643	polyadonytate binding protein-interactin hematological and neurological expressed	4.00				4.06
50	129300	W94197	Hs.110165	ribosomei prolein L26 homolog	2.55				
	129404	A1267700	Hs.317584	ESTs	18.00				
	129457	X61959	Hs.207776	aspartylg/ucosaminidase	6.50				
25	129466	L42583	Hs.334309	keralin 6A	12.94			44.00	
35	129494 129605	Al148976	Hs.112062	ESTs keratin 16 (focal non-epidermolytic palm				11.00	4.46
	129641	AF061812 AI911527	Hs.115947 Hs.11805	FSTs				12.00	4.40
	129665	AW163331	Ha.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic relic					4.70
	129703	BE388665	Hs.179999	Homo sarriers, clone IMAGE 3457003 mRNA					4.02
40	129720	AA156214	Hs.12152	APMCF1 protein	0.50				5.71
	129748 129890	M16707 Al868872	Hs.123053 Hs.282804	H4 histone, family 2 hypothetical protein FLJ22704	3.50				4.21
	129896	BE295568	Hs.13225	UDP-GalthetaGlcNAc bela 1,4- galactosylt	2.56				7.21
	129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein					4.03
45	130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34			7.00		
	130026	T40480	Hs.332112	EST		6.40			4.65
	130080	X14850	Hs.147097 Hs.172665	H2A histone family, member X methylenetetrahydrofolate dehydrogenase	2.74				4.00
	130149 130285	AW067805 AA063546	Hs.75981	ublquifn specific protease 14 (IRNA-gua	2.74		7.40		
50	130441	U83630	Hs.155637	protein kinase, DNA-activated, catalytic					3.91
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87				
	130500	AB007913	Hs.158291	KIAA0444 protein			40.40	9.60	
	130524 130541	U89995 X05608	Hs.159234 Hs.211584	forkhead box E1 (thyroid transcription f neuroflament, light polypeptide (68kD)			13.40 8.20		
55	130553	AF062649	Ha.252587	pituitary tumor-transforming 1			0.20		6.06
55	130567	AA383092	Hs.1608	replication protein A3 (14kD)			7.00		
	130577	M69241	Hs.162	insulin-1ke growth factor blading prote	3.04				
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87				
60	130648	AI458185	Hs.17298	hypothetical protein MGC2376				16.20 17.80	
00	130697 130744	L29472 H59696	Hs.1802 Hs.18747	major histocompatibility complex, class POP7 (processing of precursor, S. cerevi				17.00	5.28
	130800	Al187292	Hs.19574	hypothetical protein MGC5469					4.43
	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84				
	130869	J03626	Hs.2057 -	undine monophosphele synthetase (orotat					4.92
65	130925	AF093419 W17044	Hs.169378 Hs.327337	multiple PDZ domain protein		12.40		9.60	
	130994 131028	W17044 AI879165	Hs.32/33/ Hs.2227	ESTs CCAAT/enhancer binding protein (C/EBP),	10.21	12.40			
	131031	NM 001650	Hs.288650	aguaporin 4	TOTAL			9.80	
	131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,				9.60	
70	131058	W28545	Hs.101514	hypothetical protein FLJ10342				17.00	
	131090	Al143139	Hs.2288	visinin-like 1	2.74		8.80		
	131112 131148	H15302 AW953575	Hs.168950 Hs.303125	Homo saplens mRNA; cDNA DKFZp566A1046 (f p53-induced protein PIGPC1	3.12		0.00		
	131185	BE280074	Hs.23960	cyclin B1	3.07				
75	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07				
	131219	W25005	Hs.24395	small inducible cytokine subfemily B (Cy	2.87				
	131257	AW339037	Hs.24908	ESTs			19.20	14.67	
	131375 131460	AW293165 NM 003729	Hs.143134 Hs.27076	ESTs RNA 3'-terminal phosphale cyclase	3.50		19.20		
80	131460	At521663	Hs.334644	hypothetical protein FLJ14668	15.00				
-	131510	BE245374	Hs.27842	hypothetical protein FLJ11210			7.80		
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom			7.00		
	131786	BE000971	Hs.306083	Novel human gene mapping to chomosome 22	2.65			35.20	
85	131839 131843	AB014533 AA192315	Hs.33010 Hs.184062	KIAA0633 protein putative Rab5-interacting protein				30.20	4.11
0.5	101040			potation - appreciation of province					

	W	O 02/086	443						PCT/US02/12476
	131877	J04088	Hs.156346	topolsomerase (DNA) II atpha (170kD)	19.00				
	131885 131921	BE502341 AA456093	Hs.3402 Hs.34720	ESTs ESTs	6.48		8.40		
	131945	NM 002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00		0.40		
5	131958	NM_014062	Hs.3566	ART-4 protein					3.82
	131965	W79283 AW247017	Hs.35962 Hs.36978	ESTs melanoma antigen, family A, 3	3.03	9.80			
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30	5.00			
10	132109	AW190902	Hs.40098	cystoine knot superfamily 1, BMP antagon	21.00				
10	132114	NM_006152 AA315805	Hs.40202 Hs.94560	lymphoid-restricted membrane protein desmoclein 2		8.40			12.25
	132164	AI752235	Hs.41270	procollagen-lysine, 2-axoglutarate 5-dio	2.70				1223
	132180	NM_004460	Hs,418	fibroblest activation protein, alpha	2.71				
15	132181 132182	AW961231 NM_014210	Hs.16773 Hs.70499	Homo sapiens clone TCCCIA00427 mRNA sequi ecotropic viral integration site 2A	3.83			13.20	
13	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50			13.20	
	132277	AK001745	Hs.184628	hypothetical protein FLJ10683	4.50				
	132328	NM_014787 AK001680	Hs.44896 Hs.30488	DnaJ (Hsp40) homolog, subfamily B, membe DKFZP434F091 protein				9.20 19.80	
20	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALUS_HUMAN A			8.60	10.00	
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso			27.40		
	132543 132544	BE568452 L19778	Hs.5101	prolein regulator of cytokinesis 1 H2A histone family, membar P	4.38	7.00			
	132550	AW969253	Hs,51011 Hs,170195	bane marphagenetic protein 7 (osteogenic	2.64	7.00			
25	132552	BE621985	Hs.296922	thiopurine S-methyltransferase				15.83	
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	4.95		6.60		
	132617 132638	AF037335 AI796870	Hs.5338 Hs.54277	carbonic anhydrase XII DNA segment on chromosome X (unique) 992	4.50	8.20			
••	132653	Z15008	Hs.54451	laminin, gamme 2 (nicein (100kD), kalini	4.38				
30	132669	W38586	Hs.293981	guenine nucleolide binding protein (G pr	4.60				4.36
	132710 132771	W74001 Y10275	Hs.55279 Hs.56407	serine (or cysteine) proteinasc inhibito phosphoserine phosphetase	3.71				
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,				9.48	
35	132833	U78525	Hs.57783	eukaryotic translation initiation factor				12.00	5.83
33	132892 132906	AW834050 BE613337	Hs.9973 Hs.234896	tensin geminin	3.09			12.00	
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT					3.87
	132962 132990	AA576635 X77343	Hs.6153 Hs.334334	CGI-48 protein transcription fector AP-2 alpha (activat	3.50 6.18				
40	132990	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19				
	133000	AL042444	Hs.62402	p21/Cdp42/Rac1-ectivated kinase 1 (yeast	2.96				
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p chaperorin containing TCP1, subunit 2 (b	2.55				4.00
	133083 133086	BE244588 L17131	Hs,6456 Hs,139800	high-mobility group (nonhistone chromoso					8.96
45	133134	AF198620	Hs.65648	RNA binding most protein BA					4.28
	133155	M58583 X91662	Hs.662 Hs.66744	cerebellin 1 precursor twist (Drosophile) homolog (acrocephalos	3.00			10.80	
	133204	BE267898	Hs.254105	enolase 1, (alpha)	3.00				4,63
	133412	U41493	Hs.73112	guarine nucleotide binding protein (G pr		12.50			
50	133421 133451	AF134160 AW970028	Hs.7327 Hs.73818	cleudin 1 ubiquinol-cylochromo o reductase hinge p	2.85				4.66
	133453	A1659306	Hs.73826	protein tyrosine phosphalase, non-recept		6.80			4,00
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14				
55	133506 133615	BE582958 M62843	Hs.74348 Hs.75236	hypothetical protein MGC14353 ELAV (embryonic lethal, abnormal vision,				17.80	4,55
55	133627	NM_002047	Hs.75280	civovi-tRNA synthetase					4,85
	133649	U25849	Hs.75393	acid phosphatase 1, soluble				****	6.34
	133669 133749	NM_006925 L20852	Hs.166975 Hs.10018	splicing factor, arginine/serine-rich 5 solute carrier family 20 (phosphole tren			6.11	14.00	
60	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-			0		4.91
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5 NIPSNAP, C. elegans, homolog 1	3.07				
	133946 133973	AJ001258 N55540	Hs.173878 Hs.78026	NIPSNAP, C. elegans, homolog 1 ESTs, Weakly similar to similar to ankyr				13.00	4.60
	134047	BE262529	Hs.78771	phosphoglycerate kinase 1				10.00	3,85
65	134096	BE513171	Hs.79086	milochondrial ribosomal protein L3	2.56		8.20		
	134107	NM_005629 AW449809	Hs.187958 Hs.79150	solute carrier family 6 (neurotransmitte chaperonin containing TCP1, subunit 4 (d			8.20		4.08
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00				4.00
70	134160	T98152	Hs.79432	fibrillin 2 (congenital contractural ara			24.60		6.71
/0	134168 134185	AA398908 AA285136	Hs.181634 Hs.301914	Homo sapiens cDNA: FLJ23602 fis, clone L neuronal specific transcription factor D				14.74	6.71
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40			
	134272	X76040	Hs.278614	prolesse, serine, 15	4,50	0.00			
75	134276 134353	BE083936 AL138201	Hs.80976 Hs.82120	antigen identified by monoclonal antibod nuclear receptor subfamily 4, group A, m		9.00		16.40	
, ,	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyttransfer	2.80				
	134380	AU077143 H53497	Hs.179565 Hs.83006	minichromosome maintenance deficient (S.	4.68				3.84
	134423	H53497 AA279661	Hs.83006 Hs.83753	CGI-139 protein small nuclear ribonucleoprotein polypept					5.81
80	134470	X54942	Hs.83758	CDC28 protein kinase 2					4.21
	134498	AW246273	Hs.84131	threonyl-IRNA synthelasa		13,60			7.30
	134502	BE148534 NM_002757	Hs.84168 Hs.250870	UV-B repressed sequence, HUR 7 mitogen-activated protein kinase kinase		10.00		9.70	
0.5	134548	N95406	Hs.333495	Deleted in split-hand/split-foot 1 regio				-	4.63
85	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00				

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	134724	AF045239	Hs.321576	ring finger protein 22				12.00	
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00				
	134781	AA374372	Hs.89626	perathyroid hormone-like hormone			25.20		
5	134806	AD001528 BE268326	Hs.89718	Spermine synthase S-aminoloxidazole-4-carboxamide ribonucle					4.58
,	134859	D26488	Hs.90280 Hs.90315	KJAA0007 protein			6.20		4.79
	134891	R51083	Hs.90787	ESTs			7.40		
	134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00		7.40		
	134993	BE409809	Hs.301005	puring-rich element binding protein B					4.48
10	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50				
	135080	AI761180	Hs.94211	rod1 (required for cell differentiation,	5.00				
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00			
	135145	AW014729	Hs.95262	nuclear factor retated to kappa B bindin					4.01
15	135184	U13222	Hs.96028	forkhead box D1	40.50		7.00		
13	135286	A1583187 AW023482	Hs.9700 Hs.97849	cyclin E1 ESTs	13.50 6.46				
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to	0.46	8.80			
	135355	AK001652	Hs.99423	ATP-dependent RNA holicase	10.00	0.00			
	135371	NM_006025	Hs.997	protease, serine, 22	8.00				
20	135393	L11244	Hs.99886	complement component 4-binding protein,				14.60	

TABLE 50 force the accordance for them for the profiting being subjected. For table 55. For each probability on how to the 50 gave observement from which his originated levels were forced from the his his originated levels were forced from the his proposed obtained from the forced for obtained 50 and mRMs. These sequences were distincted table on to expended the forced from the f

	"Accessio	n" oolunrn.	
30		Unique Ecs pro ber: Gene duster no :: Genbenk ecces	
	Pkey	CAT number	Accessions
35	117079 124305 101502 109792 126034	1621717_1 242183_1 182028 754958_1 1598157_1	H82255 T971/35 AVMSS221 AVS44670 AVS44671 H593331 AVMSS221 AVS44670 AVS44670 H593331 AVMSS235 FIGUR A REGION OF HIGH TO THE
40	102768 126345 127066 127099 119243	44641_1 1653833_1 1703458_1 244301_1 1774795_1	U82021 H60077 NGFT3 1446919 W03910 F03508 EXD 144 F20140 2X3045 T26031 H70014 F03140 2X3045 T26031 T36041 H70014 F03140 H70014 F03506
45	125875 112054 126979 126992	1566433_1 1538292_1 171411_1 880655_1	H14480 N86255 R45500 F16459 AA21056 AA2100T A8565251 H107174 Z42556
50	122318 114699 114793 108305 108393	292419_1 135322_1 150742_1 111550_1 113411_1	AM2011-S M402154 AM2128 RYSSEA MA12404 AM3026 AM30254 M003021 AM01154 N003021 AM003081 AM01154 N003021 AM003081 AM01154 N003024 M001158 M01496
55	100867 123731 109700 120715 113702 115113	tigr_HT4586 genbark_AA6098 genbark_F09609 genbark_AA2927 genbark_T97307 genbark_AA2564	9 F09609 0 AA292700 1 T97307
60	101045 108554 108573 119052 126522	entrez_J05614 genbank_AA0849 genbank_AA0860 149538_1 416020_1	J06614 948 AA084948
65	126605 103768	439280_1 46922_1	AMERIERI O ANTRIESS ANTRIESS WESSED WESTER SINGUI ANTRIESS ANTRIESS WESSED WESTER SINGUI ANTRIESS ANTRIESS ANVESTER ANVESTER ANTRIESS ANTR
70			HAMBB HEART THREE WHITED AND ENDER ENDER AND ENDER ENDER AND ENDER ENDER ENDER ENDER ENDER ENDER
75			AGSSTS A-MARYS ANAMERYS ANAMERS ANAMESSES ANAM
80			ARRACES FAMILISON AND MITTERET AND MODES ON LOSSED AND STATE AND AND THE AND
85			AW10S577 A/954937 AIB11070 A4907422 AW514437 A453646) A4916977 AW517122 A4974537 A4975649 AW517139 F431737 W07688 A4153645 A4576894 A4469273 F32267 W35300 A4021161 N66610 A4406524 A4062553 A4436901 H08665 H15975 N40310

WO 02/086443 PCT/US02/12476

AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA578994 AA157491 AB40535 AA604210 AA089814 AA350421 N86243 N84281 AA203340 N95174 N86374 AA191089 AW247981 AA246013 AA693111 AA972598 AW258594 AA375595 T1219 W25185 AW243849 A288262 AA43599 W12606 A158566 AW246079 R15826 A

- 119599 geribank_W45552 W45552 5 112382 genbank_R59904 R59904 105264 geribank_AA227934 AA227934 entrez_A28102 A28102 714071_1 AA496369 AA496646 100071 123315
- 10 Table SA ahous 99 genes up-regulated nonmolers with lang circon relative to smokers with lang career. These genes were selected from 59900 problems on the Exp.(All-print): Hu30 Concor) parry. Gene expression data for each problems obtained from the analysis was expressed as average intensity (AI), a normalized value reflecting then delivate level of PMPA expression.
- 15

Flags

Livigat Cas produced lidestiffer number

Control

Livigate Case

Livigate Case

Livigate number

Livigate

Livigate 20

	Pkey	ExAcon	UnigenelD	Unigene Tille	R1	R2
25	100971	BE379727	Hs.83213	fally acid binding protein 4, adipocyte		3.64
	101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
	101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
	101304	AA001021	Hs.6685	Ihyroid hormone receptor interactor 8		12.00
	101806	AA586894	Hs.112408	\$100 celcium-binding protein A7 (psorias		2.68
30	101972	S82472	110.112.00	gb:beta -pol=DNA polymerase beta (exon e		2.11
-	102274	U30930	Ha.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
	102394	NM .003816		e disintegrin and metalloproteinase doma	7.50	
	102832	U92015		gb:Human clone 143789 defective mariner	13.50	
	103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
35	103439	X98266	110.10.10	gb:H.sapiens mRNA for ligase like protei		2.50
00	103563	L02911	Hs.150402	activin A receptor, type I	9.00	
	103857	AJ076795	Hs.45033	lacrimel proline rich protein		3.94
	104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group 1, m		12.66
40	104907	AA055829	Hs.196701	ESTs, Wealty similar to ALU1_HUMAN ALU	16.50	
	106131	BE514788	Hs.296244	SNARE protein		2.17
	106672	H47233	Hs.30643	ESTs	7.00	
	106872	T56887	Hs.18282	KIAA1134 prolein	11.50	
	106960	AA156238	Hs.32501	ESTs		2.38
45	106971	Z43848	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	9.50	
	107982	AA035375	Hs.57887	ESTs, Wealdy similar to KIAA0758 protei		2.95
	108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
	106599	AB018549	Hs.89328	MD-2 protein	13.00	
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti		2.40
50	109247	AA314907	Hs.85950	EST\$	7.00	
	109630	R44607	Hs.22872	ESTs		5.00
	110193	Al004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
	110234	H24458	Hs.32085	EST	16.50	
	110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
55	110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
	111057	T79639	Hs.14629	ESTs	16.50	
	111950	AF071594	Hs.110457	Wolf-Hirschhom syndrome candidate 1	11.00	
	112291	R53972	Hs.26026	ESTs		3.00
60	112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
60	113009	T23699	Hs.7246	ESTs		4.50
	113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
	113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	3.82
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		2.21
65	113121	T48011	Hs.8764	EST	19.50	221
03	113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	2.65
	113757	AA703095	Hs.18631	ESTs hypothetical protein FLJ23293 similar to	6.00	2.60
	113848	W52854	Hs.27099 Hs.28529	chromosome 12 open reading frame 2	0.00	6.00
	113884	Al333076	Hs.83623	nuclear receptor subfamily 1, group 1, m		4.63
70	113936 114875	W17056 AA235609	Hs.236443	Home sapiens mRNA; cDNA DKFZp664N1063 (7.00
70	114987	AA251016	Hs.87808	EST		6.00
	115460	AW958439	Hs.38613	ESTs		2.27
	115722	W91892	Hs.59609	ESTs		9.00
	116261	AA481788	Hs.190150	ESTs	9.50	5.00
75	116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
15	116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
	117178	H98675	Hs.269034	ESTs	1.00	2.68
	117757	AF088019	Hs.46732	EST	7.50	
	118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16,50	
80	118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2,50
	118657	AJ822106	Hs.49902	ESTs		2.39
	120328	AA923278	Hs.290905	ESTs. Weakly similar to protesse (H.sapi		3.50
	120404	AB023230	Hs.96427	KIAA1013 prolein	7.00	
	120524	AA261852	Hs.192905	ESTs	6.00	
85	120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	17.92	

	121558						
		AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sap		2.95	
	121676	H56037	Hs.108146	ESTs	10.00		
	121936	A)024600	Hs.98612	ESTs	15.00		
_	121938		Hs.98610	ESTs	14.00		
5	122177	AA435789	Hs.98833	EST	8.93		
	123442	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.04		
	123551	AA608837		gb:af03h12.s1 Soares_testis_NHT Homo sap	11.50		
	123756	AA609971	Hs.112795	EST	11.00		
	123861	AA620840		gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50	
10	124371	N24924	Hs.188601	ESTs	6.50		
	127477	BE328720	Hs.280651	ESTs		4.33	
	127591	Al190540	Hs.131092	ESTs		3.02	
	128252	AA455924	Hs.192228	ESTs	7.00		
	128426	A1265784	Hs.145197	ESTs		2.08	
15	128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT		2.11	
	128945	Al990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00		
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	15.50		
	129235	AW977238	Hs.126084	KIAA1055 protein		4.25	
	129506	AB020584	Hs.11217	KIAA0877 protein	6.50		
20	129595	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9		10.00	
	130160	AA305688	Hs.267695	UDP-Gal:betaGloNAc beta 1,3-galactosyllr	20.00		
	130340	D82326	Hs.239106	solute carrier family 3 (cystine, dibasi)	11.50		
	131220	AB023194	Hs.300855	KJAA0977 protein	17.50		
	131430	AJ879148	Hs.26770	fatty acid binding protein 7, brain	6.10		
25	132114	NM_006152	Hs.40202	hymphoid restricted membrane protein		6.15	
	132458	AA935315	Hs.48965	Homo segiens cDNA: FLJ21693 fis, clone C		5.58	
	132647	NM 008927	Hs.54432	sialytransferase 4B (bela-galactosidase	7.50		
	132655	D49372	Hs.54460	small Inducible cytokine subfamily A (Cy		2.53	
	132682	AI077500	Hs.54900	serologically defined colon cancer antiq		2.50	
30	132747	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein		2.83	
	132812	R50333	Hs.92186	Leman colled-coll protein		3.82	
	133337	AF085983	Hs.293676	ESTs		5.00	
	133876	AL134906	Hs.771	phosphorylase, glycogen; liver (Hers dis		3.00	
	134119	AW157837	Hs.79226	fesciculation and elongation protein zet		2.06	
35	134464	AA302983	Hs.239720	CCR4-NOT transcription complex, subunit		2.27	
	134542	M14156	Hs.85112	insulin-like growth factor 1 (somalomedi		11.50	
	135002	AA448542	Ha.251677	Ganligen 7B	87.00		
	135305	AA203555	Hs.98288	Homo sapiens cDNA FLJ14903 fis, clone PL		6.50	

TABLE 58 show the acception numbers for those primedrys leadings uniqued to 6 Table 54. For each systems on when little 16 systems during multiple from incide to 16 table 16 systems during multiple from incide to 16 table 16 systems of 16 table 16 t 45

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

Pkey CAT number Accessions

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20375. 1 AA100796 AP000599 AA019520 AA019596 AA100849 AA100849 AA108347 AA126399 AA017311 AA017332 AA085214
2030. 1 COSSESS SH 1114
2030. 1 COSSESS SH 1124
2030. 1 COSSESS SH 108562 55

103439 123551 123861 102832 101972 genbank AA412497 AA412497 WO 02/086443
Table 7A allowed Spience cover-regulated in non-sections with lang cancer relative to structers with lang cancer. These garass were selected from SHOS problems on the ExamPlyment's MLOS procerup many. Gene expression data for each problems dollaring from this analysis was expressed as everage laterally (Al), a normalized value refloring

	Eos/Affy the rolat	metrix Hu03 Ge ive level of mRf	nechip array. IA expression.	Gene expression data for each probeset obtained for	om this analysis v	vas expressed as average intensity (Al), a normalized value reflecting
5	Pkey: ExAcon: Unigene	Exemple	Eos probeset i ar Accession n number	dentifier number ember, Genbank accession number		
	Unigene	Title: Unigene	gene title			
10	R1: R2:		centile of Al fo			of Al for samples from non-smokers with adenocarcinoma, average of Al for samples from non-smokers with squamous cell
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
15	100187	D17793	Hs.78183	aido-kelo reductase family 1, member C3		164.10
	100390	£82343 X00356	Hs.18551 Hs.37058	neuroblastoma (nerve tissue) protein calcitonin/calcitonin-retated polypeptid	102.40	77.40
	100370	BE379727	Hs.83213	fatly acid binding protein 4, adipocyte	463.80	
0.0	101046	K01160		(NONE)	672.00	*
20	101066 101175	AW970254 U82671	Hs.889 Hs.36980	Charot-Leyden crystal protein melanoma antigen, family A, 2	66.00	77.20
	101497	W05150	Hs.37034	homeo box A5	62.80	17.20
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00	
25	101677	NM_000715 M88700	Hs.1012 Hs.150403	complement component 4-binding protein, dops decarboxytase (aromatic L-amino aci	186.20 80.08	
23	101941	S77583	118.100403	gb:HERVK10/HUMMTV reverse transcriptase	99.20	
	102125	NM_006456	Hs.288215	slalyltransferase		103.10
	102242	U27185 U37055	Hs.82547 Hs.278657	retinoic acid receptor responder (tazaro macrophage stimulating 1 (hepatocyte gro	67.00 71.60	
30	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	71.00	69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00	
	102669 102796	U71207 AL079646	Hs.29279 Hs.107019	eyes absent (Drosophila) homolog 2 symplekin; Hunitrigtin interacting protet		65.70 58.80
	102329	NM 006183	Hs.80962	neurotensin		268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	
	103242	X76342	Hs.389	a/cohol dehydrogenase 7 (class IV), mu o		212.10
	103260 103351	X78416 X89211	Hs.3155	casain, alpha gb:H.sapiens DNA for endogenous retrovir	64.60	130.70
40	104212	AB002298	Hs.173035	KIAA0300 protein	66.80	
40	104252	AF002246	Hs.210363	cell adhesion molecula with homology to	63.80	
	104258 105024	AF007216 AA126311	Hs.5462 Hs.9879	solute carrier family 4, sodium bicarbon ESTs	94.40 68.20	
	106260	Al097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		74.60
45	106440 106566	AA449563 BE298210	Hs.151393	glutamate-cysteine līgase, catalytic sub gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20	71.10
73	106605	AW772298	Hs.21103	Home sapiens mRNA; cDNA DKFZp564B076 (fr	83.80	
	106614	AA648459	Hs.335951	hypothetical protein AF301222		62.30
	106654 106999	AW075485 H93281	Hs.286049 Hs.10710	phosphoserinė aminotransferasa		202.40 89.60
50	108700	AA121518	Hs.193540	hypothetical protein FLJ20417 ESTs, Moderately similar to 2109260A B c		66.40
	108810	AW295647	Hs.71331	hypothetical protein MGC5350		95.50
	108857 109597	AK001468 AA989362	Hs.62180 Hs.293780	anilin (Drosophila Scraps homolog), act ESTs	85.00	63.40
_	109691	T65568	Hs.12860	EST8	00.00	58.70
55	109704	AI743880	Hs.12876	ESTs		60.60
	110942 111722	R83503 R23924	Hs.28419 Hs.23596	ESTs FST	76.40 74.60	
	112891	T03927	Hs.293147	ESTs. Moderately similar to A46010 X-II	64.80	
CO	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		76.70
60	113073 114251	N39342 H15261	Hs.103042 Hs.21948	microtubule-associated protein 1B ESTs	127,20	120.20
	115230	AA278300	Hs.124292	Homo saplens cDNA: FLJ23123 fis, clone L	174.00	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461		91.00
65	115815 115909	AW905328 AW872527	Hs.180842 Hs.59761	ribosomal protein L13 ESTs, Weakly similar to DAP1_HUMAN DEATH	66.40	226.60
05	115965	AA001732	Hs. 173233	hypothetical protein FLJ10970	82.80	220.00
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093		361.60
	116552 116571	D20508 D45652	Hs.164649	hypothetical protein DKFZp434H247 gbt:HUMGS02848 Human adult lung 3' direct	69.00 64.20	
70	118466	N66741		gb:yz33g08.s1 Morton Fetal Cochies Homo	04.20	63.50
	120484	AA253170	Hs.96473	EST	81.60	
	120983 121034	AA398209 AL389951	Hs.97537 Hs.271623	EST nucleoporin 50kD		81.10 66.20
	121423	AW973352	Hs.290585	ESTs	64.40	00.20
75	122553	AA451884	Hs.190121	ESTs		60.40
	122946	AI718702 AA487200	Hs.308026	major histocompatibility complex, class	188.60	80.20
	124472	N52517	Hs.102670	gbtab19f02.s1 Stratagene lung (937210) H EST	71.00	00.20
0.0	124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino act	. 120	104.90
80	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
	125731 - 125747	R61771 NM 002884	Hs.26912 Hs.865	ESTs RAP1A, member of RAS oncogene family	69.00	69.90
	126020	H79863	Hs.114243	ESTs		62.40
85	126547 126966	U47732	Hs.84072	transmembrane 4 superfamily member 3		62.80 60.10
0,5	120900	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra		00.10

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	127472	AA761378	Hs.192013	ESTs	70.20		
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00		
	127742	AW293496	Hs.180138	ESTs	85.20		
_	127987	Al022103	Hs.124511	ESTs	96.60		
5	128233	AW889132	Hs.11916	ribokinase		78.90	
	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90	
	128766	AW160432	Hs.296460	cranigfacial development protein 1	66.80		
	129014	AW935187	Hs.170162	KIAA 1357 protein		58.53	
	129215	AB040930	Hs.126085	K!AA1497 protein	64.20		
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80		
	130385	AW067800	Hs.155223	stanniocalcin 2		139.60	
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (hcart)		64.60	
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40		
	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20		
15	131775	AB014548	Hs.31921	KIAA0648 protein	97.80		
	132240	AB018324	Hs. 42676	KJAA0781 protein		71.00	
	132856	NM 001448	Hs.58367	glypican 4		88.40	
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20		
	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30	
20	133818	AJ110684	Hs.7645	fibringgen, B beta polypeptide	341.00		
	134264	AF149297	Hs.8087	NAG-5 protein		64.30	
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53	
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00		
	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2			
25	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30	
	135056	N75765	Hs.93765	lipome HMGIC fusion pertner			
	135309	AJ564123	Hs.42500	ADP-ribosylation factor-like 5	70.40		
25	134395 135047 135056	AA456539 AL134197 N75765	Hs.8262 Hs.93597 Hs.93765	lyscsomal-associated membrane protein 2 cyclin-dependent kinase 5, regulatory su lipome HMGIC fusion pertner	71.40 70.40	75.80 108.30	

TABLE 17 a horse the occasion combine for those primately solving subjected for 14 de 17. For each packed was the less of the packed colours marked for marked the opposition of the colours of the colou 30

35 Pkey: Unique Eos probesel identifier number CAT number: Gene diuster number Accession: Genbank eccession numbers

Phev CAT number Accessions 40

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103207 30635_4 X72790 106566 120358_1 BE298210 AIG72315 AW086489 BE286417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI395742 AI039658 A1885095 A1476470 A1287650 A1885299 A1985381 AW592624 AW340136 A1266556 AA456390 A1310815 AA464951

genbenk_D45652 genbenk_N66741 enirez_K01160 K01160 116571 45 118466 101046 N66741 101941 enirez_S77583 S77583 103351 entrez_X89211 X89211 123130 genbenk_AA487200 AA487200

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PCT/US02/12476

Table 8A shows 1720 games either up or down-regulated in lung humos or chronically diseased lung relative to a broad colloction of over 40 distinct names to Chronically diseased lung samples represent chronic non-malguant lung diseases such as thouse, emphysema, and broadfills. These genes were selected into 3849 probated so in the SouthApproach Fuzil Conscious parray, Gene operation data for each probated solar late Conscious parray. Gene question state for each probated solar late Conscious parray (Sen expression data for each probated solar late for this sandys laws expressed as exercise literately (AI), a normalized value reflecting the relative level of mRNA expression.

5 Pkey: Unique Eos probesel identifier number ExAcon: Exemplar Accession number, Genbank accession number

UnigenetD: Unigene number Unigene Title: Unigene gene fille

10 Congenie gate and Al for lung tumors divided by 90th percentile of Al for normal lung 70th percentile of Al for chronically diseased tung divided by 90th percentile of Al for normal lung Rf R2-Pkey Evacon UnigenetD Unigene Title D1 D2 15 300097 41916973 He.213603 ESTS AW189787 Hs 147474 0.55 0.54 300117 ESTS A1686661 Hs.218286 FSTs 4.26 5.44 300197 300201 AI308300 gb:ta90c06.x1 NCI_CGAP_Bm20 Homo saplen 0.62 0.83 300225 A1989963 Hs.197505 ESTs 1 68 175 20 300247 AW274682 Hs.161394 ESTs 1 08 2 28 300256 41469095 Hs 298241 Transme embrane protease, serine 3 0.86 5.80 a no 300337 41707881 Hs 202090 **ESTs** gb:HSC0FB121 normalized infant brain cDN 4,18 12.78 300362 742308 300374 AI859947 Hs.314158 ESTs 2 99 4 38 25 300387 AW270150 Hs.254516 ESTs 1 50 2.53 300440 AJ421541 Hs.146164 ESTs 3 98 5 25 300441 P10367 Hs.307921 EST, Weakly similar to Z232, HUMAN ZINC F 3 18 6.80 hypothetical protein FLJ12401 hypothetical protein FLJ20401 hypothetical protein FLJ11191 0.43 300449 41362967 Hs 132221 300469 AW135830 0.16 0.83 Hs.233955 30 300552 X85711 Hs.21838 4.10 0.75 300627 W27363 gb:ab37d01.r1 Stratagene HeLa cell s3 93 4.60 12 60 300630 AW118822 Hs.128757 ESTs 2.91 5.86 300716 AI216113 Hs 126280 hypothetical protein FLJ23393 KIAA 1542 protein KIAA 1527 protein 1 00 0.02 1.82 1 71 300738 41623332 Hs.130541 35 AA235361 4.48 8.22 300777 He 96840 Hs 188270 FSTs 1.29 1.18 300790 41492471 300832 AI688147 Hs.220615 ESTs, Weakly similar to T03829 transcrip 5.51 8 56 300836 Z44942 Hs-22958 calcium channel alpha2-della3 subunit 4 00 6.34 300838 AJ582897 Hs.192570 hypothetical protein FLJ22028 1 70 2.81 40 300878 AW449802 Hs 285901 Homo sepiens cDNA FLJ20428 fis, clone KA ESTs, Wealthy similar to T17233 hypotheti gb:ab03a10.s1 Stratagene fetal refina 93 4.56 7.91 2.23 1,58 300897 ALEGO356 Hs 127804 44504860 2.13 3.50 300926 300960 AI041019 Hs.152454 ESTs 2.74 4,46 300961 AW204069 Hs.312716 ESTs, Weakly similar to unnamed protein 1.00 1.00 45 300962 AA593373 Hs.293744 ESTS 1.46 1 51 300967 AA585209 Hs 269439 EST 0.39 1.30 Hs.148590 ESTs, Weakly similar to AF208846 1 BM-00 1.49 300987 AW450840 0.16 0.37 300988 41927208 Hs 208952 301050 AW136973 Hs.288516 ESTs, Weakly similar to S69890 mitogen ? 3.23 1 94 50 301098 AA877570 Hs.185918 ESTs 6.76 14 28 301157 AA729905 Hs.231916 ESTs 3 16 8.85 301162 Al142118 Hs.129004 ESTs 1.68 7.18 4,40 6.42 301170 AA737594 Hs 247808 301192 Hs.121188 8.33 11.59 A1808751 **ESTs** 55 301193 AA758115 Hs.128350 ESTs, Weakly similar to JC5423 2-hydroxy 4 35 7 78 301287 AW297782 Hs.255690 FSTs 1.58 1 61 301281 AA843986 Hs.190586 ESTs 2 19 1 78 301341 AIR19198 Hs.208229 ESTs 0.76 0.76 1.00 1.81 301382 AA912839 Hs.163389 **ESTs** 60 Hs.126830 1.48 1.51 301407 AW450466 **FSTs** AA975688 Ha 159955 0.51 1.46 301452 **ESTs** 301483 AW272467 Hs.254855 Untilled 2.40 5.02 301494 A)678034 Hs.131099 FSTs 2.79 3.41 301521 AI733621 Hs.133011 zinc finger protein 117 (HPF9) 0.67 0.67 65 301531 A1077462 Hs.134084 **ESTs** 2.52 Hs.73737 splicing factor, arginine/serline-rich 1 ESTs, Moderately similar to G01251 Rar p 7.41 11 92 301580 41878959 Hs.27453 10.70 301676 F05865 Hs.108323 ubiquitin-conjugating enzyme E2E 2 (homo 2.70 4 22 301690 301718 F07744 Hs.7987 DKFZP434F162 proh 4 20 8 78 70 AA384252 Hs.286132 D15F37 (pseudogene) an/lin (Drosophila Scraps homotog), act integrin, alpha 2 (CD49B, alpha 2 subuni 5.93 7.04 301804 AA581004 Hs 62180 1 70 0.76 1.58 301822 X17033 Hs 271986 R20002 Hs.6823 hypothetical protein FLJ10430 1.00 1.00 301846 ESTs, Weakly similar to pH sensitive max gb:yc97g09.r1 Soares infant brain 1NIB H 2.88 5.49

aldo-keto reductase family 1, member B11

Homo sapiens BAC clone RP11-120J2 from 7 ESTs

gonadolropin-releasing hormone 2

KIAA0674 protein transcriptional adaptor 2 (ADA2, yeast, hypothetical protein FLJ11252

paired box gene 9

Hs.13861

Hs.27973

301868 T71508

301905 AI991127 Hs.117202 ESTs

301948 AA244641 Hs.116724

301960 AW070252

302011 T91418 Hs.125156

302016 302041 NM 001501 Hs.129715

302072 A 1238384 Hs 132576

302094 Al286176 Hs.6786 ESTs

302095 AW044300 Hs.137506

302148

N40834 Hs.23495

AW269618 Hs.23244

75 301882 T78054

80

85

2.28 3.80

1.00 100

5 28 2.28

5.38 6.48

3.03

1.00 1 25

0.71 0.99

160 171

0.52 1 20

2.75 4.93

3.04 3.87

	w	O 02/08	5443		
	302155	AI088485	Hs.144759	ESTs	0.45
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33
	302202	AF097159	Hs.159140	UDP-GalthetaGlcNAc beta 1,4- galactosylt	0.52
5	302206	AJ937193	Hs.41143	phosphoinositide specific phospholipase	2.76
5	302209 302235	AF047445 AL049987	Hs.159297 Hs.166361	kitler cett lectin-like receptor subfami Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.00 1.68
	302230	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38
	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27
10	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54
	302384	Y08982	Hs.202676	synaptonemal complex protein 2 CD3-epsilon-associated protein; antisens	2.63
	302406 302409	U86751 AF155156	Hs.211956 Hs.218028	adaptor-related protein complex 4, apsil	5.82
	302408	AB028977	Hs.225974	KIAA1054 protein	3.66
15	302432	AL 080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr	2.44
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophita) homolo	0.44
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:a-1,3-D-mannosid	4.18
	302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85
20	302472 302476	AA317451 AF182294	Hs.6335 Hs.241578	SW/VSNF related, matrix associated, acti U6 snRNA-associated Sm-like protein LSm8	2.04 1.44
20	302476	T80660	Hs.230424	Homo sapions cDNA FLJ13540 fis, clone PL	0.51
	302490	AA885502	Hs.187032	ESTs	2.64
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34
0.5	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00
25	302630	AB029488	Hs.272100	SMS3 protein	0.52 1.00
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.58
	302638	AA463798 X57723	Hs.102696 Hs.198273	MCT-1 protein NADH dehydrogenase (ubiquinone) 1 beta s	2,72
	302655	AJ227892	Hs.146274	ESTs	1,00
30	302656	AW293005	Hs.70704	Homo saplens, clone IMAGE:2823731, mRNA,	2,97
	302668	AA580691	Hs.180789	S164 projein	0.80
	302679	H65022		gb:yu66g11.r1 Weizmann Offactory Epithel	1.68
	302680	AW192334	Hs.38218	ESTs	2.70
35	302697 302705	AJ001408 U09060		gb:Homo sepiens mRNA for immunoglobulin qb:Humen immunoglobulin heavy chain, V-r	3.91
33	302711	108442		gb:Human autonomously replicating sequen	2.20
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54
	302742	L12069		gb:Homo sapiers (clone WR4.10VH) anti-th	4.28
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57
40	302771	H98476 AJ245067	Hs.42522	ESTs gb:Homo sepiers mRNA for immunoglobulin	2.94 3.49
	302789 302795	AJ245007 AJ245313	Hs.272838	hypothetical protein FLJ 10494	0.80
	302802	Y08250	FIS. 27 2030	gb:H.sepiens mRNA for variable region of	1.13
	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14
45	302812	N31301	Hs.152864	hypothetical protein FLJ20051	3.04
	302847	X98940		gb:H.sapiens reerranged Ig heavy chain (1.80
	302885	AL137763	Hs.132127	hypothetical protein LOCS7822 ESTs, Weakly similar to T17330 hypotheti	1.00 0.53
	302943 302977	AI581344 AW263124	Hs.127812 Hs.315111	hypothetical protein FLJ 12894	2.45
50	303006	AF078950	Hs.24139	Homo sapiens cDNA; FLJ23137 ffs, clone L	4.88
50	303011	AF090405	1224100	gb:Homo sapiens clone 2A1 scFV aniibody	1.41
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51
	303081	AF151882	Hs.27693	poplidylprolyl isomerase (cyclophilin)-l	0.72
55	303077 303090	AF163305 AA443259	Hs.146286	glt:H.sapiens T-cell receptor mRNA kinesin family member 13A	1.17
22	303091	AF192913	Hs.140280 Hs.130683	zinc finger protein 180 (HHZ168)	2.50
	303094	AF195513	Hs.278953	Pur-gamma	5.38 3.26
	303095	AF202051	Hs.134079	NM23-H8	3.26
	303131	AW081061	Hs.103180	DC2 protein	2.02
60	303195	AA082211	Hs.233936	mycsin, light polypeptide, regulatory, n ESTs	1.32 0.77
	303196	AA082298 AA581439	Hs.59710 Hs.152328	ESIS ESTs	0.24
	303218	AA333538	Hs.204501	hypothetical protein FLJ10534	3.58
	303234	AA132255	Hs.143951	ESTs	2.28
65	303251	AW340037	Hs.115897	protocadherin 12	0.38
	303295	AA205625	Hs.208067	ESTs	2.30
	303297	T80072	Hs.13423	Homo septens clone 24468 mRNA sequence	1.86 0.10
	303316 303467	AF033122 AA398801	Hs.14125 Hs.323397	p53 regulated PA26 nuclear protein	4,54
70	303506	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09
, 0	303552	AA359799	Hs.224662	ESTs, Weakly similar to unnamed protein	1.00
	303598	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	4.96
	303637	AF056083	Hs.24879	phosphetidic acid phosphatase type 2C	2.06
75	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00
13	303756 303856	A1738488 AA968589	Hs.115838 Hs.180532	ESTs	1.76
	303896	AA968589 N88597	Hs.113503	glucose phosphale isomerase karyopherin (importin) bela 3	2.30
	303907	AW467774	Hs.171880	polymerses (RNA) II (DNA directed) polyp	3,10
	303946	AW474196	Hs.306637	Homo segiens cDNA FLJ12363 fis. clone MA	5.06
80	303978	AW513315			5.14
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83
	303990	AW515465		glocu71s11x1 NCI_CGAP_Md8 Homo sepiens glocu51s15x1 NCI_CGAP_U12 Homo sepiens	1.15 2.20
	303999	AW516449 AW516611		chrn70h11x1 NCI_CGAP_Ov39 Homo senions	4.85
85	304006	AW517947		gbzxp7cb11.x1 NCI_CGAP_Ov39 Homo sapiens gbzxb56hc2.x1 NCI_CGAP_Ut2 Homo sapiens	3,21
				•	

1.15 (0.84 (0.94 (

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	W	O 02/08	6443			
	304008	AW518198	Hs.3297	ribosomei protein S27a	6.50	11.0
	304009	AW518206 T03036	Hs.181165	eukaryofic translation elongation factor	1.88	3.27 3.55
	304024 304026	T03160		gb:FB21B7 Fetal brain, Stratagene Homo s gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
5	304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.4
	304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.4
	304046 304061	T54903 T61521		gbcyb42d06.s1 Strategene fetal spleen (9 gbcyb73g01.s1 Strategene ovary (937217)	6.18 2.64	12.11 8.23
	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
10	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.6
	304114	R78946		ob:vi87c02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122 304155	H28966 H68696		gb:ym31a06.s1 Scores infant brain 1NIB H gb:yr78b06.s1 Scores felal liver spleen	1.00	2.76 1.18
	304100	N56929		ob:vv82d08.s1 Soares multiple aderosis	4.28	11.3
15	304234	W81608		gb:zd88h06.s1 Scares_fetal_heart_NbHH19W	6.47	11.0
	304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34 3.40	1.16
	304270 304287	AA069711 AA079286	Hs.297753 Hs.78466	vimentin protessome (prosome, macropain) 26S sub	2.93	5.40 4.42
	304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.9
20	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430 304456	AA347682 AA411240		gb:EST54044 Fetal heart II Homo sapiens gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00 3.33
	304456	AA464716		gb:zx82c11.s1 Soares ovary turnor NbHOT H	2.18	1.15
	304526	AA476427		ab:2x02e05.s1 Soares total felus Nb2HF8	5.38	14.1
25	304542	AA482602	Hs.169476	glycaraldehyde-3-phosphale dehydrogenase	4.16	8.23
	304546 304607	AA486074 AA513322	Hs.297681	serine (or cysteine) proteínase inhibito gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	0.55 1.95	1.20 2.10
	304640	AA524440	Hs.111334	ferriin, light polypeptide	2.10	2.83
	304650	AA527489	Hs.3463	ninosampi arateia S23	3.33	12.8
30	304735	AA576453		gb:nm75h11.s1 NCI_CGAP_Co9 Homo sapiens gb:nn13g09.s1 NCI_CGAP_Co12 Homo sapiens	1.33	0.88
	304760 304849	AA580401 AA588157	Hs.13801	gb:nn13g09.s1 NCI_CGAP_Co12 Homo sapiens KIAA1685 protein	3.68 2.77	8.14 3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.0
	304921	AA603092	Hs.297753	vimentin	2.47	4.24
35	304966	AA613893	Hs.282435	ESTs	6.78	11.6
	304987 305016	AA618044 AA626876	Hs.300697	immunoglobulin heavy constant gamma 3 (G gb:zu8@h06.s1 Soares_testls_NHT Homo sap	6.46	1.23 10.1
	305034	AA630128		ob:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA841012		gb:eb99:04.s1 Stratagene lung (937210) H gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	5.68	11.5
40	305111	AA644187	Hs.303405	ESIS	1.48	1.37 4.61
	305148 305159	AA654070 AA859168	Hs.275668	gb:nt01g08.s1 NCI_CGAP_Lym3 Homo saplens EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955	114.210000	gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
4.5	305232	AA670052	Hs.169476	glycereldehyde-3-phosphate dehydrogenase	0.78	1.18
45	305235 305245	AA670480 AA676695	Hs,81328	gb:ag37e01.s1 Jia bone marrow stroma Hom nuclear factor of kappa light polypeptid	3.11 4.38	8.66 7.53
	305312	AA700201	F18,0 320	ab:zi44607.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.183019	EST	1.20	1.40
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16 5.86	0.68 9.87
30	305413 305447	AA724659 AA737858		gb:ai10f08.s1 Soares_parathyroid_tumor_N gb:nx10c08.s1 NCL_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528 305612	AA789158 AA782347	Hs.272572	gb:nz12e05.s1 NCL_CGAP_GCB1 Homo sapiens hemoglobin, alpha 2	6.44	9.10 0.79
33	305614	AA782866	M\$.272012	gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribotomal rentein S18	7.57	10.2
	305637	AA806124		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo saplens gb:oe29c12.s1 NCI_CGAP_Pr25 Homo saplens	4.78	12.4
60	305639 305650	AA806138 AA807709		gb:re29c12.s1 NCI_CGAP_P725 Homo sapiens gb:rw31e04.s1 NCI_CGAP_GCB0 Homo sapiens4	0.89	0.70 8.71
00	305690	AA813477		gb:al67a05.s1 Soares_lestis_NHT Homo sap	4.91	9.40
	305728	AA828156	Hs.73742	ribosomal protein, large, PO	0.19	0.81
	305728 305759	AA828209 AA835353		gb:of34a02.s1 NCI_CGAP_Kid6 Homo sepiens gb:ak72b06.s1 Barslead spleen HPLRB2 Hom	5.12	9.29 4.11
65	305792	AA845256		gb:ak84a08.s1 Barslead spleen HPLRB2 Hom	2.34	4,25
05	305864	AA864374	Hs.73742	nibosomal protein, large, PO	0.30	1.40
	305901	AA872968		objobe3b08 of NCL CGAP Kid5 Homo seniers	2.10	5.21
	305910 306015	AA875981 AA897116		gb:rx21h02.s1 NCL_CGAP_GC3 Homo sapiens gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s1	0.32	1,01 1,12
70	306013	AA897221	Hs.109058	ribosomel protein S6 kinase, 90kD, polyp	5.21	7.90
, ,	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soaros_NFL_T_GBC_S1 Homo s	7.38 7.19	20.6 13.4
	306065 306104	AA906725 AA910956		gb:ok/8g02.s1 NCI_CGAP_GC4 Home sapiens gb:ok85h11.s1 NCI_CGAP_Kid3 Home sapiens	6.50	9.13
75	306109	AA911861			4.21	5.25
	306148	AA917409	Hs.288036	IRNA isopenterrylpyrophosphate transferes gb:oo60g04.s1 NCL_CGAP_Lu5 Homo sapiens gb:oi53h05.s1 NCL_CGAP_HN3 Homo sapiens	2.20	2.70
	305242	AA932805 AA936900		gb:oo60g04:s1 NCI_CGAP_Lu5 Homo sapiens	2.84 1.60	5.35 1.12
	306268 306325	AA953072	Hs.210546	goxis3h05.s1 NCL_CGAP_HN3 Homo sapiens interteukin 21 receptor	1.65	2.26
80	306353	AA961382	Hs.275865	ribosomul molein S18	3.78	6.32
	306375	AA968650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
	306396 306428	AA970223 AA975110	Hs.191228	gb:op09d05.s1 NCI_CGAP_Kid6 Homo sapiens hypothetical protein FLJ20284	0.95 3.19	2.45 4.10
	306442	AA976899	mg. 181220	nh nn 35 nn 9 e 1 NCL CGAP GC4 Homo saniens	4.67	7.44
85	306446	AA977348		gb:oq72e12.s1 NCI_CGAP_Kid6 Homo saplens	3.92	6.27

\$306459 AM79186 116-5593		W	O 02/08	36443			
100619					ab:ap33c06.s1 Soores_NFL_T_GBC_S1 Hamo s	3.35	5.77
\$\ \text{SSSSS} \times \text{AddSSSSS} \times \text{AddSSSSSS} \times \text{AddSSSSSS} \times \times \text{AddSSSSSS} \times \text{AddSSSSSSS} \times AddSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		306467	AA983506	Hs.163593	ribosomal protein L18a	3.72	5.37
\$\ \text{Signature} \tag{5.00657} 5.006					gb:or84d07.s1 NCI_CGAP_Lu5 Homo sapiens		
2006252 A-0502408 1.0 1.	-			Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R		
2006252 A-0502408 1.0 1.	2		AA994530		gbroub /e08.s1 NCI_CGAP_BrZ Homo sapiers		
3,08698 AUXXXXII N. 16,06176 (1) 10 10 10 10 10 10 10 10 10 10 10 10 10		306572	AA300000 AA006248		about8c10 c1 NCL CGAP Kid5 Home sariers	1.42	3.13
30,000075 ADDIZION 1,000076 ADDIZION				Hs.169476	givoeraldehyde-3-phosphate dehydrogenase	4.91	8.68
15		306605	AI000497	Hs.119500	ribosomal protein, large P2		
\$300750 AUX7290 H.307610 Sorro, Lorde, Jank H. Homos sap 1.85 1.85 1.87 1.07 1.07 1.07 1.07 1.07 1.07 1.07 1.0	10		AI004024		gbxxu11b07.x1 Soares_NFL_T_GBC_S1 Homo s		
2007022 AUS22656 Ha. 2007070 AUS22675			Al005603	Hs.284136	PRO2047 protein		
15 2017/21 AUGUSTON AUGUS				U- 207670		1.00	1.10
15 000751 A002589 000751 A002589 A		306702	AM27350	Hs 272572			
2007677 A009905 Mil-2011 Mil-2012 Source, Jeffs June 1, 1991 Mil-2012 Mil-20	15			100212012	objow70h12.s1 Soares fetal_liver_spleen_	3.91	5.21
200897 AM3987 200895 AM3987 200895 AM3987 200895 AM3988 200895 AM3988 200895 AM3988 AM39888 AM3988 AM3988 AM3988 AM3988 AM3988 AM3988 AM3988 AM3988 AM3		306767	AI038963	Hs.249118	ESTs	3.33	6.06
20 306858 A1125111 307031 A112714 H.1.19122 307041 A112724 H.1.19123 307051 A112724 H.1.19123					gbzqa75h12.x1 Soares_fetal_heart_NbHH19W		
20 00685 M145152 307081 M167439 307091 M167439 3070		306897			gbxqa33c06.s1 Soores_NhHMPu_S1 Homo sapi		
2007035 AH46774 https://doi.org/10.1007035 AH46775 https://doi.org/10.1007035 AH46776 https://doi.org/10.1007035 AH46776 https://doi.org/10.1007035 AH46776 https://doi.org/10.1007037 A	20		AITZSTTT		go:amoorus.s1 Baisteau spieen niPLRB2 nutil	1.72	1 58
307941 M144250	20			He 110122	nhosomal protein L13s		
25 377161 A187429 A187259 A1		307041	AI144243	1,211.0122	gb:gb85b12.x1 Soares_fetal_heart_NbHH19W		
2.5 207297 2007978 14111353 14711353 14711354 147113					gb:xx70h06.s1 Soares_NhHMPu_S1 Homo sapi		8.52
207317 AUG9820 Mi-14/123	2.5		AJ189251		gb:qc99g06.x1 Soares_pregnant_uterus_NbH	3.55	
\$\\ \) \$\\ \\ \) \$\\ \) \$\\ \\ \) \$\\ \\ \) \$\\ \\ \) \$\\ \) \$\\ \\ \) \$\\ \\ \\ \) \$\\ \\ \\ \\ \) \$\\ \\ \\ \\ \\ \) \$\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	25				ferfitin, light polypeptide	2.46	
20 374		307317	AJ208303	HS.147333	COSS		
\$\\ \text{307476} \text{Add F176} \text{in 1.77937} \text{200726} \text{200726} \text{200726} \text{200726} \text{200726} \text{200726} \text{200726} \text{200726} \text{200726} \text{200726} \text{200726} \text{200726} \qq\q\q \qq\q\q\q\q\q\qq\q\q\q\q\q\q\q\q\q\q\q						2.02	3.73
30 37415 AJ20195 (1.1792) 2019		307410	A/241715	Hs.77039	ribosomel protein S3A	0.72	0.48
S07426	30	307415	AJ242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
\$\ \text{307161} \ \text{207165} \ \text{307161} \ \text{207165} \ \text{307166} \ \text{207166} \ \text{307166} \ 30716		307423	AJ243206	Hs.179573	collagen, type I, alpha 2		
35 SITSE1 A251555 SIT					gb:qh30g11.x1 Sosres_NFL_T_GBC_S1 Homo s	3.18	7.67
\$1.00					gcqt/2003x1 Soares_MinMr0_S1 noine sapi		11.20
307009 A200205 307019 A301428 40 30716 A301428 307701 A301428 3077	35				obrook5a12x1 Soores felal lung NhHI.19W		15.51
201897 301894 3					glxgm01f02.x1 Soares_NhHMPu_S1 Homo sapi		7.19
\$\\ \) \$\\ \) \$\\ \) \$\\ \) \$\\ \) \$\\ \) \$\\ \) \$\\ \) \$\\ \\ \) \$\\ \) \$\\ \\ \\ \) \$\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\		307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
40 307716 A335406 M32727 A355506 M32727					gb:tb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
\$\\ \frac{8}{3}\) \$\\ \text{2077} \\ \text{3}\) \$\\ \text{3}\) \$	40		Al318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S HI		
107760 ASIZ287	40			HB.83/53		1.51	
\$87764 ASSET216			AI342387		about 27507 v.1 Conner areasset interior Mini-		
\$70787 NBST189 (1987) 1885 1789 (1987) 1		307764	Al342731		glxgo26a07.x1 NCI_CGAP_Lu5 Homo saplens	4.52	12.58
\$70787 NBST189 (1987) 1885 1789 (1987) 1		307783	Al347274		gb:tp05d02.x1 NCI_CGAP_Co16 Homo sepiens		
\$1,000 \$1,000 \$2,000 \$1,	45				gb:qt18f09.x1 NCI_CGAP_GC4 Homo saplers	6.57	9.61
\$ \text{S07820} \times \text		307807			gb:qt09d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	
\$ 0.07839 0.35872 (a) 1.62572 (b) 1.62573 (b) 1.62573 (c) 1.62573					abunitant of MCI CGAP Codd Home conjens	7.94	
2007 Add 200				Hs.276737	EST Weakly similar to RSHLI22 ribosomal		3.32
S07997 A-M-Set 29 March 2015 March 201	50		Al365541		gb:qz08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	
\$ 380012 A458240 H.287216 H.28745 H.28					gbtg02h05.x1 NCl_CGAP_CLL1 Homo sapiens	3.13	4.99
55 380213 ACRES 1 2001 ACRES 2 2001 ACRES 1 2001 ACRES 2		307997	A/434512	Hs.181165	eukaryotic translation elongation factor		
55 \$88223 ACEST22 LASS 1977 \$100 \$				HS.203442	eb-tissing v1 NCL CGAP Lym12 Home conies	3.79	
\$809.00 A469824 H.27597 A56982 A76982	5.5			Hs.251577	hemoolobin, alpha 1		0.88
200899 AM69839 Hz 1269 17					glyceraldehyde-3-phosphale dehydrogenase	4.36	6.06
508101 A479920 14479321 144		308059		Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R		
500 1016 AFF 1820 1821 1822 1							
308154 AUGO0200 308171 AUG	60			Hs.181185	enkaryotic translation elongation tactor	1.30	
308154 AUGO0020 308171 AUG	00	308100		He 200444	EGT COLLECT STREET HOLT TO SHIP COLLECT	270	
26871 ALSSEASE Lab Laboration ALSSEASE Lab				110000411	gb:lr/93d08.x1 NCI_CGAP_Ut2 Homo sapiens	0.66	1.33
5 30213 ASS7145 30214 ASS7145 30219 ASS7145 30219 ASS7246 H. E32219 30219 ASS7246 H. E32229 30210 ASS724 ASS7256 H. E322940 30210 ASS724 ASS7256 H. E322940 30210 ASS724 ASS7256 H. E322940 30210 ASS725 ASS725 ASS725 H. E322940 30210 ASS725 ASS725 ASS725 H. E322940 30210 ASS725 ASS7		308171	AI523632		ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
\$\ \) \$\ \\ \) \$\ \\ \) \$\ \\ \) \$\ \\ \) \$\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	65			Hs.278572	anaplastic lymphoma kinasa (Ki-1)	2.43	2.14
80219 ASS7246 https://doi.org/10.1001/	00	306213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD		
508271 ASSTORAGE NEW ASSTORA					gg:P12.1_13_HUS.F tumor2 Homo expires cD		
200319 A850983 Hel.1519 Hel.1519				He 252259	ribosomal crotein S3	2.40	6.35
00 303822 AH513519 Ha.105216 SAA4655 profile 1.24					eukaryotic translation elongation factor	2.45	3.33
208413 ARXIVESS M. Int. 199311 SETS TOP TOP TO THE CONTROL OF THE	70	308362	Al613519	Hs.105749	KIAA0653 protein		
\$38444 ART/245 \$127117 \$57. Moderately similar to 190556 myosi \$4.77 \$2.77 \$39859 ART/1909 \$30859 ART/1909 \$30859 ART/1909 \$30850 ART/1909				Hs.196511	ESTs	3.16	4.82
75 308898 AFF 18279 ghard 572.12 il Barshood undu HPL 488 Horno 2000 554 AFF 18279 ghard 572.12 il Barshood undu HPL 482 Horno 2000 554 AFF 18279 ghard 572.12 il Barshood undu HPL 482 Horno 2000 554 AFF 18279 ghard 572.12 il Barshood undu HPL 482 Horno 2000 554 AFF 18279 ghard 572.12 il Barshood undu HPL 482 Horno 2000 554 AFF 18279 ghard 572.12 il Barshood undu HPL 482 HORNO 2000 554 AFF 18279 ghard 572.12 il Barshood undu HPL 482 HORNO 2000 554 AFF 18279 ghard 572.12 il Barshood undu HPL 482 HORNO 2000 554 AFF 18279 ghard 572.12 il Barshood undu HPL 482 HORNO 2000 554 AFF 18279 ghard 572.12 il Barshood undu HPL 482 HORNO 2000 554 AFF 18279 ghard 572 il Barshood undu HPL 482 HORNO 2000 554 AFF 18279 ghard 572 il					KIAA152/ protein		
(2) 308899 Aff 19803 30815 Aff 19803 (a) Compared prior of Part 1 de section dans le PL/Reil Homo 322 512 512 512 513 50815 Aff 19803 (a) Compared prior of Part 1 de section dans le PL/Reil Homo completa 102 52 513 513 513 513 513 513 513 513 513 513				ns.zr/117	oh:se51o12 v1 Randead anda HPI RBS Home		
90815 AT18939 Hs.(107174) 308313 AT18930 hs.(107	75				nb:as47d07.x1 Barslead aorta HPLRB6 Homo		5.12
38843 Al/15540 ght/15124 MC, COAP, D/M Brown sinjeries 389 349 2000 2000 2000 2000 2000 2000 2000 20		308615	Al738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
38873 AR76145 gen/30fe161 ND, CGSP-CLI Hono capiene 022 039 038 AR76145 ND (CSSP-CLI Hono capiene 022 039 038 ND (CSSP-CLI HONO capiene 022 039 038 ND (CSSP-CLI HONO capiene 022 039 038 ND (CSSP-CLI HONO capiene 022 038 ND (CSSP-CLI HONO capien		308643	AI745040		obstr19a12 v1 NCL CGAP Ov23 Homo sagiens	3.98	3.69
80 308722 AB07405 Hz.29408 ESTS 5.317 6.30 308778 AB11109 2008778 AB11109 200878 AB11109 200878 AB11109 200878 AB11109 200878 AB11107 Hz.2186 20087901c translation elempsition factor 2.94 5.15 308808 AB18289 308892 AB2411 Hz.21724 2008786 AB12411 Hz.21724 AB1241 Hz.21724 AB12411 Hz.21724 AB1241 AB12411 Hz.21724 AB1241 AB1241					nhwi09c10.x1 NCI_CGAP_CLL1 Homo sapiens		
98778 AB11109 gb:h04c11x1 NCI_CGAP_OV23 Home sepiens 1.00 1.00 987872 AB11767 Hs.2186 eizervoller installed belengtinfin factor 2.94 5.15 98988 AB18289 gb:hx526/1x1 NCI_CGAP_P722 Hono sepiens 4.41 8.34 989273 AB24118 Hs.217431 gmenin AV	80			No 250 (60			
308782 Al811767 Hs.2186 outcaryofic translation elong/ation factor 2.94 5.15 308808 Al818299 gbxx52e01.xt NCL_CGAP_Pr22 Homo sapiens 4.41 8.34 308893 Al824118 Hs.217433 aprent/in 2.41	80			ns.259408			1.00
308808 Al818289 gb:wk52c01.x1 NCL_CGAP_Pr22 Homo sapiens 4.41 8.34 308893 Al82418 Hs 217493 gcnerin A2 1.85 1.92		308782		Hs.2186	enkarvolic translation elongation factor	2.94	5.15
308823 AIR24118 He 217403 general A2 1.85 1.92		308808	AJ818289		gb:wk52c01.x1 NCI_CGAP_Pr22 Homo sapiens	4.41	8.34
O.D 308875 AVS32332 gb:sl48g03.x1 Barstead colon HPLM87 Homo 2.52 3.80	0.5	308823	Al824118	Hs.217493	annevin A2		1.92
	63	308875	M832332		BossinedRoyXJ Related colou unrusRl Hould	2.02	3.00

	w	O 02/08	5443			
	306879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	308886	AI833240		clost76d10.x1 Barstead colon HPLRB7 Homo	3.06	2.65
	306896	AI858845		gb:wl32d10.x1 NCI_CGAP_Ut1 Home sapiens	2.45	3.44
-	308934	AI865023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
5	308966	AI870704		gb:wl47h01.x1 NCI_CGAP_Ut1 Homo sepiens	1.00	1.00
	308979	AI873111		gb:wl52n05.x1 NCI_CGAP_Brn25 Homo sapien gb:tq39l01.x1 NCI_CGAP_Ut1 Homo sapiens	7,15 0.61	11.10
	309045 309051	AI910902 AI911975		gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
	309069	A917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
10	309083	Al922426	Hs.119598	ribosomal protein L3	2.39	3.34
10	309105	AI925503	Hs.265884	ESTs	5.54	17.78
	309122	AJ928178		gb:wc95a11.x1 NCI_CGAP_Kid11 Homo sapien	1.00	2.92
	309128	AJ928816	Hs.180842	rihosomal protein I 13	1.38	5.55
	309164	AJ937761		gb:wp84b09.x1 NCI_CGAP_Bm25 Homo sapien	2.43	3.11
15	309177	AJ951118		gb:wx63g05.x1 NCI_CGAP_Br18 Homo sepiens	0.81	0.97
	309288	AJ991525	Hs.299426	ESTs	4.86 4.36	7,46 9,43
	309299	AW003478		gb:wq66c06.x1 NCI_CGAP_GC6 Homo sepiens	2.88	7.54
	309303	AW004823	Hs.244144	gb:ws93a08.x1 NCI_CGAP_Co3 Homo sepiens EST	4.30	7.14
20	309411 309437	AW085201 AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
20	309459	AW117645	Hs.65114	kerstin 18	2.88	4.55
	309476	AV/129368	US'001 IA	gb:xe14b05.x1 NCI_CGAP_Ut4 Homo sapiens	2.08	6,60
	309499	AW136325	Hs.279771	Homo seciens clone PP1596 unknown mRNA	2.82	3.55
	309529	AW150807	Hs.181357	taminin recoolor 1 (67kD, ribosomal pro	4.78	3.95
25	309532	AW151119		cb;xq33e10.x1 NCL_CGAP_Ut1 Homo sapiens	1.18	4.40
	309626	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.0
	309641	AW194230	Hs.253100	EST, Moderately similar to GHHU Ig gamm	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.2
20	309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00 5.45	1.00 9.61
30	309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	1.41	1.25
	309700	AW241170	Hs.179661	tubulin, beta polypeptide gb:xq36h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00	8.35
	309747 309769	AW264889 AW272346		gb:xs13c10:x1 NCI_CGAP_Kid11 Homo sapien	5.76	11.9
	309782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
35	309783	AW275401	Hs.254798	EST	1.00	4.11
20	309799	AW276964		gb:xp58h01.x1 NCi_CGAP_Ov39 Homo sapiens	1.68	1.44
	309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
	309903	AW339071	Hs.300697	immunoglobulin heavy constant gamme 3 (G	1.05	1.18
	309923	AW340684		gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
40	309928	AW341418		gb:hd08c03x1 Soares_NFL_T_GBC_S1 Homes gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homes	7.41 1.20	13.7
	309931	AW341683		gb:hd13d01.x1 Soares_NFL_1_GBC_S1 Home s	4.90	18.2
	309933	AW341936	Hs.257111	gb:hb73f10.x1 NCI_CGAP_Ut2 Homo saplens hypothetical protein MGC3265	1.99	3.07
	309964 310002	AW449111 Al439096	Hs.323079	Homo sapiers mRNA; cDNA DKFZp564P116 (fr	0.20	0.47
45	310002	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
43	310098	AI685841	Hs.161354	ESTs	0.31	0.76
	310109	AI203094	Hs.148633	ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
	310115	Al811317	Hs.223796	ESTs	1.25	0.84
50	310121	AW195642	Hs.148901	ESTs	1.00	2.71
	310146	Al206614	Hs.197422	ESTs	9.50	15.3
	310193	AI827853	Hs.147562	ESTs	2.85 4.26	4.18 10.6
	310255	AW450439	Hs.153378	ESTs	3.28	4.40
55	310261	AI240483 AI915771	Hs.201217 Hs.74170	ESTs metallothionein 1E (functional)	0.26	0.86
22	310264	AI242102	Hs.213636	ESTs	5.43	8.19
	310273	AI243332	Hs.156055	ESTs	3.15	8.06
	310290	AW013815	Hs.149103	ESTs	2.19	3.12
	310333	AI253200	Hs.145402	ESTs	1.17	1.91
60	310346	AI261340	Hs.145517	ESTs	4.81	9.95
	310385	A1263392	Hs.158151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444	AW196632	Hs.252956	ESTs	0.85	1.01
	310446	AI275715	Hs.145926	ESTs	2.18	3.85 5.19
65	310468	Al984074	Hs.196398	ESTs ESTs	1.00	1.00
	310477	AI948801	Hs.171073		3.87	8.12
	310512 310514	AW275603 AI681145	Hs.200712 Hs.160724	ESTs ESTs	3.30	7.33
	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
70	310524	Al302654	Hs.208024	ESTs	3.26	3,46
	310584	AI653007	Hs.156304	ESTs	2.39	4.08
	310608	AI962234	Hs.196102	ESTs	5.60	6.49
	310624	AI341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AI814373	Hs.164175	ESTs	1.85	1.71
75	310648	AI347863	Hs. 156672	ESTs	0.17 5.40	0.69
	310694	A1654370	Hs.157752	Homo sapiens mRNA full length insert cDN	4.82	6.27
	310695 310714	AI472124 AI418446	Hs.157757 Hs.157882	ESTs ESTs	1.76	3.51
	310714 310722	AI418446 AI989803	Hs.157882 Hs.157289	ESTS ESTS	1.14	6.85
80	310756	AI916560	Hs.158707	ESTS	8.46	13.0
00	310764	AI376769	Hs.167172	ESTs	4.76	7.37
	310848	AI459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
0.5	310854	AI421677	Hs.161332	ESTs	6.37	7.94
85	310858	AI871000	Hs.161330	ESTs	6.07	9.84

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	310864	Al924558	Hs,161399	ESTs	0.87	0.78
	310875 310896	T47764 AW157731	Hs.132917 Hs.270982	ESTs. Moderately similar to ALU7. HUMAN A	1.00 7.07	3.63 16.68
	310990	AW195634	Hs.170401	ESTs, Moderatory surmer to ALD7_HOMAN A	1.00	1.00
5	310955	AJ560210	Hs.263912	ESTs	10.08	17.66
	310957	AW190974	Hs.196918 Hs.171050	ESTs	2.18 3.06	3.18 6.64
	311000 311012	AJ521830 AW298070	Hs.241097	ESTs ESTs	1.23	3.77
	311034	AJ564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
10	311074	AW290922	Hs.199848	ESTs	6.04	14,19
	311134	A1990849 AW450552	Hs.196971 Hs.205457	ESTs periaxin	3.54 0.65	6.96 0.95
	311187	AI638374	Hs.224189	ESTs	2.46	2.78
10	311220	A1656040	Hs.196532	ESTs	1.10	2.52
15	311230 311236	AJ989808 AJ653378	Hs.197663 Hs.197674	ESTs ESTs	1.41 2,18	1.75 2.11
	311242	AW016812	Hs.200266	ESTS	0.63	5.11
	311258	A)671221	Hs.199887	ESTs	1.00	1.41
20	311277	AW072813	Hs.270868 Hs.291829	ESTs, Moderately similar to ALU4_HUMAN A ESTs	2.56 1.04	1.94 2.69
20	311294 311308	AA826425 F12664	Hs.291829 Hs.49000	ESTS	1,96	6.70
	311351	AI682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2,80	6.06
25	311405 311409	AW290961 Al698839	Hs.201815	ESTs gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.80 3.84	11.66 6.94
23	311420	Al936291	Hs.209867	ESTs	5.30	12.58
	311443	Al791521	Hs.192206	ESTs	4.39	6.09
	311467	Al934909 Al933672	Hs.175377 Hs.211399	ESTs ESTs	1.00 2.76	1.04 5.61
30	3114/9	R57390	Hs.211399 Hs.301064	ests arfaofin 1	2.50	5.73
50	311495	AW300077	Hs.221358	ESTs .	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87 1.33
	311534 311537	AW130351 Al805121	Hs.243549 Hs.211828	ESTs ESTs	0.31 3.69	5.85
35	311543	AI681360	Hs.201259	ESTs	1.73	1.34
	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557 311558	AI819230 Z44432	Hs.211238 Hs.63126	Interleukin-1 homolog 1 KIAA1292 protein	1.00	1.00 3.41
	311559	AW006271	Hs.265848	similar to rat myomegalin	2.68	5.90
40	311563	AI922143	Hs.211334	ESTs	2.39	3.32
	311586	AI827834 AW450675	Hs.211227	ESTs . ESTs	2.47 1.00	3.85 1.00
	311816 311621	AVV450675 AI924307	Hs.212709 Hs.213464	ESTs	4.18	6.74
	311635	AI928456	Hs 213081	ESTs	2.17	3.76
45	311888	AW193874	Hs.240044	ESTs	2.60	3.12
	311672	R11807 AW183738	Hs.20914 Hs.232644	hypothetical protein FLJ23056 FSTs	2.79 0.19	5.18 0.96
	311700	R49601	Hs. 171495	retingic acid receptor, beta	6.28	8.83
	311714	AW131785	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	5.00	8.17
50	311735	AW294416	Hs.144687	Homo sapieris cDNA FLJ12981 fis, clone NT ESTs	0.96 1.00	0.72 1.95
	311743 311783	T99079 AI682478	Hs.191194 Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AI056769	Hs.133512	ESTs	1.34	3.97
55	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52 3.58	13.32 3.91
33	311819 311823	AW265275 AI089422	Hs.254325 Hs.131297	ESTs ESTs	1,40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTS	0.88	0.87
60	311896	AW206447 N28365	Hs.22579	go:UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su Homo sapiens clone CDABP0036 mRNA sequen	1.66 1.66	1.13
00	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	AJ597963	Hs.118726	ESTs	1.88	3.02
	311959 311960	T67262 AW440133	Hs.124733 Hs.189690	ESTs ESTs	2.02	2.33 6.62
65	311960	AW440133 AI382726	Hs.189590 Hs.182434	ESTS ESTS	5.80	8.14
00	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78460	Hs.13941	ESTs	0.12	1.39
	312028 312046	T78886 AJ580018	Hs.284450 Hs.268591	ESTs ESTs	3,78 4.11	4.92 7.32
70	312046	T83748	Hs.268594	ESTS ESTS	2.36	3.08
	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760 T91809	Hs.13685 Hs.121296	ESTS ESTs	1.60 0.68	1.15 0.85
	312093 312094	Z78390	HS.121296	gb:HSZ78390 Human fetal brain S. Meler-E	3.05	4.48
75	312097	AJ352096	Hs.112180	zinc finger protein 148 (pHZ-52)	4.52	9.70
	312118	T85332	Hs.178294	ESTs	2.40	2.60
	312128 312147	AI052609 T89855	Hs.17631 Hs.195648	Horno sapiens cDNA FLJ20118 fls, clone CO ESTs	2.39 0.67	3.53 1.03
	312147	AA953383	Hs.195548 Hs.127554	ESTS	5.85	10.60
80	312179	AJ052572	Hs.269864	ESTs	2.41	3.32
	312201 312207	AI928365 H90213	Hs.91139	solute carrier family 1 (neuronal/epithe ESTs	0.24 2.20	0.89 4.55
	312220	H90213 N74613	Hs.191330	gbcze55e07.s1 Soares fetal liver spicon	4.28	11.13
0.5	312252	Al128388	Hs.143655	ESTs	1.64	1.57
85	312304	AA491949	Hs.269392	ESTs	0.12	2.47

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	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs	0.44	1.74
-	312331	AA825512	Hs 289101	glucose regulated protein, 58kD	3.73	5.96
5	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363 312375	A1675558 A1375096	Hs.181867 Hs.172405	ESTs cell division cycle 27	10.08 2.78	16.73 3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
	312389	AI863140	116.172717	gbdz43h12.x1 NCI_CGAP_Bm52 Homo sapien	2.37	3.96
10	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	AI167637	Hs. 146924	ESTs	1.11	1.00
	312507	Al168177	Hs.143653	ESTs	5.89	8.24
15	312520	Al742591	Hs.205392	ESTs	3.30	8.92
	312548	A1566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35068	ESTs	0.40	0.77 0.94
	312583 312599	AI193122 AI865073	Hs.124141	ESTs ESTs	0.13 3.75	5.29
20	312599	AA046451	Hs.125720 Hs.165200	ESTS ESTS	6.78	12.93
20	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	A1240582	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
	312817	H75459	Hs 233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8,93	13.78
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71 4.25
30	312925	N90868	Hs.271695	ESTs ESTs	1.00	1.17
30	312936 312975	AI681581 AI640506	Hs.121525 He 203119	ESTS, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs. Violatily satisfact to ALOY_HOMAN ALOYS	0.80	1.05
	312960	AA497043	Hs.115685	ESTs	3.12	3.60
	312984	N25871	Hs.177337	ESTs	2.03	2.13
35	313000	Al147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96	1.39
	313039	Al419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
	313049	AW293055	Hs.119357	ESTs	6.44	10.73
40	313056	Al651930	Hs.135684	ESTs ESTs	1.51 0.25	2.04 1.50
40	313058 313070	D81015 AI422023	Hs.125382 Hs.161338	ESTS	8.56	11.60
	313070	A)676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.169677	ESTs	3.28	5.06
	313136	N59284	Hs.288010	ESTs	0.49	1.36
45	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238189	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00 0.74	3.87 2.06
50	313265 313267	N93466	Hs.121764 Hs.129583	ESTs, Weakly similar to lesticular tekti ESTs	0.74	1.30
50	313207	A1770008 A1027604	Hs.159650	ESTs	6.68	9.57
	313275	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
	313292	Al362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
	313325	Al420611	Hs.127832	ESTs	1.20	2.27
55	313357	AW074848	Hs.201501	ESTs	4.02	5.33
	313393	Al874685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	AI241540	Hs.132933	ESTs	6.57	15.07 3.01
60	313417 313457	AA741151 AA576052	Hs.137323 Hs.193223	ESTs Horno sapiens cDNA FLJ11646 fis, clone HE	0.63 2.78	4.70
00	313457	AA076002 AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313556	AA628517	Hs.118502	ESTs	0.23	0.70
	313569	Al273419	Hs.135146	hypothetical protein FLJ 13984	1.88	1.00
65	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	Al753075	Hs.104627	Homo sapiens cDNA FLJ 10158 fis, clone HE	1.00	1.72
	313662	AA740151	Hs.130425 *	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00 5.80
70	313672 313690	AW468891 AW93591	Hs.122948 Hs.78146	ESTs platelet/endolhelial cell adhesion molec	3.46 0.51	0.97
70	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412	112.100411	gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
	313774	AW136836	Hs.144583	ESTs	1.38	1.19
75	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1,15	0.91
	313834	AW418779 AI538438	Hs.114889	ESTs ESTs	0.68 5.74	3.14 8.88
80	313835 313852	AI538438 H18633	Hs.159087 Hs.123641	ESTs protein tyrosine phosphatase, receptor t	0.16	1.14
ou	313852	AW470806	Hs.123641 Hs.275002	ESTs prosine prospinatase, receptor t	2.09	4.06
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	FSTe	5.28	6.83
0.5	313883	AI949384		ebmu76d01.s1 NCL CGAP_Alv1 Home sapiens	2.90	10.91
85	313915	AI969390	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	1.00	1.00

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	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AJ870175	Hs.13967	ESTs	0.46	0.75
5	313983 314035	AJ829133 AA164199	Hs.226780 Hs.270152	ESTs ESTs	4.10 5.88	6.40 7.90
,	314037	AW300048	Hs.275272	ESTS	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103 314107	AI028477 AA806113	Hs.132775 Hs.189025	ESTs ESTs	2.90	5.29 1.66
10	314113	AA218986	Hs.118854	ESTS	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp647C244 (fr	2.53	3.32
	314126	AA226431		gb:nc18b12.s1 NCL_CGAP_Pr1 Home sapiens	3.13	5,08
15	314128	AA935633	Hs.194628	ESTs	2.90 4.15	6.35
15	314151 314184	AA236163 AW061795	Hs:202430 Hs:233465	ESTs ESTs	3,44	4.65
	314192	AW290975	Hs.118923	ESTS	1.00	1,23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98 0.38	7.16 1.94
20	314262 314320	AW086215 AA811598	Hs.246096 Hs.275809	ESTs ESTs	3.34	5.66
	314332	ALQ37551	Hs.95612	ESTS	2.85	2.09
	314335	AA267443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
0.5	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
25	314351 314376	AA292275 Al628633	Hs.193746 Hs.324679	ESTs ESTs	3.07 4.10	3.77 6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AJ217440	Hs.143873	ESTs	0.58	2.49
••	314466	AA767818	Hs.122707	ESTs	2.53	2.62
30	314478	AL043807	Hs.125507	DEAD-box protein	3.94 1.30	5.65 1.44
	314482 314506	AA833655	Hs 134182 Hs 206868	ESTs Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
	314529	AL046412	Hs.202151	ESTs	3.43	6.87
35	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
	314562 314579	AJ564127 AW197442	Hs.143493 Hs.116998	ESTs ESTs	2.29 3.87	5.27 5.75
	314579	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
	314585	AA918474	Hs.216363	ESTs	1.06	1.40
40	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ 10570 fis, clone NT	1.00	1.00
	314592 314603	AA435761 AA418024	Hs.192148 Hs.270670	ESTs ESTs	0.90 4.56	2.60 6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
	314606	AA418241	Hs.188767	ESTs	2.97	4.55
45	314648	AA878419		gb:EST391378 MAGE resequences, MAGP Homo!	1.42	1.36
	314699 314701	Al038719 Al754634	Hs:132801 Hs:131987	ESTs ESTs	3.66	4.97 0.90
	314710	A1669131	Hs.290989	EST	3.40	7.52
	314750	A1095005	Hs.135174	ESTs	2.80	6.54
50	314767	AW135412	Hs.164002	ESTs	3.20	4.26
	314801 314817	AA481027 Al694139	Hs.109045 Hs.192855	hypothetical protein FLJ10498 ESTs	1.00 0.91	1.00 0.99
	314835	AI281370	Hs.76064	ribosomal replain I 27a	5.75	7.44
	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sagien	1.68	4.34
55	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940 314941	AW452768 AA515902	Hs.162045 Hs.130650	ESTs ESTs	10.10 0.31	16.20 1.02
	314941	AA5159UZ AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
	314955	AA521382	Hs.192534	ESTs	2.59	3.90
60	314973	AW273128	Hs 300268	ESTs	1.05	1.25
	315004 315006	AA527941 AJ538613	Hs.325351 Hs.298241	EST	5.64 0.52	13.63 1.78
	315033	AI493046	Hs.146133	Transmembrane prolease, serine 3 ESTs	2.46	1.00
	315035	AJ569476	Hs.177135	ESTs	0.34	1.33
65	315056	AJ202703	Hs.152414	ESTs	2.10	264
	315069	AJ821517	Hs.105866 Hs.152423	ESTs Homo sapiens cDNA: FLJ21274 fis. clone C	1.00	1.30 1.00
	315071 315073	AA552690 AW452948	Hs.152423 Hs.257631	Homo sapiens curva: FLJ212/4 tis, clone C ESTs	1.78	1.52
	315078	AA568548	Hs.190616	ESTS	3.00	3.79
70	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175 315193	AI025842 AI241331	Hs.152530 Hs.131765	ESTs ESTs	1.06	1.91 0.97
	315196	AA972756	Hs.44898	Homo saplens clone TCCCTA00151 mRNA sequ	0.48	1.96
75	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	Al474433	Hs.179556	ESTs	5.37	9.36
	315353 315397	AW452608 AA218940	Hs.279610	hypothetical protein FLJ10493 tidgetin-like 1	1.00	1.30 2.24
	315403	AA218940 AW362980	Hs.137516 Hs.163924	ESTs	2.04	5.23
80	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454	Al239473		gbqh38f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
	315455 315473	AW393391 A)681671	Hs.156919	ESTs ESTs, Moderately similar to OVCA1	3.78 0.89	5.76 2.15
	315483	AW512763	Hs.312671 Hs.222024	transcription factor BMAL2	2.32	1.96
85	315526	Al193048	Hs.128685	ESTs	1.67	1.78

	w	O 02/08	6443			
	315530	A(200852	Hs.127780	ESTs	1.05	1.01
	315541	Al168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.256578	ESTs	1.00	2.22
	315562	AA737415	Hs.152826	ESTs	2.66	2.48
5	315577	AW513545 41368399	Hs. 17283 Hs. 140489	hypothetical protein FLJ 10890 FSTs	2.20 1.00	2.25 1.04
	315587 315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AN1072367 AA364078	Hs.258189	ESTs	7.44	12.56
	315634	AA837085	Hs.220585	ESTs	0.50	1.40
10	315668	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	Al932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742 AI418055	Hs.155556 Hs.161160	hypothelical protein FLJ20202 ESTs	2.18 2.88	3.77 2.63
	315707 315730	H25899	Hs. 161160 Hs. 201591	ESTS	0.11	0.60
15	315745	Al821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177	1121101000	gb:zi15a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	315820	Al652022	Hs.258785	ESTs	2.35	3.01
20	315878 315905	AA683336 AI821911	Hs. 189046 Hs. 209452	ESTs ESTs	2.12 1.03	2.64 1.97
20	315923	AI821911 AI052789	Hs.209452 Hs.133263	ESTS ESTS	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
	316001	Al248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
25	316011	AW516953	Hs 201372	ESTs	0.35 6.56	1.63
	316012 316040	AA764950 AI983409	Hs.119898 Hs.189226	ESTs ESTs	5.69	8.13 10.69
	316048	Al720759	Hs.189220 Hs.224971	ESTS ESTS	2.84	10.45
	316076	AV297895	Hs.116424	ESTS ESTS	0.30	1.05
30	316124	Al308862	Hs.167028	ESTs	1.00	1.43
	316151	AI806016	Hs.156520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs ESTs	4.92 1.48	6.94 1.60
35	316232 316275	AW297853 Al671041	Hs.251203 Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
55	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
40	316346	A1028478	Hs.157447	ESTs	3.51	6.69 4.33
40	316365 316380	A1627845 A1393378	Hs.210776 Hs.164496	ESTs ESTs	2.50 1.16	2.16
	316470	AAB09902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTS	2.46	2.89
	316514	AA768037	Hs.291671	ESTs ·	4.70	6.04
45	316519	AI929097		gb:od10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520 Al125586	Hs.122082	ÉSTS ESTS	1.00 2.61	2.89 3.72
	316633 316700	AW172316	Hs.127955 Hs.252961	ESTs, Wealdy similar to ALU1_HUMAN ALU S	3.46	4.64
	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4,45	6.95
50	316713	A)090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	A1440266	Hs.170673	ESTs, Wealtly similar to AF126780 1 retin	0.20	1.45
	316787	AW369770	Hs.130351	ESTs	4.05 2.25	5.53 3.82
	316809	AA825839 AA922060	Hs.202238 Hs.132471	ESTs ESTs	1.00	1.32
55	316811 316812	AW135045	Hs.232001	ESTS ESTS	3.28	4.70
55	316818	AA827176	Hs.124316	ESTS	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
	316827	AI380429	Hs.172445	ESTs	0.72	1.56
60	316891	AW298119	Hs.202536	ESTs	1.64	2.97
00	316951 316970	AA134365 AA860172	Hs.57548 Hs.132406	ESTs -	1.45	1.08 1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
	317001	Al627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
65	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs ESTs	6.18	12.72 2.66
	317128 317129	AA971374 H12523	Hs,125674 Hs,78521	Homo sapiens cDNA: FLJ21193 fis, clone C	1.87 4.12	6.64
	317137	AW341567	Hs.125710	ESTs	2.82	5.12
70	317196	A1348258	Hs.153412	ESTs	1.98	2.51
	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130064	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc/osteonectin, owov and kazal-like d	2.74	0.86
75	317266 317282	AA906289 AJ807444	Hs.203614 Hs.176101	ESTs ESTs	1.00 2.60	1.00 4.21
15	317282	AW370882	Hs.176101 Hs.222080	ESTS ESTS	1.96	3,49
	317302	AA908709	Hs,135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2,28
0.0	317320	AA927151	Hs.130452	ESTs	3.58	8.13
80	317413	AW341701	Hs.126622	ESTs ESTs	2.08 3.06	4.92 4.79
	317417 317452	AA918420 AA972965	Hs.145378 Hs.135568	ESTs	3.06 4.22	9.21
	317519	AA9/2900 AIR59695	Hs.126960	ESTs	1.88	4.15
÷.	317521	AI824338	Hs.126891	ESTs	3.12	4,55
85	317529	AI916517	Hs.126865	ESTs	2.73	3.34

		0.03/00/	112			
		O 02/080		ESTs	1.00	2.43
	317570	AJ733361 AA938663	Hs.127122 Hs.199628	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.56
-	317627	AI346110	Hs.132553	ESTs	1.50	1.39
5	317650	AJ733310	Hs.127346 Hs.127785	ESTs ESTs	0.48 4.18	1.46 7.14
	317659 317674	AA961216 AW294909	Hs.12/785 Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
10	317692	Al307659	Hs.174794	ESTs	5.33	9.59
10	317701	AI674774	Hs.128014	ESTs	1.00 5.13	1.00 7.81
	317711 317722	AI733015 AI733373	Hs.272189 Hs.128119	ESTs ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
	317777	Al143525	Hs.47313	KIAA0258 gene product	1,00	2.48
15	317799	Al498273	Hs.128808	ESTs	1.78	2.11
	317803 317821	AA983251 AJ368158	Hs.128899 Hs.70983	ESTs PTPL1-associated RhoGAP 1	0.80 0.17	1.06 0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
20	317861	AW341064	Hs.129119	ESTs	2.18	5.93
	317865 317869	A1298794 AW295184	Hs.129130 Hs.129142	ESTs deoxyribonucisase II beta	4.48 0.44	8.20 0.99
	317881	AW250104 AIR27248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
	317890	AJ915599	Hs.129225	ESTs	4.68	7.48
25	317899	A1952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
	317986	A1005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28 5.12	1.66 9.97
	318001 318016	AW235697 AI016694	Hs.130980 Hs.256921	ESTs ESTs	1.86	4.50
	318023	AW243058	Hs.131155	ESTS	2.92	5.22
30	318054	AW449270	Hs.232140	ESTs	3.92	6.37
	318068	A1024540	Hs.131574	ESTs	1.21	1.27
	318117	A1208304	Hs.250114 Hs.133272	ESTs ESTs, Weakly similar to ALUC_HUMAN !!!!	0.86 5.90	1.17
	318187	Al792585 Al077540	Hs 134090	ESTS, Weakly Stilled to ALOG_HORART III	1,05	0.90
35	318240	A)085377	Hs.143610	ESTs	3.10	2.40
	318255	A1082892	Hs.134662	ESTs	0.02	1.05
	318266	AJ554341	Hs.271443	ESTs	6.12 4.98	10.55 7.90
	318330 318389	A1093840 A1493501	Hs.143758 Hs.170974	ESTs ESTs	2.46	5.62
40	318428	A1949409	Hs.194591	ESTs	0.77	0.45
	318458	Al149783	Hs.158438	ESTs	3.54	4.92
	318467	Al151395	Hs.144834	ESTs ESTs	4.56 2.08	5.62 4.05
	318473 318478	AJ939339 AJ693927	Hs.146883 Hs.265165	ESTS	4.22	8.07
45	318487	AI167877	Hs.143716	ESTs	1.47	1.05
	318488	AJ217431	Hs.144709	ESTs	1.40	4.14
	318491	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84 2.58	1.90 5.20
	318499 318537	T25451 AA377908	Hs.13254	gb:PTHI188 HTCDL1 Homo sepiens cDNA 5/3 ESTs	3.26	4.18
50	318538	N28825	Hs.74034	Homo saciens clone 24651 mRNA sequence	0.35	1.07
50	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761 Hs.49007	ESTs, Weakly similar to unnamed protein	1.91	1.98 6.22
55	318580 318587	T34571 AA779704	Hs.168830	poly(A) polymerase alpha Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
55	318596	AJ470235	Hs.172696	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprolein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39 1.72	1.04 3.57
60	318637 318648	AA243539 T77141	Hs.9196 Hs.184411	hypothetical protein albumin	6.27	9.91
00	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318571	AA186823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T58115	Hs.10336	ESTs Homo saxions cDNA: FLI21238 fis. clone C	1.00 3.05	2.19 3.18
65	318711 318725	AI936475 AI962487	Hs.101282 Hs.242990	ESTs	1,08	2.46
05	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24963	Hs.23766	ESTs	1.00	3.01
70	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD FSTs	2.70 3.90	3.86 7.13
70	318816 318865	F07873 H10818	Hs.21273	gb:ym04f10.r1 Soares infant brain 1NI8 H	2.25	3.56
	318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
75	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31 1.03	7.00 0.91
13	318901 318925	AW368520 Z43577	Hs.301528 Hs.21470	L-kynurenine/alpha-aminoadipale aminotra ESTs	2.23	3.80
	318936	AI219221	Hs.308298	ESTs	1.86	7,16
	318982	Z44140	Hs.269622	ESTs	5.84	9.79
90	318986	Z44186	Hs.169161	ESTs, Highly simitar to MAON_HUMAN NADP-	1.00	1.00
80	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38 1.00	6.11 1.07
	319103 319170	H05896 R13678	Hs.4993 Hs.285306	KIAA1313 protein putative selenocysteine lyaso	3.79	5.03
	319196	F07953	Hs.16065	putative G-protein coupled receptor	1.00	2.98
85	319199	F07361	Hs.13306	ESTs	3.53	5.66 7.26
83	319242	F11472	Hs.12839	ESTs	5.87	1.20

1985 1983		w	O 02/086	5443			
1997 1998					Homo canione of INA: EL 121027 tis clone H	1.81	1.57
\$ 19220 11:1474 bit-20073 Co. 4.4 profess) Co. 4.4 profess) Co. 4.4 profess			F11802		FSTs		
\$ 319522 AASTS158 In: 12775 \$ 319527 WIGST IN 18-20243 \$ 319528 WIGST IN 18						4.80	10.40
10 1972 1975 19	_						211
10 1987 19	5				ESTs		
10 31923 F12119 th. 1285 ESTs Control of the property of the prope				Hs.79059	transforming growth factor, bela recepto		
10 31837 Add 1973		319291	W86578	Hs.285243	hypothetical protein HLJ22029	0.26	4.60
10 18/207 18/20				HS.12003	ED IS shill COCCEDE to assembly of leftest broke of NI		
15 1869 18	10	319370		He 325823	ESTs Moderately similar to ALUS HUMAN A		
3 35829 AASSTAL (b.1919) 3 35427 ROSCOS (b.1919) 3 35427 ROSCOS (b.1919) 3 35427 ROSCOS (b.1919) 3 35428 ROSCOS (b.1919) 3 35428 ROSCOS (b.1919) 3 35429 ROSCOS (b.1919) 3 354				Hs.13911		1.26	2.43
15 316447 105006 https://doi.org/10.0014/10.0016/steps-plane 2.00 3.54 phys/902/97.1 Stores field for spiken 2.00 4.00 4.00 992/97.1 Stores field for spiken 2.00 4.00 992/97.1 Stores field for spiken 2.00 2.00 2.00 2.00 2.00 2.00 2.00 2.0		319396				0.70	
13-144.5 TECRS00. https://doi.org/10.1451/1451.5 TECRS00. https://doi.org/10.1451/1451.5 TECRS00. https://doi.org/10.1451/1451.5 TECRS00. https://doi.org/10.1451/1451/1451/1451/1451/1451/1451/1451		319396	AA359754	Hs.191196	ESTs		3.59
319443 RRB050 https://doi.org/10.1001/31.3001 https://doi.org/	15		R05329		gb;ye91b04.r1 Soares fetal liver spleen		
319467 AACREACO March 11991 ESTs E	15	319425	T82930		gb.yd3907.r1 Soares fetal liver spieen		
1986 Allessed Miles Mi							5.68
29 31947 19653 1.65 31946 All 74.69 1.62 1.62 31956 All 74.69 1.62 31956 19688 1.62 1.62 31956 19688 1.62 1.62 31956 19689 1.62 31956 19689 1.62 31956 19689 1.62 31956 19699 1.62 31956 19699 1.62 31956 19699 1.62 31956 19699 1.62 31956 19699 1.62 31956 1.62 31956 1.62 1.62 31956 1.62 1.62 31956					ESTs, ready sittles to recent to constitution		
1996 1997							
\$1966 AUSEA/19 1.820779 2.00 2.25 2.00 2.	20	319480	R06933		ESTs	1.00	1.00
\$\frac{1}{3}\$\fr		319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen		
25 318623 786666 https://doi.org/10.1009/s10992 77.0009 https://doi.org/10.10092 77.0009 https://doi.org/10.10092 77.0009 https://doi.org/10.10092 77.0009 https://doi.org/10.10092 77.00092 77.0009 https://doi.org/10.10092 77.000							
\$\frac{1}{3}\frac{1}\frac{1}{3}		319508	T99896	Hs.270104	ESTs, Moderately similar to ALUS_HUMAN A		
319566 RIGRES 319506 ANGERIS 319506 RIFES 319507 ANGERIS 319506 ANGERIS 319506 ANGERIS 319506 ANGERIS 319507 ANGERIS	25				ESTS		
\$1,950.20	23			HS. 14300	ehad 22h 12 et Coorea fotal liver enlana	6.44	
1982 1982			AARDS106	Ne 20403			
3 19566 078606 in ±2.0526 1.00 1.			T82998				4.82
\$\frac{1}{3}\frac{1}				Hs.283683	chromosome 8 open reading frame 4		0.82
1961 H-657 1962	30		R11679	Hs.297753			
1995 APT/1985 199				Hs.12293	hypothetical protein FLJ21103	3.06	4.24
315627 1					gicym19c10.r1 Soares infant brain 1NIB H		
\$1,950							
\$\frac{1}{31964}\$ \text{HSQSS}\$ \text{h2-106}\$ \text{EST}\$ \text	35			HS.100004			
1982 1982	22			He 21208	ESTe Moderately similar to 4 Chain 4 H		
1970 1970		319662	H06382	Hs.21400	ESTS	1.58	
\$\frac{4}{3}\) \$\frac{1}{3}\) \$\frac{1}{3}\) \$\frac{1}{3}\] \$\fr					ESTs		
\$ 19872 1785855 1422464 18915		319742	T77668	Hs.21182	ESTs	2.48	3.13
\$19789 A.321552 to 117144 \$1800 A.321552 to 117145 \$1800 A.321552 to 11	40						
1985 1982						4.36	
1985 1985		319788		HS.117414			
\$\frac{4.5}{3.0000} \times \frac{1.000}{3.0000} \times \frac{1.0000}{3.0000} \times \frac{1.0000}{3.0000} \times		319805		HS.27130U	N. accientions of mouse poyours		1.32
1987 178517 148508 128	45	319834		110.204000	nh/zm61n01 r1 Stratagene fibroblast /937	0.30	0.94
## 1982 A-45556 https://doi.org/10.1009/j.meg/10.1009/j.		319878	178517	Hs.13941	ESTs	3.99	6.44
\$1,950.50 \$1,950.60 \$1,9		319882	AA258981	Hs.291392	ESTs ·		7.36
\$16944 \$176266 \$161267 \$1612							3.21
1996	50	319935	H79460				
\$1,925 \$	30		1/9248	H8.133510		3.31	4.05
20007 A-305(14) 20007 B-2007					Human DNA sequence from clone RPS-890F0		
50,000 180/287 180/288 180/287 180/288 180/287 180/288 180/287 180/2		320007	44336314	110.100000	nh-EST40943 Endometrial tumor Homo sanie		
\$2,000 HISTORY 1-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2		320018	T83263		gb;yd40h09,r1 Soares fetal liver spleen	2.77	5.14
200400 A-233271 https://doi.org/10.1001/10	55	320030	H63789		ESTs. Weakly similar to KIAA0638 protein		6.69
2000					ESTs, Weakly similar to A46010 X-linked		3.27
\$20003 AG/74(6) th; 20264 \$6000 febra febra \$5.00 febra; \$2000 febra febra \$2000 febra febra \$2000 febra febra \$2000 febra febra \$2000 febra f		320040	AA233671	Hs.87164	hypothetical protein FLJ14001		
500 145/136			T86564	Hs.302256			
200096 MVH1007 hal.14811 CDCC Spell dividing spok 45, Scoronic 1.00	60						
\$201.00 \$1	00	320090	430411307	No.11/31J	CDC45 (cell division curls 45 S corpuis		
\$\frac{1}{5}\$ \frac{2}{30168}\$ \$\frac{1}{164.175}\$ \$\frac{1}						2.27	
20198 J.WH (2020) 14.17229 ETS 20198 J.WH (2020) 14.17229 ETS 20199 J.WH (2020) 14.17229 ETS		320140	H94179	Hs.119023			1.00
20156 REZ/201 Hand Sapher CMM F. LI (2016 Is, done) EE 2.85 4.35		320188		Hs.172318	ESTs	1.26	1.00
201599 178656 https://doi.org/10.1001/10	65						
202033 AL05227 https://doi.org/10.1003/10.				Hs.24321		2.85	4.53
2007 AA27964 http://discourse.gov/marchina.adgen				Hs.29792			
20229 AFGS8610 to 127711 20225 AFGS8610 to 127711 20225 AFGS8610 to 127711 20225 AFGS8698 to 12725 20221 to 12725 20221 to 12725 20221 to 12725 20225 20225 to 12725 20225 to		320203		HS.124776	homo sapiens mkna; curva ukr-zpocent 110 (1	1.00	1.10
\$\\ \) \$10225	70					0.18	
002211 193199 19424683 ESTS Gyrolds-coppled incorple 55 139	, ,	320225			G antioen, family B. 1 (prostate associa	5.26	13.75
75 300287 ALG6537 in 5132971 in supplies in RIAN £300 ALG6537 in 5132971 in supplies in RIAN £300 ALG6537 in 513297			H03139				1,93
75 32028 HS019 https://dx.doi.org/10.1009/10.1		320260	NM_003608	Hs.131924	G protein-coupled receptor 65		4.56
\$3,0252 AF07374 https://doi.org/10.1009/10.1	75				Homo sapiens mRNA: cDNA DKFZp564P016 (fr	1.00	1.92
\$30325 Alf6978 h.1,58861 consciols control of the c	/5				Homo sagiens cDNA FLJ10664 fis, clone NT		
\$20330 AFGEROM = \(\frac{1.41660}{1.4000} \) = \(\frac{1.41660}{1.4000} \) = \(\frac{1.4160}{1.4000} \) = \(\frac{1.4160}{		320322		Hs.139322		1.41	1.01
30009 H10927 Ma2914A Hone resignes DMR FLJ M478 fix, chose HE 1,81 2.32 50008 H10952 Ma2914B ESTs 100 32 2 50140 R22291 H22396 ESTs 100 32 2 50140 R23291 H23296 ESTs 2014 R2396 ESTs 2014 R2396 R2391 R							1.26
80 300388 H18695 - Hs.31266 ESTs 1.00 3.22 300402 R22291 Hs.23386 Homo sapises clone FLOX76 PRO2852 mRMA, 1.41 1.35 300413 AA233711 Hs.173269 ESTs 2.21 3.61 300422 R62765 Hs.124136 ESTs 11.25 20.78 200436 AA23352 Hs.2358591 ESTs 2.22 3.49		320330					
3.0402 R2291 Hs. 23988 Homo sapians clone FL0578 PR02852 mRM., 1.4f 1.36 3.0414 A.033711 Hs. 173296 SETS 3.0422 R62786 Hs. 124136 ESTS 1.25 3.0404 A.253352 Hs. 23965 SETS 2.22 3.49	80	320388	H16065	. Hs 31286	FSTs		3.22
320413 AA203711 Hs.173289 EBTs 2.31 3.61 320432 R62786 Hs.124136 ESTs 11,25 20,78 		320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
320432 R62786 Hs.124136 ESTs 11.25 20.78 320436 AA253362 Hs.293663 ESTs 2.22 3.49		320413	AA203711	Hs.173269	ESTs	2.31	3.61
		320432	R62786	Hs.124136			
O.3 320438 W24546 H6.5669 ESTS 3.53 8.14	0.5	320436	AA253352	Hs.293663	ESTs	2.22	
	03	32/0438	W24548	H5.5669	ESIS	3.53	0.14

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	320448	Al240233	Hs.80887	v-yes-1 Yameguchi sarcome viral related	1.42	3.46
	320448	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	folistatin-like 1	0.65	1.18
	320499	R32555	Hs.24321	Homo sepiens cDNA FLJ12028 fis, clone HE	3.44	7.15
5	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87 5.63
	320527 320536	R34672 AA331732	Hs.324522 Hs.137224	ESTs ESTs	3.16 2.83	5.83
10	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1,28	1.00
10	320564	AF056209	Hs.159396	peolidylolycine alpha-amidating monogxyg	1.22	0.81
	320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80506	small nuclear ribonucleoprotein polypept	1.00	6.25
1.5	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00 0.14	1.53
	320651 320664	AA489268 Al904216	Hs.111334 Hs.91251	ferrifin, light polypeptide hypothetical protein FLU11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AJ445591		gb:yq04a10.r1 Soares felal liver spicen	1.06 1.35	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	0.04	0.82
25	320771 320794	Al793266 AA281993	Hs-117176 Hs-91226	poly(A)-binding protein, nuclear 1 ESTs	2.96	4.33
23	320734	AF100780	Hs. 194679	WNT1 inductible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	artemin	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1,06	1.75
	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
30	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	A)473796	Hs. 135904	ESTs	1.00	1.00
	320896 320921	AB002155 R94038	Hs.271590 Hs.199538	uroplakin 1B inhibin, beta C	5.90 2.20	2.55 1.17
	320927	A1205786	Hs.199536 Hs.213923	FSTs	0.18	1.46
35	320957	A1878933	Hs.92023	oore histone macroH2A2.2	1.67	2.18
55	320997	H22544	100000	gb:yn69111.r1 Soares adult brain N2b5HB5	3.26	3.52
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321046	H27794	Hs.269055	ESTs	2.69	4.25
40	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56 0.53
40	321059 321062	A1092824 R87955	Hs.126465 Hs.241411	ESTs Home sapiens mRNA full length insert cDN	2.76	5.20
	321062	AF131782	Hs.241411 Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
	321102	AA018306	HS-24 1430	gb:zg40d08.r1 Scares retina N2b4HR Homo	1.79	4.27
	321130	H43750	Hs.125494	ESTs	1.00	3.14
45	321142	A1817933	Hs.298351	ASPL prolein	8.73	15.38
	321155	AA336635	Hs.99598	hynothelical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39 4.46
	321170 321199	N53742 AW386512	Hs. 172982	ESTs	5.69	8.01
50	321199	H54178	Hs.226469	gb:yy56d10.s1 Soares_multiple_sclerosis_ Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
50	321225	AL080073	Hs-251414	Homo saplens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hp. 18192	Ser/Arn-related nuclear matrix protein (1.00	1.00
	321244	AF068654		gb:Homo sapiens isolale AN.1 immunoglobu	2.18	9.13
	321270	R83560		gb:yv76c06.s1 Soares fetal liver spieen	3.80	5.26
55	321317	Al937060	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041 AB033100	Hs.137507 Hs.300646	KIAA1215 protein KIAA protein (simitar to mouse paladin)	0.44	0.93
	321325 321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
	321356	R93443	Hs.271770	ESTs	3.10	4.66
60	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	AI369667	Hs.132743	ESTs	1.13	0,97
	321430	U05890		gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60 0.42	3.11 0.72
65	321467	X13075 AA514198	Hs.38540	gb:Human 2a12 mRNA for kappa-immunoglobu ESTs	2.46	6.50
03	321468 321491	AA514198 H70665	Hs.292549	ESTS	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTS	2.28	3.86
	321510	AA703650	Hs.255748	ESTs	2.14	3.94
70	321513	H84972	Hs.106551	ESTs	2.78	5.37
	321516	A1382803	Hs.159235	ESTs	3.06	7.19
	321565	AJ525773	Hs.266514	hypothetical protein FLJ11342	4.89 1.00	7.82 1.73
	321577 321581	H84260 AA019964	Hs.28803	gb:ys90g04.r1 Sceres rotina N2b5HR Homo ESTs	4.88	6.73
75	321582	AA143755	Hs.28803 Hs.21858	trinucleotide repeat containing 3	1.00	2.08
, ,	321587	H95531	13121000	gb:ys76e02.r1 Soares refina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
00	321642	AW085917	Hs.247084	ESTs	1.52	1.38
80	321669	H95404	Hs.294110	ESTS	2.17	2.45 6.95
	321687	AA625149	Un concer	gb:ef70e12.r1 Soares_NhHMPu_S1 Home sapi	4.31	
	321688	H97646 AA700017	Hs.123158 Hs.173737	Homo sapiens cDNA FLJ 12830 fils, clone NT ras-related C3 botulinum toxin substrate	2.82 0.51	3.28 1.08
	321693 321700	N55160	Hs.167260	ESTs	4.57	7.46
85	321701	AW390923	Hs.42568	ESTs	1.00	1.00

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	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97 1.00	5.26 1.00
	321775 321777	Al694875 Al637993	Hs.202312 Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca Homo sapiens clone N11 NTera2D1 teratoca	1.00	0.45
5	321779	N42729	Hs.163835	FSTs	0.90	0.90
	321829	D61993	Hs.8966	tumor endothelial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809 Hs.46901	ESTs KIAA1462 protein	6.49 0.28	9.58 0.95
10	321883 321899	AA426494 N55158	Hs.29468	ESTs	0.39	0.95
10	321911	AF026944	Hs.293797	ESTs	6.20	10.7
	321949	R49202	Hs.181694	EST	4.62	10.5
	321955	AI651866	Hs.195689	ESTs ESTs	2.89 0.32	5.47 1.25
15	321956 321987	AL110177 AL133612	Hs.132882 Hs.272759	KIAA1457 protein	1.00	1.83
13	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.00	1.90
20	322044 322057	AW340926 N92197	Hs.154679	gb:xy51b10.x1 NCl_CGAP_Lu34.1 Homo sapie synaptoleomin 1	3.20 1.55	9.67 1.07
20	322057	NS2197 Al341937	HS.1540/8	nivel10e03 v1 NC1 CGAP GC4 Homo spriens	4.59	7.68
	322070	U80769	Hs.210322	gb:qt10e03.x1 NCI_CGAP_GC4 Homo sapiens Homo sapiens mRNA for KIAA1766 protein,	2.78	4,52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
25	322091	AI819863	Hs.106243	ESTS	1.59	1.75 5.27
23	322125 322130	R93901 R98978	Hs. 117767	gb:yq16c12.r1 Soares fetal liver spicen ESTs	10.12	16.4
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		nb:vr88b03.r1 Soares fetal liver spicen	4.09	6.67
20	322173	H52567		gb:yl85d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
30	322178	H56535 H92891		gb:yl88g03.r1 Soares_pineal_gland_N3HPG gb:yl94c02.s1 Soares_pineal_gland_N3HPG	0.44 4.52	2.54 7.50
	322179 322186	H92891 H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs. 211516	ESTs	2.20	5.04
	322212	AF087995	Hs.134877	ESTs	3.42	4.84
35	322221	Al890619	Hs. 179662	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	Al640193 AF086283	Hs.226389	ESTs gb:zd46(01.r1 Soares_fetal_heart_NbHH19W ESTs	3.62	1.00
	322278 322284	AF066263 AI792140	Hs.49265	FSTs	0.66	2.76
	322288	AL037273	Hs.7886	pellno (Drosophila) homolog 1	0.71	0.70
40	322320	AF086419		gb:zd78d03.r1 Soares_felal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin	2.92 8.50	4.44 11.5
	322339 322366	W17348 AW404274	Hs.122492	gb:zb18c07.x5 Soeres_fetal_lung_NbHL19W hypothetical protein	0.61	1.34
	322372	W25624	Hs.153943	ESTs	7.37	12.0
45	322374	AI394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.5
	322378	AF064819	Hs.201877	DESC1 protein	1.00 7.09	1.00
	322388 322416	AI815730 AA223183	Hs.247474 Hs.298442	hypothetical protein FLJ21032 adaptor-related protein complex 3, mu 1	3.20	5.80
	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
50	322425	W37943	Hs.34892	KIAA1323 prolein	0.83	1,00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.6 2.23
	322465 322467	AA137152 AF116826	Hs.286049 Hs.180340	phosphoserine aminotransferase putative protein-tyrosine kinase	3.41 1.00	1.30
55	322407	AA744286	Hs.266935	IRNA selenocysteine associated protein	1.75	2.03
50	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359 AI916847	Hs.270947	gb:Homo sapiens full length insert cDNA ESTs	1.25 4.57	8.81
60	322566	W87285	Hs.269587	ESTS	1.00	1.42
• • •	322585	AA837622		ob:zh69c01.r1 Soares folal liver soleen_	4.18	6.94
	322635	AA679064		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352 AIR28854	Hs.256042 Hs.258538	ESTs striatin, calmodulin-binding protein	2.94 0.48	4.64
65	322653	AA011522	HS.258538	gb:zl03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
05	322687	AJ110759		db:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	Al110872	Hs.279812	PRO0327 protein	1.80	1.72
70	322708	AF113674	Hs.283773	clone FLB1727 hypothetical protein FLJ11109	1.00 3.28	3.43
70	322712 322766	AA021328 AW068805	Hs.23607 Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1,53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	Al608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
75	322810	Al962276	Hs.127444 Hs.293616	ESTs	4.09 1.20	6.90 1.63
13	322818 322820	AW043782 AI377755	Hs.293616 Hs.120695	ESTs ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Ha,279727	Homo sacions cDNA FLJ14035 fls, clone HE	5.26	1.22
90	322887	A1986306	Hs.86149	phosphoinosital 3-phosphate-binding prot	2.80	2.24
80	322913	AI733737 AI825940	Hs.68837 Hs.211192	ESTs ESTs	2.38 4.02	6.61 5.79
	322926 322929	ARI25940 AI365585	Hs.211192 Hs.146246	ESTs	0.30	1.14
	322968	AI905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
0.5	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
85	322981	AA493252	Hs.159577	ESTs	2.26	2.61

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	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AJ733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
_	323025	AL157565	Hs.315369	Home sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
5	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46 3.08	1.90 5.64
	323064 323098	AL119341 AI700025	Hs.49359 Hs.270471	Homo sapiens mRNA; cDNA DKFZp547E052 (fr ESTs	2.31	4.49
	323102	AL119913	Hs.163615	ESTS	5.38	11.64
10	323155	AL135041	113.103010	ab:DKFZo762K2310 r1 762 (synonym; hmei2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
1.5	323232	AA148722	Hs.224680	ESTs	0.45	1.35
15	323266	AW003362	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281 323283	AI697556 AA256014	Hs.292659 Hs.86682	ESTs Home sapiens cDNA: FLI21578 fis, clone C	12.68	15.05
	323203	AA226310	Hs.191501	ESTs	4.42	9.61
	323316	AL134620	Hs.280175	ESTs	2.98	5.93
20	323334	Al336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
25	323359	AA234172	Hs.137418	ESTs	0.34	1.18 3.71
25	323360 323405	AA716061 AW139550	Hs.161719 Hs.115173	ESTs ESTs	3.01 1.90	8.81
	323420	AW139550 A1672386	Hs.263780	ESTS	0.29	1.01
	323434	AW081455	Hs.120219	ESTS	2.27	1.92
	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapien	0.43	0.80
30	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	A1652287		gb:EST382593 MAGE resequences, MAGK Homo2. ESTs	.21	3.08
35	323515	AA282274	Hs.256083 Hs.104613	ESTs	2.69 1.20	3.40 1.09
33	323541 323545	Al185116 Al814405	Hs.104613 Hs.224569	RP42 homolog ESTs	1.25	1.09
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fls, clone C	0.27	0.72
	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
	323878	AL042121	Hs.20880	ESTs	3.33	5.10
40	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323748	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06 3.42	3.70 8.13
45	323856	AA355264 T18988	Hs.267604 Hs.293668	hypothetical protein FLJ10450 ESTs	5.97	12.51
45	323857	AA341774	Hs.129212	ESTS	3.17	4.52
	323876	AL042492	Hs.147313	ESTA	0.36	1.00
	323885	AA344308	Hs.128427	Homo saplens BAC clone RP11-335J18 from	2.31	3.33
	323911	AL043212	Hs.92550	ESTs	4.38	5.41
50	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	Al869984	Hs.182906	ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34 1.00	10.07 5.03
	324036 324055	A1472078 AA528794	Hs.303662 Hs.128844	ESTs ESTs	0.86	1.00
55	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
-	324072	AA381829	1101212010	gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4,30
	324129	AJ381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
60	324132	AW504860	Hs.288836	hypothetical prolein FLJ12673	4.24 6.96	6.21 10.69
	324214 324227	AA412395 AA295552	Hs.225740 Hs.28631	ESTs Homo sepiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324227	AA295552 AL047634	Hs.231913	ESTs	2.42	4.05
	324275	AA429088	Hs.98523	ESTS	3.62	5.38
65	324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
	324290	AA432032	Hs.304420	ESTs	3.71	4.34
	324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
	324312	Al198841	Hs.128173	ESTs	4.06	5.91
70	324325	AL138153	Hs.300410	ESTs	5.88	8.25
/0	324338 324341	AL138357 AW197734	Hs.145078 Hs.99807	regulator of differentiation (in S. pomb ESTs, Weakly similar to unnamed protein	0.87 1.28	1.25
	324341	AW452016	Hs.293232	ESTS, Weatry sintag to unioniou protein	2.54	3.46
	324343	AA452306	Hs.270319	ESTs	5.85	8.36
	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
75	324384	AA453396	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	Al924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73 0.71	2.17 1.90
80	324497 324510	AW152624 AI148353	Hs.136340 Hs.287425	ESTs, Weakly similar to unnamed protein Homo septens cDNA FLJ11589 fis, clone HE	1.00	1.00
00	324510	AA492588	FID-201420	glong99c08.s1 NCL_CGAP_Thy1 Homo sapiens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11,36
	324633	AA572994	Hs.325489	ESTs ·	2.92	4.22
0.5	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324675	AW014734	Hs.157969	ESTs	0.39	0.73

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### 1.50 1.50					hundheling podein El 111011	0.93	0.93
\$2,000 \$4,000 \$1,000 \$2,000 \$1,000 \$				Hs.21275		1.57	
\$ 32001 A819826 h.1.4555 short O.Sphraederine (self-Courspin) 1.00 5.55 short O.Sphraederine (self-Courspin						1.55	1.34
2-2622	_	324801	AJ819924	Hs.14553	sterol O-acytransferase (acyt-Coenzyme	1.00	6.56
### ## ### ### ### ### ### ### ### ###	5				gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens		
2-3686 ASSET ASS			AA843926	Hs.124434		2.00	
1-30 1-30					ESTS Could profes yield protein COOK florence		0.43
10					Homo saniens nDNA: FL.122785 fis. clone K	1.68	1.21
2-28685	10		AA806794	Hs 131511	ESTa		5.61
Seesay August		324889	D31010		gb:HUMI.12147 Human fetal lung Homo sapie	2.20	
15 159895 150897 1517000 1517000 151700 151				Hs.265459	ESTs, Moderatoly similar to ALU2_HUMAN A		
15 1688 170897 1.111000 1.110000 1.100000 1.100000 1.1000000 1.100000000 1.10000000000						3.37	0.01
1,000 1,00	1.5	324958	AA625076	HS.132892	protocachenn zu		
	13					5.24	10.22
2016 Aufoliside 1		325105			ESTs	1.00	1.00
20		325108	AA401863		ESTs		
226149 091117 1.4.179761 ESTh	20		D83901		ESTs		
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SECTION SECT		325149				6.50	
25 SECRETA 26 SECRETA 26 SECRETA 26 SECRETA 26 SECRETA 27 SECRETA 28 SEC		325107	HI033002	16.15/012	2010	6.18	
25540 C29 C32 C3						2.64	4.12
15,556 24,29 25,577 25	25	325328					
20373							0.33
2003/16 0.88 1.65		325367					1 22
2004 2004 2004 2004 2004 2004 2004 2004 2004 2005		126380					
26/471 8-6 17.52	30					6.76	14.14
200507 2		325471					
35 205569 7,88 21.40 1.00 1.00 1.00 1.00 1.00 1.00 1.00							
25566 4.00 5.05		325557				5.51	826
2,5569 4.20 5.54	2.5						
1.00	33					4.20	5.24
40 255597 2,59 13.40 25559 13.40 25559 13.40 25559 25578 4.8 12.50 25578 4.8 12.50 25578 4.8 12.50 25578 4.8 12.50 25578 4.8 12.50 25578 4.8 12.50 25578 4.8 12.50 25578 4.8 12.50 25578 4.8 12.50 25578 4.8 12.50 25578 4.7 1		325585				1.10	1.13
40 22658		325587				1.00	1.00
255665 0.66	40					2.98	
15696 0.55 1.55	40					0.76	0.70
20718 4.8 2.0							1.55
45 257789 0.55 0.58 0.58 0.58 0.58 0.58 0.58 0.58						4.48	9.20
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2016 4.74 7.18	45					2.42	
1,000 1,00						7.88	9.83
50 325525 7.76 15.86 7.76 15.86 7.76 15.86 7.76 15.86 7.76 15.86 7.76 15.86 7.76 15.86 7.76 15.86 7.76 15.86 7.76 15.86 7.76 15.86 7.76 7.76 15.86 7.76 7.76 7.76 7.76 7.76 7.76 7.76 7		325819					
50 200625 244 10.00 200625 245 245 10.00 200625 245 245 245 245 245 245 245 245 245 2						7.78	15.98
25544 3.66 5.03	50					2.04	10.60
105666 0.51 0.00		325932					7.36
\$2500		325941				3.66	9.03
\$55 \$\frac{52606}{250006}\$\$\frac{1.57}{250006}\$\$\fr		325969					7.40
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20009 3.50 5.56 6.00 2.00 2.00 2.00 2.00 2.00 2.00 2.0	55	326046				7.21	14.72
Colored Colo		326099				3.60	5.98
60 325165 0.48 1.11 325169 0.13 2.08 1.11 325169 0.13 2.08 2.08 2.08 2.08 2.08 2.08 2.08 2.08		325108				1.27	1.06
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Section S.50 S.00	ου	325165				0.45	0.45
20220 7,00 12,01 1		326 109					
55 32674 100 6.08 52674 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 52674 52674 526850 526850 52674 526850 526850 52674 526850 526850 52674 526850 5268		326230					
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200902 1,00 1,00 1,00 2,0003 1,00 1,0	70	326592				2.77	4.01
20093 1,00 1,31 1,00 1,31 1,00 1,31 1,00 1,31 1,00 1,31 1,00 1,31 1,00		326605				2.01	2.53
75 328720 0.19 0.05 328720 2.34 7.00 328772 2.34 7.00 3287742 2.34 7.00 3287742 2.34 7.00 3287742 2.36 7.00 328742 2.30 7.00 328742 2.30 7.00 328840 2.00 3.00 328840 2.00 1.00 328841 1.00 1.00 328841 1.00 1.00 328841 1.00 1.00 328841 1.00 1.00 328841 1.00 1.00 328841 1.00 1.00 328841 3.00 3288		326692					
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26916 3.00 4.56 2.00 4.50 4.50 4.50 4.50 4.50 4.50 4.50 4	, 5					0.25	0.83
\$1 35984 0.41 1.70 \$25984 \$0 35982 \$2 22 33 35984 \$0 35989 \$1.09 1.20 \$27015 \$27016 \$27016 \$32704 \$355 6.3 \$255 6.3 \$270175 \$355 6.3 \$355 6.2 \$255 6.3 \$270175 \$355 6.3 \$255 6		326818				3.09	4.56
80 336963 202 3.80 326961 1.09 1.20 327035 1.00 6.04 327040 3.05 4.22 327043 3.55 6.31		326936					
326961 1.09 1.20 327038 1.00 8.04 327040 3.05 4.22 3270783 3.35 6.31	90	326964				2.02	1.70
327056 1.00 8.04 327040 3.05 4.22 3270763 3.55 6.31	80	326963					1.20
327040 3.05 4.22 327053 3.55 6.31		327036				1.00	8.04
197063 3.55 6.31		327040				3.05	4.22
6.5 SZ7075 1.59 1.40	0.5	327053					
	85	327075				1.59	1.40

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	327085 327130	
	327156	
5	327220 327224	
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	327321 327332	
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	327442 327467	
15	327467 327473	
	327483 327562	
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20	327606	
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25	327776	
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	327984 328004	
30	328021 328068	
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35	328157 328196	
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40	328299 328342	
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	328369 328381	
45	328461 328481	
10	328500 328630	
50	328608	
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	328664 328666	
55	328698	
	328700 328708	
	328735 328743	
60	328808	
	328861 328908	
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65	328934 328949	
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	329011 329033	
70	329037 329067	
70	329134	
	329157 329178	
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	329224	
	329228 329288	
80	329337 329541	
	329560	
	329588 329643	
85	329703	

2.50 3.74 6.55 1.72 6.65 1.72 6.65 1.72 1.73 1.73 1.74 1.75 12.57 6.594 6.104 6.202 6.202 6.203 6.204 6.203 6.204 6.203 6.204 6.203

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	329764				5.78	15.5 5.44
	329816 329860			•	2.09 3.13	10.7
	329993				7.83	14.2
5	330020				5.58	13.1
	330036				3.32	5.57 7.97
	330052				4.31 1.34	1.76
	330088				4.70	12.4
10	330093				0.44	1.08
	330100				3.47	4.83
	330106 330107				2.14 3.17	6.87
	330120				5.61	11.8
15	330123				4.50	12.7
	330208				1.55	7.62
	330263 330300				2.81	4.96
	330313				3.00	4.41
20	330366				0.67	0.76
	330372 330385	AA449749	1) (000m4	karyopherin alpha 5 (importin alpha 6)	4.76 2.14	11.8 2.15
	330385	AA449749 D14669	Hs.182971 Hs.154387	KIAA0103 gene product	0.40	1.18
	330468	L10343	Hs.112341	protesse inhibitor 3, skin-derived (SKAL	1.11	0.94
25	330472	L24203	Hs.82237	ataxia telangiectasia group D-associated	1.67	1.17
	330478 330493	L38486 M27826	Hs.296049	microfibritar-associated protein 4 endogenous retroviral protease	0.46 1.07	1.07
	330495	M31328	Hs.267319 Hs.71642	guanine nucleotide binding protein (G pr	0.97	0.98
	330506	M61906	Hs.6241	nhosohoinositide-3-kinasa, regulatory su	0.17	3.60
30	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
	330537	U19765	Hs.2110 Hs.183671	zinc finger protein 9 (a cellular retrov	2.81 3.91	2.07
	330547 330551	U32989 U39840	Hs.183671 Hs.299867	tryptophen 2,3-dioxygenase hepatocyte nuclear factor 3, alpha	1.15	1.0
	330568	U56244	10200001	(NONE)	2.83	4.79
35	330599	U90437		ab:Human RP1 homolog mRNA, 3UTR region	2.08	1.5
	330601 330606	U90916 X02419	Hs.82845 Hs.77274	Homo sapiens cDNA: FLJ21930 fis, clone H plasminogen activator, wokinase	0.89 1.87	1.3
	330609	X04741	Hs.76118	ubiquifin carboxyl-terminal esterase L1	1.83	1.3
	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.19
40	330630	X78669	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644 330650	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83 1.25	1.1:
	330660	Z68228 AA347868	Hs.2340 Hs.139293	junction plakeglobin ESTs, Weakly similar to ALU7_HUMAN ALU S	15.50	29.0
	330692	AA017045	Hs.6702	EST ₈	1,00	1.00
45	330707	AA133891	Hs.293690	ESTs	0.20	1.3
	330715 330717	AA233707 AA233928	Hs.11671 Hs.52620	Homo sepiens cDNA FLJ11570 fis, clone HE Integrin, beta 8	0.12 6.62	1.44 6.43
	330772	AA243580	Hs.34382	ESTs	1.40	1.68
	330740	AA297746	Hs.22654	Homo sepiens voltage gated sodium channe	0.27	2.0
50	330742	AA400979	Hs.25691	recentor (calcitonin) activity modifying	0.44	0.90 3.23
	330744 330751	AA406142 AA428286	Hs.12393 Hs.29643	dTDP-D-glucose 4,6-dehydratase Homo sapiens cDNA FLJ13103 lls, clone NT	1,66	1.5
	330780	AA448883	Hs.30469	FSTs	0.52	0.9
	330763	A4450200	Hs.274337	hypothetical protein FLJ20666	0.37	0.9
55	330786 330790	D60374 T48538	Hs.49136 Hs.105807	ESTs, Moderately similar to ALU7_HUMAN A ESTs	0.78	0.8 3.1
	330790	AA015730	Hs.265398	ESTs, Weakly similar to transformation-r	0.37	2.0
	330827	AA040332	Hs.12744	ESTs	1.60	1.0
CO	330844	AA053037	Hs.86803	ESTs	0.93	1.1
60	330901 330931	AA157818 F01443	Hs.267319 Hs.284256	endogenous retroviral protease hypothetical protein FLJ14033 similar to	1.02 0.24	1.00
	330952	H02855	Hs.29967	ESTs	90.0	1.3
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.2
65	330968	H16568	Hs.23748	ESTs	0.48 0.29	0.9
65	331014 331046	H98597 N66563	Hs.30340 Hs.191358	hypothetical protein KIAA 1165 ESTs	0.29	8.9
	331040	N75081	Hs.157148	Homo saciens cDNA FLJ11883 fis, clone HE	1.24	1.0
	331099	R36671	Hs.83937	hypothetical protein	0.75	1.0
70	331108	R41408	Hs.21983	ESTs	1.00	2.7
70	331131 331135	R54797 R61398	Hs.4197	gb:yg87b07.s1 Soares infant brain 1NIB H ESTs	6.04	10.0
	331170	T23461	Hs.159293	ESTs	2.63	4.2
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.7
25	331183	T40769	Hs.8469	ESTs	1.00	3.0
75	331203 331271	T82310 AA059347	Hs 82226	(NONE) glycoprotein (transmembrane) nmb	1.70 1.20	3.8 3.1
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.3
	331327	AA281076	Hs.109221	ESTe	2.09	2.4
80	331341	AA303125	Hs.23240	Homo sapiens cDNA FLJ13496 fis, done PL	0.72	2.4 0.9
٥U	331359 331363	AA416979 AA421562	Hs.46901 Hs.91011	KIAA1462 protein antarior gradient 2 (Xenepus laevis) hom	1.02	0.8
	331378	AA448881	Hs.49282	hypothetical protein FLJ11068	1.03	1.2
	331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.0
85	331402 331422	AA505135 F10802	Hs.44037 Hs.163628	ESTs ESTs, Moderately similar to ALU7_HUMAN	1.80	3.9
0,5	351422	r IUdUZ	FIG. 103020	Ed 15, Intractatory a table to ALO7_FORMAN		1.0

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	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531	N51343	18.20010	abovz15aG4.s1 Soares multiple scierosis	0.98	1.68
	331547	N54811		gbxxd74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
-	331578	N67960	Hs.249989	ESTs	0.11	0.57
5	331589	N71027 N89861	Hs.152618 Hs.112110	ESTs PTD007 protein	1.09 0.93	1.38 0.76
	331606 331614	N92293	Hs.240272	EST FIDOS protein	0.17	1.34
	331668	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
10	331676	W79834	Hs.58559	ESTs, Weakly similar to rholden (M.musc	0.08 8.72	1.07 4.27
	331681 331692	W65712 W93592	Hs.119571 Hs.152213	collagen, type III, alpha 1 (Ehlers-Dani wingless-type MMTV integration site fami	0.94	0.54
	331717	AA190688	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1,34
	331718	AA191404	Hs.104072	ESTs	6.80	11.77
15	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc FST	0.73 2.77	0.59 4.08
	331831 331852	AA412031 AA418988	Hs.97901 Hs.98314	ES I Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
	331943	AA453418	Hs.21275	hypothelical protein FLJ11011	0.36	1.88
20	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990	AA478102	Hs.139631	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19 1.27	0.78 1.03
	332027 332029	AA489671 AA489697	Hs.65641 Hs.145053	hypothetical protein FLJ20073 ESTs	0.30	1.62
25	332029	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA496019	Hs_201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
	332074	AA599012		gb:ae41e11.s1 Gessler Wilms lumor Homo s	0.19	2.00 1.18
30	332083 332085	AA600200 AA600353	Hs.166546 Hs.173933	KIAA1080 protein; Golgi-associated, gamm nuclear factor VA	0.30	1.50
30	332125	AA609661	Hs.312447	ESTs	0.22	0.62
	332177	F10812	Hs.101433	ESTs	0.22 8.21	18.03
	332180	H03348	Hs.7327	claudin 1	2.27	1.57
2.5	332185	H10356	Hs.101689	ESTs	0.09	1.18
35	332203	H49388 N48891	Hs.317769 Hs.101915	EST Stargardt disease 3 (autosomal dominant)	8.05 0.78	5.02 0.85
	332232 332240	N48891 N54803	Hs.324267	ESTs, Weakly similar to pulative p 150 [0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
	332275	R06838	Hs.26530	serum deprivation response (phosphalidy)	0.27	0.76
40	332280	R38100	Hs.146381	RNA binding motif protein, X chromosome	0.39 5.24	1.88
	332299 332304	R69250 R74041	Hs.21201 Hs.101539	nectin 3; DKFZP566B0846 protein ESTs	1.44	3,18
	332304	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1,32
	332384	M11433	Hs.101850	refinel-binding protein 1, cellular	1.71	0.88
45	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.11112	ESTs	0.68 31.54	1.00
	332453 332458	L00205 M33493	Hs.111758 Hs.250700	karatin 6A tryptase beta 1	0.51	1,00
	332504	AA063917	Hs.15106	chromosome 14 open reading frame 1	0.79	1,24
50	332525	M17252	Hs-278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70
	332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteina-rich motor nauron 1	0.22 0.93	1.46 1.49
	332539 332559	AA412528 M13955	Hs.20183 Hs.166189	ESTs, Weakly similar to AF164793 1 prote cytckeratin 2	0.35	1.13
55	332563	N92924	Hs.274407	prolease, serina, 16 (thymus)	1.00	1,00
	332565	AA234896	Hs-25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methyl Cp G binding protein 2 (Rett syndr	0.53	0.59
	332634	\$38953	Hs.283750 Hs.50640	tenascin XA	1.00	1.16 1.70
60	332638 332640	AA283034 AA417152	Hs.5101	JAK binding protein protein regulator of cytokinesi's 1	6.15	1.16
00	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070 Hs.114765	v-myc avian myelocytomatosis viral oncog myeloiditymphoid or mixed-lineage leukem	1,00	1.44
03	332736 332758	L13773 X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ 10902	1.44	1.56
	332792	77 1100204		.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1.70	1.19
	332816				1.85	2.47
70	332858				1.04 3.48	1.57 8.04
	332906				1.00	1.00
	332912				1.06	4.40
	332922				1.00	1.00
75	332956				0.42	0.88
	332959				1.96	6.34
	332982				0.56	0.99
	332984				1,47	2.01
80	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76 1.92	3.70 1,21
	333122 333123				1.92	1,21
85	333123 333138				0.47	0.52

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	333139 333140
5	333221 333260 333380 333387 333512
10	333524 333585 333603 333604 333618 333627
15	333627 333628 333650 333678 333750
20	333763 333767 333768 333769 333772
25	333777 333846 333884 333887 333891
30	333892 333904 333906 333948 33948
35	333966 333968 334061 334094 334113
40	334181 334183 334167 334219 334222 334223
45	334223 334239 334255 334333 334378 334382 334492
50	334562
55	334616 334633 334648 334767 334866 334691
60	334934 334934 334945 334967 334990
65	335015 335093 335120 335125 335179
70	335188 335211 335288 335289 3353861 335379
75	335414 335416 335496 335497
80	335548 335551 335558 335586 335619 339520
85	335620 335621 335682

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	WO 02/086443
	335686 335755
	335784 335814
5	335815
	335823 335835 336851
10	335868 335896
	335936 335948
	335963 335995
15	336021 336034
	336038
20	336107 336205 336275
	336275 336292
	336292 336331 336419
25	336632 336633
	336634 336635 336636
30	336637
	336638 336659
	336675 336684
35	336694 336716
	336721 336796 336900
40	335948
	337028 337043 337046
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43	337128 337162 337183
	337184 337192
50	337194
	337259 337268 337299 337325 337389
55	337325 337325
55	337493 337497
	337500 337549
60	337603 337605
	127674
65	337755 337786 337809
	337862 337871
	337958 338008
70	338033 338083
	338110 338112
75	338145 338148 338158
	338161
80	338179 338182
ου	338189 338197
	338199 338215 338279
85	3382/9 338316

252420 0.2011 1.002 1.00

	WO 02/086443			PCT/US02/12476
	338322	3.23	7.39	
	338357	4.10	11.39	
	336359	10.12	21.59	
	338366	0.69	1.02	
5	338374	0.40	1.18	
_	338414	0.47	1.06	
	338418	6.12	13.86	
	338469	3,09	5,11	
	338501	6.28	10.32	
10	338506	6.97	12.41	
	338523	3,10	5.84	
	338549	1.70	2.70	
	338561	0,79	0.81	
	338662	1,72	1,46	
15	338671	0.17	0.91	
	339676	2.10	15.86	
	338726	1.20	1.09	
	338779	0.12	0.57	
	338804	0.99	1.67	
20	338836	1.00	1.00	
	338871	4.30	9.81	
	338872	5.02	12.81	
	338879	0.23	1.12	
	338937	6.55	12.26	
25	338966	1.76	5.42	
	338993	1.00	2.40	
	339047	5.26	10.81	
	339100	5.10	6.88	
	339114	1.00	1.70	
30	339121	1.00	3.75	
	339170	10.36	19.67	
	339229	4.08	13.48	
	339264	2.64	3.83	
	339293	1.73	1.94	
35				

TABLE 68 shows the assisting markes for lease Playe in Table & basing uniqued Vis. For each probable the base field to general customer can make it in a special country of the probability of the probabil

45 Pkey CAT number Accessions 322044 187363 1 AW340926 AA249063 N86075 Al341937 AW003063 U34725 AA904742 322060 44320_1 50 321430 42705_1 X57414 X57415 321467 43034_1 X13075 X13076 322125 46779_1 R93901 AF075073 R93902 46861_1 46873_1 H69434 AF085958 H69846 322166 322173 H52567 H52557 AF085970 H52164 55 322178 46882_1 H56535 AF085980 H56712 H92891 AF085982 H92777 322179 46885_1 1615102_1 H84849 H84252 H84260 H86664 H85320 1615333_1 H95531 H95521 H84529 321577 321587 111953 1 AA070412 AA102346 AA061885 60 320997 627492_1 H22544 H46842 AI204929 322278 47271_1 W69304 AF086283 W69200

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Pkey: Unique Eos probeset Identifier number CAT number: Gene diuster number Accession: Genbank accession numbers

321687 218439_1 AA825149 AA313030 AA313052 H97463 313883 129439_1 AA665089 AA135130 AA484059 AA102419 AW877765 322320 47422_1 814584 1 W79150 AF086419 AI668646 AI734214 W17348 322339 314648 293660_1 AW979268 AA878419 AA431342 AA431628 300201 682222_1 25196_-2 Al308300 Al308296 306897 A1093967 323155 979809_1 AL120701 AL135041 AL121524 AF147359 T58511 T58980 322527 38927_1 WRR010 WR0126

322585 473768_2 300362 1574395_1 Z42308 H23514 322635 82296 1 AA005129 AA679084 AA694399 322664 85042_1 AA011522 AA702841 AA011691 AA330797 315454 380580_1 AI239464 AI239473 AA625812 AI208703 322687 37372_1 327472_1 AF074666 A\110759 AF090902 AI903735 AA491283 AI694953 AW976903 AA761362 314957

\$07753 657691, 1 AS917274 AW644024 \$07072 289502, 1 AS91722 AS91829 NYSSCSSOS AW65802 AA381742 \$07092 289502, 1 AS91722 AS91829 NYSSCSSOS AW65802 AA381742 \$07092 271461, 1 AA46274 VYZYSS AS917803 BENDRASS AW687803 BEDT9817 \$07092 1 AW67817 AA677034 \$07092 1 AW67817 AA677034

315791 403558_1 AA67477 A4677004 324003 233642_1 AL116754 AA33202 H36001 316519 442685_1 AA67455 AA768376 300926 333127_1 AA504860 AA504911

	wo	02/0864	43 PCT/US02/12476
	324580	328264 1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	A/692552 A/393343 A/800510 A/377711 F24263 A/A661876
-	324889	1515978_1	D31010 D30991 D31168 D31166 D31465
5	302697	43219_1	AJ001409 AJ001410
	302711	45419_1	L08442 D51348
	302742 318499	458_39 364430_1	L12061 T25451 AA585296 AA585306
	310624	34624 4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
10	302847	458_105	X98941 X98942 X98943 X98953 X98949
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	303598	270283_1	AA382814 AA402411 AA412355
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	320007	1815987_1	T83263 T85731 T85730
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	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
25	312389	902067_1	Al863140 V860703 R43474 H14957 R66522 R11908
23	319611 312437	1565863_1 291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131
	312437	291472_1	AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717
			AW063311 AA429538
	311896	579192 1	AW206447 Al248530 Al084433 Al400976 R16553
30	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158 321199	410938_1 212379_1	H79670 H47798 AA700289 N34524 AA306071 AW954803 AA502335 AM33430 AI203997 AW026670 AW266328 AW850787 AA317664 AW993843 AW835572
	321199	212079_1	AW385512 Al334966 W32951 H62656 H53902 R88904 AW835732
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	314126	177666_1 743644_1	AA226431 AA226569 AA488748
	320714		R91883 AI446591
40	306442	AA976899	
40	306446	AA977348	
	306458 306510	AA978186 AA988548	
	306557	AA994530	
	306572	AA995686	•
45	306582	AA998248	
	306666	AI004024	
	306686 306751	AI015615 AI032589	
	308011	AI439473	
50	306892	AI092465	
	308106	AI476803	
	308164	Al500600	
	306956	Al125111	
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55	308216	A1557135	
	308219	Al557246	
	308588	A/718299	
	308599	AI719893	
60	308643	AI745040	
	308673 308697	Al760864 Al767143	
	308778	AI811109	
	308776	Al818289	
65	308875	AI832332	
	308886	A1833240	
	308898	AI858845	
	308966 308979	AJ870704 AJ873111	
70	303011	41689_1	AF090405 AF090407 AF090406
, .	303077	44060_1	AF163305 AF163307 AF163303
	305016	AA626876	
	305034	AA630128	
75	305072 305148	AA641012 AA654070	
15	305190	AA665955	
	303978	AW513315	
	303990	AW515465	¥
00	303998	AW516449	
80	303999	AW516611	
	305235 305312	AA670480 AA700201	
	305312	AA724659	
0.5	306447	AA737856	
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	we	02/086443	
	305614	AA782866	
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_	305650	AA807709	
5	305690 305728	AA813477 AA828209	
	305759	AA835353	
	305792	AA845256	
10	307041	AI144243 AI167439	
	307181	Al189251	
	305901 305910	AA872968 AA875981	
	307415	AI242118	
15	307426 307517	Al243364 Al275055	
	307551	AI281556	
	307561 307608	AI282207 AI290295	
20	307691	Al318285	
	307730 307760	Al336092 Al342387	
	307764	Al342731	
25	307796	AJ350556	
23	309045 309051	AI910902 AI911975	
	307807	Al351799	
	307808 307820	Al351826 Al355761	
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	309122 309164	AI928178 AI937761	
	309177	AI951118	
35	307902 309299	AI380462 AWQQ478	
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	309476 309532	AW129368 AW151119	
	309747	AW264889	
40	309769 309799	AW272346	
	309799	AW276964 AW299916	
	302679	311853_1 H6502	2 AA186889
45	309923 309928	AW340684 AW341418	
	309931	AW341683	
	309933 302705	AW341938 31765 1 10906	0 U09061
50	302789	34161_1 AJ245	067 AJ245070
30	304008 304024	AW517947 T03036	
	304026	T03160	
	304028	T03266	
55	304046 304061	T54803 T61521	
	304063 302802	T62536 34487 1 Y0826	0 Y08245
	304114	R78946	0 100240
60	304155	H68696 N56929	
00	304203 304234	W81608	
	304348 304430	AA179868 AA347682	
	304456	AA411240	
65	304521 304526	AA464716 AA476427	
	304607	AA513322	
	304735	AA576453 AA580401	
70	304760 306015	AA897116	
	306063	AA906316	
	306065 306104	AA906725 AA910956	
75	306109	AA911861	
/3	306242 306288	AA932805 AA936900	
	306396	AA970223	
	330568 330599	NOT_FOUND_entre: 1532312 U9043	z U56244
80	331131	genbank_R54797	R54797
	331203 331531	NOT_FOUND_entre:	T82310 N51343
	331547	genbank_N51343 467396_1 AA828	597 N54811
85	332074	genbank_AA599012	AA599012

WO 02/086443 TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Unique number corresponding to an Ece probesed Sequence source. The 7 dig functions in this outsine are Gendoals Identifier (G) numbers. "Dunham Lel et." refers to the publication entitled "the DNA equipment of human formounce 2C Dunham of all, Nature (1999) 402-495-495. Indicates DNA strand from which comes were predicted. Ref: Strand.

	Nt_position:	Indicates nucleotide		
10				
	Pkey	Ref Strand	Nt_position	
	332792	Dunham, I. et.al.	Plus	73381-73768
	332816	Durham, Letal.	Plus	359844-360030
15	332906	Dunham, I. et.al.	Plus	1923101-1923205
	332911 332912	Dunham, I. et.al.	Plus Plus	1961767-1961858 1962120-1962246
	332922	Dunham I et al.	Plus	2009620-2009738
	332956	Dunham, I. et.al. Dunham, I. et.al. Dunham, I. et.al.		2510528-2510658
20	332959	Dunham, I. et.al.	Plus	2518145-2518213
	333138 333139	Dunham, I. et.al.	Plus Plus Plus Plus Plus Plus	3369205-3369323 3369495-3369571
	333221	Dunham, I. et.al. Dunham, I. et.al.	Plus	3978070-3978187
	333380	Dunham, I. et.al.	Plus	4904775-4904846
25	333387	Dunnam, I. et.al.	Mus	4910935-4910997 5560510-5560564
		Dunham, I. al.al. Dunham, I. et.al.	Plus	5612620-5612780
	333585	Dunham, Let.al.		6234778-6234894
20	333618	Dunham, l. at.al.	Plus Plus	6562391-6562566
30	333627 333628	Dunham, I. at.al.	Plus	6620584-6620903 6629004-6629233
	333650	Dunham, I. at.al. Dunham, I. at.al.	Plus Plus	6796852-6797128
	333678	Dunham, L et.al.	Phie	7068223-7068288 7608165-7608234 7692491-7692630
35	333750	Dunham, I. et.al.	Plus	7608165-7608234
33	333763 333767	Dunham, I. at.al. Dunham, I. at.al.	Plus Plus	7692491-7692630 7694407-7694623
		Dunham, I. et.al.	Plus	7695440,7695697
	333769	Dunham, I. et.al.	Plus	7696625-7696707
40 .	333772	Dunham, I. et.al.	Plus	7706773-7706902
40 .		Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	7746805-7746916 8008623-8008757
		Dunham, I. et.al.	Plus	8153960-8154161
	333887	Dunham, I. et.al.	Plus	8154882-8155025
45	333891 333892	Dunham, I. et.al.	Plus	8156437-8156709 8156825-8157001
73	222040	Dunham, I. et.al. Dunham, I. et.al.	Plus	8583497-8583627
	333954	Dunham, I. et.al.	Plus	6563186-6563335
	333988	Dunham, Let.al.	Plus Plus Plus Plus	8655643-8655826
50	333968 334061	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	8681004-8681241 9686941-9687077
50		Dunham, I. et.al.	Plus	9889953-9890105
	334113	Durham, I. et.al.	Plus	10282459-10282597
	334161	Dunham, I. at.al.	Plus Plus	10599033-10599180
55	334219 334239	Dunham, I. et.al. Dunham, I. et.al.	Plus	12716160-12716384 13056569-13056693
	334333	Durham, I. et.al.	Plus	13603544-13603657
	334378	Dunham, I. at.al.	Plus	13907239-13907370
	334382 334562	Dunham, I. at.al. Dunham, I. et.al.	Plus Plus	13915866-13916036 14987847-14987940
60		Dunham, I. et.al.	Plus	15032740-15032817
	334616	Durham, I. at.al.	Plus	15176123-15176470
		Dunham, I. et.al.	Plus Plus	15333206-153333305 18872214-18872317
		Dunham, I. at.al. Dunham, I. et.al.	Pius	19299770-19299944
65	334934	Dunham I et al	Phie	20103970-20104058
	335015	Dunham, I. at.al.	Plus	20682792-20682945
	335120 335125	Dunnam, I. at.at.	Plus	21436286-21436384 21441390-21441471
	335129	Dunham, I. et.al.	Plus	21634405-21634526
70	335188	Dunham, I. et.al.	Plus	21669118-21669328
	335211	Dunham, I. et.al.	Plus	21774611-21774680
	335361 335379	Dunham, f. et.al. Dunham, f. et.al.	Plus	22807292-22807445 22899306-22899420
	335414	Dunham, t. et.al.	Plus	23235546-23235684
75	335416	Dunham, I. at.al.	Plus	23237354-23237465
	335496 335497	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus Plus Plus Plus Plus Plus Plus	24164386-24164545 24167686-24167869
		Dunham, I. et.al.	Plus	24740167-24740347
	335586	Dunham, I. et.al.	Plus	24990333-24990497
80	335686	Dunham, I. et.al.		25439839-25439920
	335784 335823	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	25942710-25942792 26365925-26366004
	335983	Dunham, I. et.al.	Plus	27938968-27939070
0.5	335995	Dunham, I. et.al.	Plus	28009044-28009184
85	336021	Dunham, I. et.al.	Plus	28686482-28686559

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	336034	Dunham, I. et.al.	Plus	29014404-29014590
	336038	Dunham, I. et.al.	Plus	29022963-29023165
	336107	Dunham, Letal.	Plus Plus	29987731-29987869 963890-985529
5	336632 336633	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	983890-985829 985591-985221
5	336634	Dunham, I. et.al.	Phic	986296-986670
	336635	Dunham, I. et.al.	Plus	987908-988364
	336636	Dunham, I. et.al.	Plus	988418-989185
10	336637 336638	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	989276-990813 991906-993240
10	336659	Dunnam, r. et.al. Dunham, t. et.al.	Plus	1896402-1896478
	336694	Dunham, Let.al.	Plus	2420546-2420616
	336721	Dunham, I. et.al.	Plus	3371522-3371586
1.5	336900	Dunham, Letal	Plus	10236423-10236523
15	336948 337028	Dunhem, I. et.al.	Plus Plus	12692290-12692381 16644817-16644942
	337026	Dunham, I. et.al. Dunham, I. et.al.	Plus	17821742-17821922
	337162	Dunham, Let.el.	Plus	23478943-23479145
	337183	Dunham, Let.al.	Plus	23943606-23943696
20	337184	Dunham, Let.al.	Plus	23973949-23974016
	337268 337299	Dunham, Letal. Dunham, Letal.	Plus Plus	28011979-28012034 29022656-29022775
	337389	Dunham, I. et.al. Dunham, I. et.al.	Plus	31401509-31401579
	337493	Dunham, Letal.	Plus	33330760-333330981
25	337549	Dunham, Let.et.	Plus	34474472-34474531
	337755	Dunham, Letal.	Plus	3971764-3971900
	337809	Dunham, I. et.al.	Plus Plus	4449069-4449193 5443027-5443101
	337871 337958	Dunham, I. et.al. Dunham, I. et.al.	Plus	6969162-6969270
30	338008	Dunham, 1. et.al.	Plus	7697068-7697236
-	338033	Dunham, I. et.al.	Plus	8092128-8092271
	338110	Dunham, I, et.al.	Plus	10384481-10384621
	338112	Dunham, Letal.	Plus	10391398-10391600
35	338145	Dunham, I. et.al.	Plus Plus	11386629-11386692 11448985-11449085
33	338148 338179	Dunham, I. et.al. Dunham, I. et.el.	Plus	12808775-12808833
	338197	Dunham, I. et.el.	Dine	13638107-13638181
	338279	Dunham, I, ot.el.	Plus	16168944-16169091
40	338318	Dunhern, I. et.al.	Plus	17089711-17089988
40	338322	Dunham, Let.al.	Plus Plus	17132477-17132547 18062184-18062402
	338357 338359	Dunham, Letel. Dunham, Letel.	Plus	18074402-18074501
	338366	Dunham, I. et.el.	Plus	18252026-18252189
	338374	Dunham, Let.el.	Plus	18371200-18371282
45	338414	Dunham, Let.el.	Plus	19345573-19345660
	338418	Durham, Let.el.	Plus	19435506-19435596 21244713-21244828
	338501 338506	Dunham, Let.el. Dunham, Let.el.	Plus Plus	21221871-21221953
	338523	Dunham, I. et.al.	Plus	21509763-21509864
50	338662	Dunham, Let.al.	Plus	24404720-24404899
	338804	Dunham, J. et el.	Plus	27236005-27236108
	338836 338879	Dunham, I. et.el. Dunham, I. et.al.	Plus Plus	27792166-27792272
	338079	Dunham, I. et.al.	Plus	28410653-28410734 29160655-29160725
55	338993	Dunham, I. et.el.	Plus	30077787-30078184 30760793-30760968
	339047	Durham, Let.al.	Plus	30760793-30760968
	339100	Dunham, I. et.al.	Plus	31141580-31141765
	339114 339121	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	31456454-31456519 31583467-31583536
60	339121	Dunham, I. et.al.	Plus	32216399-32218527
•••	339293	Dunham, I, et.al.	Plus	33223671-33223819
	332858	Dunham, Let.al.	Minus	1339607-1339397
	332982	Dunham, I. et.al.	Minus	2628296-2628109
65	332984 332998	Dunham, Let.et. Dunham, Let.at.	Minus Minus	2632606-2632457 2711704-2711565
05	333058	Dunham, Letat.	Minus	3028925-3028811
	333097	Dunham, I. et.al.	Minus	3204124-3204036
	333121	Dunham, Let.al.	Minus	3308446-3308358
70	333122	Dunham, Let.al.	Minus	3309596-3309531
70	333123 333140	Dunham, Let.el. Dunham, Let.at.	Minus Minus	3310817-3310749 3377220-3376309
	333260	Dunham, I. et.al.	Minus	4308400-4308304
	333603	Durham, I. et.al.	Minus	6466335-6465727
	333504	Dunham, i. et.al.	Minus	6467090-6466768
75	333904	Dunham, I. et.al.	Minus	8217374-8217261
	333906	Dunham, I. et.al.	Minus Minus	8218238-8218063 11832582-11832508
	334183 334187	Dunham, I. et.al. Dunham, I. et.al.	Minus	11832582-11832508
	334222	Dunham, Letat	Minus	12732417-12732289
80	334223	Durham, Let.at.	Mnus	12734365-12734269
	334255	Dunham, Let.el.	Minus	13200776-13200692
	334492	Durham, Let.al.	Minus	14478333-14478172 15363301-15363222
	334648 334787	Dunham, Let.al. Dunham, Let.al.	Minus Minus	15363301-15363222 16299093-16298937
85	334933	Dunham, Let.al.	Minus	20078117-20077991

	W	O 02/086 Dunham	443		
	334945 334967	Dunham, Dunham,	l. et.al.	Minus Minus	20138885-20138637 20173311-20173218
	334990	Dunham,	l. et.al.	Minus	20173311-20173218
5	335093	Dunham,	l. ct.al.	Minus	21297367-21297214
3	335288 335289	Dunham, Dunham,	l. et.al.	Minus Minus	22304275-22303770 22305950-22305708
	335548	Dunham,	l. et.al.	Minus	24662773-24662673
	335551 335619	Dunham, Dunham,	l. ct.al.	Minus Minus	24679828-24678961 25082677-25082498
10	335620	Dunham, I	l. et.al.	Minus	25092561-25092434
	335621 335682	Dunham,	Lotal	Minus Minus	25098878-25098767 25421215-25421093
	335755	Dunham, I Dunham, I	. et.al.	Minus	25763806-25763747
15	335814	Dunham, I	, et.al.	Minus	26320043-26319845
13	335815 335835	Dunham, I Dunham, I	rtal	Minus Minus	26320518-26320421 26393311-26393245
	335851	Dunham, I	. et.al.	Minus	26604863-26604742
	335868 335896	Dunham, I Dunham, I		Minus Minus	26711437-26711300 26977639-26977558
20	335936	Dunham, !	. et.al.	Minus	27360474-27360400
	335948 336066	Dunham, i	.ct.al.	Minus	27555924-27555788
	336205	Dunham, I Dunham, I	. et.al. . et.al.	Minus Minus	29241080-29240842 30477456-30477311
25	336275	Dunham, I	. et.al.	Minus	30477456-30477311 32085675-32086536
23	336292 336331	Dunham, I Dunham, I	ot al	Minus Minus	32818035-32817927 33594527-33594371
	335419	Dunham, I	.et.a.	Minus	34052568-34052445
	336675 336684	Dunham, I Dunham, I		Minus Minus	2020758-2020664
30	336716	Dunham, !	. et.al.	Minus	2158060-2157993 3259952-3259862
	336798	Dunham, i	. et.a/.	Minus Minus	5888954-5888757
	337043 337046	Dunham, I Dunham, I	et.al.	Minus	17407330-17407251 17610892-17610821
35	337128	Dunham, 1	. ct.al.	Minus	22215251-22215034
33	337192 337194	Dunham, I Dunham, I	. St.al.	Minus Minus	24591853-24691771 24610510-24610359
	337229	Dunham, I	et.al.	Minus	26716579-26716481
	337325 337497	Dunham, I Dunham, I		Minus Minus	30015948-30015800
40	337500	Dunham, t	et.al.	Minus	33371317-33371258 33376212-33376158
	337603 337606	Dunham, I	et.al.	Mnus Mnus	1299296-1299194
	337671	Dunham, I Dunham, I	. et.al.	46	1346555-1346397 3260634-3260547
45	337786	Dunham, I	et.al.	Minus	3260634-3260547 4133203-4133081
+3	337862 338083	Dunham, I Dunham, I	atal	Minus Minus	5347658-5347550 9318438-9318301
	338158	Dunham, I	et.al.	Mnus	11794465-11794343
	338161 338182	Dunham, I. Dunham, I.	et al.	Mnus Minus	12124716-12124658 12824919-12824827
50	338189	Dunham, I	et.al.	Minus	12878594-12878478
	338199 338215	Dunham, I. Dunham, I.	st.sl.	Minus Minus	13760865-13760780 14055447-14055355
	338469	Dunham, I.	atal	Minus	20520297 20520242
55	338549 338561	Dunham, I.	al.al.	Minus	22049171-22049081 22311966-22311856
,,,	338671	Dunham, I. Dunham, I	et.al.	Minus Minus	24508421-24508346
	338676	Dunham, I.	atal.	Minus	24637427-24637369
	338726 338779	Dunham, I. Dunham, I.	et.al.	Minus Minus	25926206-25925618 27030151-27029795
50	338871	Dunham, I.	at at	Minus	28301708-28301611
	338872 338966	Dunham, I. Dunham, I.	etal.	Minus Minus	28300921-28300790 29614876-29614749
	339229	Dunham, I.	et.al.	Minus	32722330-32722199 32975145-32975053
55	339264 325228	Dunham, I. 6381940	etal. Plus	Minus 2630-2694	32975145-32975053
,,,	325235	6381943	Minus	162154-162	264
	329588	3962484	Plus	1169-1619	
	329560 329541	3962491 3983503	Plus Minus	2095-2990 2765-3069	
70	325328	5866875	Plus	86780-8685	
	325340 325373	6017033 5866920	Minus Minus	166656-166 1136686-11	B19 36777
	325367	5866920	Minus	922881-922	968
75	325389 325436	5866921 5866939	Plus Minus	239672-239 29778-2990	759
, 5	325498	5866967	Plus	173372,173	930
	325471 325557	6017034	Minus Plus	289268-289 50921-5105	342
	325559	6249595	Minus	118590-119	172
30	325560	6249595 6249599	Minus	133794-133	981
	325569 325587	6249599 6682462	Plus Plus	79927-8021 126724-126	
	325585	6682462	Plus	73476-7357	4
35	325597 325639	5866992 5867002	Plus Plus	1065020-10 253525-253	55089 608

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	325739	5867038	Minus	205138-205269 207533-207690
	325740	5867038	Minus	207533-207690
	325792	6469828	Minus	1018-1176
5	325735 325685	6552447 6682468	Minus Pius	269122-269190 117397-117483
-	325686	6682468	Plus	118337-118439
	325819	6682490	Minus	130314-130370
	329764	6048195	Minus	109733-109968 135994-140138
10	329703 329643	6065793 6448539	Minus Plus	139994-140138 53403-53537
10	329816	6624888	Minus	70296-70423
	329860	6687260	Minus	163474-163605
	325883	5867087	Plus	22498-22663
15	325895 325925	5867097 5867124	Plus Plus	358317-358476 115749-115962
10	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969	5867153	Pius	101911-102061
20	325971 329993	5867153 4567166	Plus Minus	105841-106035 101307-101434
20	330020	6671887	Plus	172397-172491
	326163	5867168	Minus	7831-8035
	326274	5867171	Minus	410289-410404
25	326025 326046	5867176 5867182	Plus Minus	70854-70915 62668-62825
23	326099	ERC7186	Minus	661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62929
30	326189	5867212	Plus	69288-69413
30	326204 326230	5867218 5867230	Minus Minus	148088-148200 301868-301972
	330052	4567182	Plus	352560-352963
	330036	6042048	Plus	117120-117216
35	326360	5867293	Plus	13627-13844
22	326589 326393	5867320 5867341	Plus Plus	22760-22919 41702-41841
	326505	5887435	Minus	8818-8949
	326515	5867439	Plus	36683-36809
40	326592	6138928	Plus	23689-23826
40	330107 330106	6015249 6015249	Minus Minus	100091-100282 99443-99778
	330100	6015253	Plus	21166-21301
	330093	6015278	Plus	1043-1199
45	330068	6015293	Plus	37517-37638 59613-59770
43	330086 330120	6015302 6671864	Minus Minus	59613-59770 127553-127658
	330123	6671869	Minus	35311-35406
	326742	5867611	Minus	96187-96248
50	328805	5887837	Plus	24656-24749
20	326818 326720	6117831 6552456	Minus	15199-15309 84525-84677
	328770	8598307	Minus	513603-513668
	326692	6682502	Plus	117697-117899 335002-335095 18023-16581
55	326693 326983	6682502	Minus Minus	335002-335095
22	326993	5887657 5867660	Plus	18023-16581
	326936	8004448	Minus	10217-10357
	328984	8489838	Plus	10217-10357 75340-75458
60	327040	6531965	Plus	783670-783817
00	327053 327075	6531965 8531965	Plus	2247257-224743 4041318-404143
	327085	6631966	Plus	4734947-473508
	327036	6531965	Plus	319951-320040
65	327130 327158	6531976	Plus	20247-22343
03	327156	5866841 5867481	Minus Plus	2462-2620 48583-48773
	327332	5867516	Minus	56361-56532
	327220	5867526	Minus	65701-65781
70	327224	5867534	Plus	188468-188544 99745-99836
70	327321 327361	6249562 6552412	Minus Minus	61013-62130
	327396	5867743	Plus	8702-8820
	327414	5867750	Plus	102461-102586
75	327442	5867759	Plus	111483-111618
15	327467 327473	5867772 5867775	Plus Plus	88030-88151 75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
00	327562	5867804	Mnus	343989-344474
80	327568 327606	5867811	Minus	46152-46287 200262-200495
	327611	6004463 5867868	Plus Minus	175063-175392
	327642	5867891	Minus	2513-2743
85	327654	5867910	Minus	97564-97710
00	327734	5867940	Minus	31003-31583

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327775	5867964	Mhus			
327796	5867982	Plus			
327840	6249578	Minus			

130791-130871 85267.85405

73066-73206

66517-66931

101503-101634

157407-157887

289920-290014 263545-263635

80378-80491

73326-73615

16551-16729

42133-42438

95240-95428

66611-66677

713478-714590

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764089-764203

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270724-270798

662758-662848

217275-217336

59098-59481 334973-335406

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108317-108403

117002-117059

771755-771889 846342-846448

43552-43619

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85470-85673

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317461-317688

146417-147652

29959-30018 145940-146155

179177-179463

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467155-467222

8987-9180

75371-75583

29408-29684

68114-68854 89389-89455

76734-76853

778-901

3246-3302

327984 5868216 Plus 15 5902482 328021 Plus 328068 6117819 Plus 328264 6381912 Plus 330300 2905862 Minus 328608 5868222 Minus 20 328600 5868229 Minus 328616 5868239

Plus 328623 5868246 Minus 328632 5868247 Plus 328666 5868254 Minus 25 328698 5868264 Minus 328700 5868264 Plus 328708 5868271 5868289 Minus Plus 328735 328743 328806 5868289 Plus Plus

30 5868324 328299 5868366 Minus 328342 5868383 Plus 328365 5868387 Minus 5868388 328389 Plus 35 328381 5868392 Plus 328451 5868425 Minus 328481 5868449 Minus 328500 5868464 Plus 328530 5868482 Plus 40 328664 6004473 Plus Minus Plus 328861 6381928

328908 5888493 328933 5868500 Plus Plus 328934 5868500 45 328949 6456785 Minus 330313 6042030 5868542 Minus Plus Plus Minus 329005 330366 2944106 330372 6580495 50 329033 5868561 Minus 329037 5868562 Minus

329057 5868591 Minus 329134 5888679 Plus Minus Plus Plus Minus 329157 5868687 55 329178 5868704 329192 5868716 329194 5868716 5868720 5868728 329204 Minus Plus Minus 329224 60 329228 5868728 329288 5868771 Plus

329337 5888806

329011 6682532 Plus

WO 02/086443 PCT/US02/12476 TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-reguisted in lung bunors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granuformatous and carcinoid tumons) relative to normal body (issues. These genes were selected from about 99990 probesels on the Exalifymetrix Hu03 Genechip array.

- Table 18 alone the acception numbers for those Proxy below (bigoest). For table 194. For each probact we have been tested the given dustine number from which the opportunities of the proper of the proxy of the property of 10
 - Table 9C show the genomic positioning for those Pkey's tacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15	ExAcon: Exe		l idenlifier number number, Genbank accession number								
	Uninene Title: Unio	ene gene title									
20		 Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small call carcinomas, granulomatous and carcinoid tumors) divided by the average of normal tune samples 									
20	R2: Ave	age or normal lu	ng samples sensit kung disease samples (indudiae benedifis, ameh	rooma fibrosis alo	electasis, asthme) divided by the average of normal lung samples						
	NZ. AVO	ago ut notrinate	from one access semples friends and processes, only	ocena, narono, un	accepting arrange by the arrange at the second second						
	Pkey ExApon	Unigene?D	Unigene Title	R1	R2						
0.5	400195	-	NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00						
25	400205		NM_006265*:Homo sapiens RAD21 (S. pombe)	15.80	396.00						
	400220		Eas Control	2.28 7.68	2.84 9.72						
	400277 400285		Eos Control Eos Control	1.00	1.00						
	400268 X06256	Hs.149609	Integrin, alphe 5 (fibronectin receptor,	1,04	2.24						
30	400289 X07820	Hs.2258	metrix metalloproteinase 10 (strometysin	132.45	4.00						
	400298 AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00						
	400301 X03635	Hs.1657	estrogen receptor 1	1.00	1.00						
	400303 AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65						
35	400328 X87344	Hs.180062	tronsporter 2, ATP-binding casselle, sub	0.87 156.55	1.80 253.00						
33	400419 AF084545 400512		Terget NM_030678*:Homo sapiens cylochrome P450,	1,00	200						
	400617 AF242388		lengsin	3.67	87.00						
	400560		NM 030878*Homo septens cytochrome P450,	1.00	1,00						
	400664		NM_002425:Homo sapions matrix metallopro	20.26	45.00						
40	400666		NM_002425:Homo saplens matrix metallopro	1.36	1.07						
	400666		NM_002425:Homo sapions metrix metallopro	3.26	3.22						
	400749		NM_003105*:Homo sapiens sortiin-related	1.00 7.63	91.00						
	400763 401027		Terget Exon Target Exon	1.00	1.00						
45	401093		C12000586*xxii6330167 dbi BAA86477.1 (A	1.00	155.00						
10	401203		Terget Exon	1.00	86.00						
	401212		C12000457*:xi\7512178\pir\T30337 polypt	1.00	400.00						
	401411		ENSP00000247172*.HYPOTHETICAL 126.2 kDa	1.00	72.00						
	401435		C14000397 3 7499898 pir T33295 hypoth	1.00	64.00						
50	401464 AF039241		histone deacetylase 5	3.82 2.02	49.00 40.00						
	401714 401747		ENSP00000241802*:CDNA FLJ11007 FIS, CLON Homo sapiens kerain 17 (KRT17)	128.43	68.00						
	401760		Target Exon	1,74	35.00						
	401780		NM_005557*:Homo sapiens keratin 16 (foca	26,47	10.50						
55	401781		Target Exon	10.33	4.61						
	401785		NM_002275":Homo saplens keratin 15 (KRT1	4.13	2.70						
	401797		Target Exon	1.44	2.10						
	401961		NM_021626:Homo saplens serine carboxypep	1.41	1.86 177.00						
60	401985 AF053004 401994		class I cytokine receptor Target Exon	61.84	47.00						
00	402075		ENSP00000251056*:Plasma membrane calcium	1.00	1.00						
	402280		NM_001436*:Homo saplens fibrillarin (FBL	1.58	1.39						
	402265		Target Exon	2.09	35.00						
	402297		Target Exon	1.00	92.00						
65	402408		NM_030920*:Homo sapiens hypothetical pro	28.87	13,00						
	402420		C1000823*:gi[10432400]emb[CAC10290.1] (A	1.00 7.44	1.44 243.00						
	402674 402602		Target Exon NM_001397:Homo sapiens endothelin convor	1.00	70.00						
	402994		NM_002463*:Homo sapiens myxovirus (influ	1.37	1.43						
70	403137		NM 005381*:Homo sepiens nucleolin (NCL).	1.00	19.00						
, 0	403306 NM_00682	5	transmembrane protein (63kD), endoplasmi	1.00	43,00						
	403329		Target Exon	1.00	61.00						
	403381		ENSP00000231844*:Ecotropic virus integra	1.00	119.00						
75	403478		NM_022342:Homo sapiens kinesin protein 9	28.13 20.23	136.00 76.00						
75	403485		C3001813*glj12737279 refPXP_012163.1 k	6.30	29.33						
	403627 403715		Target Exon Target Exon	1.30	35.00						
	404044		ENSP00000237855**DJ398G3.2 (NOVEL PROTEI	1.00	54.00						
	404076		NM_016020*:Homo sapiens CGI-75 protein (14.29	91.00						
80	404101		C8000950:gl/423560/pirj/A47318 RNA-blndi	1.00	1.00						
	404140		NM_006510:Homo sapiens ret finger protei	1.42	1.44						
	404165		ENSP00000244562:NRH dehydrogenase (quino	1.00 1.00	54,00						
	404185		Target Exon NM 005936:Homo sapiens myeloid/lymphoid	5.93	117.00 13.77						
85	404210 404253		NM_021058*:Homo sapiens HZB histone fami	1,00	1.00						
00	404200		mm_oz rodo a romo esquello i izza insiglic idili								

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	404287	O 02/086	143	O6001909:gi[704441]dbj[BAA18909.1] (D298	29.71	42.00
	404298			C5001238*gjj121715jspjP26697jGTA3_CHiCK	1.30	1.00
	404347			Tarrat Extra	1.00	1.00
	404440			NM_021048:Homo sapiens melanoma antigen.	1.00	15.00
5	404721			NM_005596*:Homo sepiens nuclear factor I	1.00	60.00
	404794	NM_000078		cholesteryl ester transfer protein, plas	1.07	1.38
	404854 404877			Target Exon NM_005365:Homo saplens melanoma antigen,	1.61	2.01 1.00
	404927			Target Exon	1.00	1.00
10	404996			Target Exon	1.00	1.00
	405449			CY000047*nil11427234beffXP 009399.11 z	1.00	1.00
	405568			NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
	405572			Target Exon	0.76	1.14
15	405646 405676	BE336714		C12000200gij4557225[ref]NP_000005.1] al cytochrome c-1	1.01	1.28
13	405770	DE330714		NM_002362:Homo sapiens melanoma antigen.	45.52	37.00
	405932			C15000305:gl[3806122[gb]AAC69198.1] (AF0	1,99	1,99
	406137			NM .000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
20	406360			Target Exon	1.00	35.00
20	406399 406467			NM_003122*:Homo seplens serine protesse	1.00 1.00	1.00
	406621	X57809	Hs.181125	Target Exon immunoglobulin lambda locus	1.41	1,74
	406642	AJ245210	110.101125	d:Homo sagiane mRNA for immunoglobulin	2.16	3.91
	406663	U24683	Hs-293441	immunosfobulin heavy constant mu	2.07	2.93
25	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	15.00	51.00
	406673	M34996	Hs.198253	major histocompatibility complex, class	0.98	3.09
	406676	X58399	Hs.81221	Human L2-9 transcript of unrearranged im	1.30 1.33	1.53
	406678 406685	U77534 M18728		gb:Human clone 1A11 immunoglobulin varia ob:Human nonspecific crossreading antig	1.46	2.85
30	406687	M31126	Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
-	406690	M29540	Hs.220529	carcingembryonic antigen-related cell ad	226.37	350.00
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.01	2.52
	406815	AA833930	Hs.288036	tRNA isopenieny/pyrophosphate transferas	20.25	32.00
35	406851 406964	AA609784 M21305		major histocompatibility complex, class gb:Human alpha salellite and salellite 3	0.75 38.15	1.91
33	406967	M21305 M24349		go:Human perathyroid hormone-fike protei	1.00	1.00
	406974	M57293		gb:Human paralityroid hormone-related pep	1.00	1.00
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.77	1.10
40	407128	R83312	Hs.237260	EST	1.00	1.00
40	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
	407168 407239	R45175 AA078350	Hs.117183 Hs.87848	ESTs leukccyte immunoglobufin-like receptor,	2.16 1.10	18.00 1.57
	407242	M18728	U9'01'040	gb:Human nonspecific crossreacting antig	1.12	2.85
	407244	M10014	Hs.75431	fibrinogen, gamme polypeptide	3.24	16.38
45	407289	AA135159	Hs.203349	Homo saciens cDNA FLJ12149 fis, clone MA	3.53	3,68
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74 0.06	73.00
	407366 407378	AF026942	Hs.271530 Hs.57778	gb:Homo saplens cig33 mRNA, pertial sequ ESTs, Moderately similar to 138022 hypot	1.00	8.25 26.00
	407430	AA299284 AF169361	HS.5///6	gb:Homo sapiens protein tyrosine phospha	1.00	25.00
50	407453	AJ132067		gb:Homo sapiens mRNA for exonemal dynein	1.00	75.00
	407577	AW131324	Hs.246759	hypothetical protein MGC12538	1.00	1.00
	407634	AW016569	Hs.136414	UDP-GloVAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
	407710	AW022727	Hs.23616	ESTs .	1.00 1.89	28.00 1.31
55	407720 407746	ABC37776 AK001962	Hs.38002	KIAA1355 protein hypothetical protein FLJ11100	1.00	1.00
55	407756	AA116021	Hs.38260	ubiguitin specific protesse 18	4.51	5.00
	407758	D50915	Hs.38355	KIAA0125 gene product	1.00	28.00
	407782	AA608956	Hs.112619	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
60	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	7.88	3.83
00	407790 407811	AI027274 AW190902	Hs.40098	Homo sapiens cDNA FLJ14866 fis, clone PL cysieine knot superfamily 1, BMP antagon	3.63 89.96	42.00 109.00
	407839	AA045144	Hs.161596	ESTs	173,91	108.00
	407944	R34008	Hs.239727	desmocoltin 2	111.30	70.00
	408000	L11690	Hs.620	bullous pemphigold antigan 1 (230/240kD)	151.17	8.00
65	408031	AA081395	Hs.42173	Homo sepions cDNA FLJ10366 fis, clone NT	9.91	93.00
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	195.78 1.00	231.00
	408070	AW148852 AW968904	Hs.123073	gb:xf05d05.x1 NCL_CGAP_Bm3S Home sapien CDC2-related protein kinasa 7	37.84	61.00
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	0.85	1.71
70	406212	AA297567	Hs.43728	hypothatical protein	5.88	7.91
	408243	Y00787	Hs.624	interleukin 8	4.27	9.98
	408349	BE546947	Hs.44276	homeo box C10	3.79	3.46
	406353	BE439838 AI382803	Hs.44298	mitochondrial ribosomal protein S17 FSTs	1.88 1.00	1.65 73.00
75	408354 408369	R38438	Hs.159235 Hs.182575	solute carrier family 15 (H???? transport	1.41	16.50
, 5	408380	AF123050	Hs.44532	diubiquitin	15,19	37.22
	408482	NM_000676	Hs.45743	adenosine A2b receptor	1.85	1.19
	408522	AJ541214	Hs.46320	Small profine rich protein SPRK [human,	1.98	1.24
90	408536	AW381532	Hs.135188	ESTs	1.55	1.50
80	408545 408572	AW235405 AA065811	Hs.253690 Hs.228588	ESTs, Moderately similar to ALU4_HUMAN A	1.00 1.00	1.00 44.00
	408572	AAU55511 AW963372	Hs.225558 Hs.46677	PRO2000 protein	107.16	55.00
	408660	AA525775		ESTs, Moderately similar to PC4259 ferri	1.00	1.00
	408761	AA057264	Hs-238936	ESTs, Waskly similar to (defline not ava	52.24	141.00
85	408771	AW732573	Hs.47584	potassium voltage gated channel, delayed	3.05	109,00

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	W	O 02/086	443			
	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790 408805	AW580227	Hs.47860 Hs.48269	neurotrophic tyrosine kinase, receptor, vaccinia related kinase 1	41.19 24.67	61.00 45.00
	408841	H69912 AW438865	Hs.256862	PSTs	1.00	58.00
5	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	1.00	89,00
-	408908	BE296227	Hs.250822	serino/threoning kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guarine nucleotide binding protein (G pr	1.00	1.00
	408996 409015	AI979168 BE389387	Hs.344096 Hs.49767	g'ycoprolein (transmembrane) nmb NM_004553:Homo sapiens NADH dehydrogenas	3.71 1.44	5.50 1.24
10	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Ov	4.28	5.32
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.0
	409077	AA401369	Hs.190721	ESTs	1.00	17.01
	409093 409103	BE243834 AF251237	Hs.50441	CGI-04 protein XAGE-1 protein	2.02 80.44	1.93
15	409103	AF251237 AL136877	Hs.112208 Hs.50758	SMC4 /chrichital mainlenance of chromoso	14.87	6,00
	409187	AF154830	Hs.50966	carbamoyl-phosphale synthelase 1, miloch	1.00	1.00
	409228	A)654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1,00
	409234	AI879419	Hs.27206	ESTs ESTs	1.00 11.90	1.00
20	409268 409269	AA525304 AA576953	Hs.187579 Hs.22972	hypothetical protein FLJ13352	1.00	1,00
20	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168,91	35.0
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (niceln (100kD), kalini	79.74 1.45	96.00 2.10
25	409430 409446	R21945 Al561173	Hs.346735 Hs.67688	splicing factor, arginine/serine-rich 5 ESTs	1.45	4.00
23	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.0
	409522	AA075382		qb:zm87b03.s1 Stratagene ovarien cancor	15.98	141.0
	409582	AA401369	Hs.190721	ESTs	1.00	17.0
30	409632 409705	W74001 M37762	Hs.55279 Hs.56023	serine (or cysteine) profeinase inhibito brain-derived neurotrophic factor	292.12 1.00	79.00 82.00
30	409710	M3/762 AT789160	Hs.108681	Homo sapiens brain (umor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo seplens mRNA; cDNA DKFZp586P2321 (f	20.75	51.0
35	409757	NM_001898	Hs.123114	cystatin SN gbtUl-HF-BR0p-ajr-f-11-0-ULr1 NIH_MGC_5	22.46 1.00	15.80
33	409866 409893	AW502152 AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.00
	409902	Al337658	Hs.156351	ESTs	25.92	50,00
	409935	AW511413	Hs.278025	ESTs	2.63	2.11
40	409956 409958	AW103364	Hs.727	inhibin, bela A (activin A, activin AB a	2.17 0.91	4.01 2.07
40	409958 410001	NM_001523 AB041036	Hs.57697 Hs.57771	hyaluronan synthese 1 kalikrein 11	1.04	2.28
	410032	BE065965	ns.o///	ab;RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.0
45	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
45	410048 410076	W78487 T05387	Hs.58218 Hs.7991	profine oxidase homolog ESTs	1.03 1.12	1.44
	410102	AW248508	Hs.279727	Homo septens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311928	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
50	410193 410274	AJ132592 AA381807	Hs.59757 Hs.81782	zinc finger protein 281 hypoxia-inducible protein 2	42,01 1,72	51.00 1.32
	410274	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182633	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
	410348	AW182663	Hs.95469	ESTs	1.00	1.00
55	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
	410418 410438	D31382 AB037756	Hs.63325 Hs.45207	transmembrane protease, serine 4 hypothetical protein KIAA1335	4.30 1.00	2.03
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
	410555	W27235	Hs.64311	a disintentin and metalingrateinase dome	23.99	1.41
60	410561	BE540255	Hs.6994	Homo saplens cDNA: FLJ22044 fis, clone H	10,04	1.00
	410681 410781	AW246890 Al375672	Hs.65425 Hs.165028	calbindin 1, (28kD) ESTs	10.88	18.92 57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobultr-like receptor,	1.62	3.78
	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
65	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58 84.00
	411152 411248	BE069199 AA551538	Hs.334605	gb:QV3-BT0379-010300-105-g03 BT0379 Homo Homo sspiens cDNA FLJ14408 fis, clone HE	1.00 1.82	1.45
	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
70	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
	411402 411573	BE297855 AB029000	Hs.69855 Hs.70823	NRAS-related gene KIAA1077 protein	1.00 11.40	46.00 11.35
	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	1.08	1.90
	411617	AA247994	Hs.90063	neurocalc'n delta	1.74	2.57
75	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
	411773	NM_006799 AF245505	Hs.72026	prolease, sorino, 21 (lostisin)	1.34 2.19	2.19 2.79
	411789 411800	AF245505 N39342	Hs.72157 Hs.103042	Adlican microtubule-associated protein 1B	23,34	34,00
	411945	AL033527	Hs.92137	v-mvc avian myelocytomatosis viral oncog	1,00	8.00
80	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
	412140	AA219691	Hs.73625	RAR6 interaction, kinesin-like (rabkines	118.48 1.98	92.00
	412276 412464	BE262621 T78141	Hs.73798 Hs.22826	macrophage migration inhibitory factor (ESTs, Weakly similar to ISS214 salivary	1,16	1.49
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
85	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

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	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	14.65	47.00
	412719	AW016610	Hs.816	ESTs	332-46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54,90	1.00
5	412811	H06382 AL037159	Hs.74619	ESTs protessome (prosome, macropain) 26S subu	1.00 1.63	11,00
,	412817 412863	AA121673	Hs.59757	zine finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	intedeukin enhancer binding factor 2, 4	2.19	2.05
10	413011 413048	AW068115 M93221	Hs.821 Hs.75182	biglycan mannose receptor, C type 1	0.30	6.23
10	413048	AL035737	Hs.75184	chitinase 3-like 1 (carfilage glycoprole	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	oměthine decarboxylase 1	1.92	2.59
15	413223	A1732182 T64858	Hs.191866 Hs.21433	ESTs	5.73 0.99	27.00 1.06
13	413248	154838	Hs.75257	hypothesical protein DKFZp547J036 stam-loop (histone) binding protein	1.00	18,00
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
20	413364	BE536218	Hs.137516	fidgetin-like 1	1.00	1.00
20	413385 413409	M34455 A)638418	Hs.840 Hs.1440	indoleamine-pyrrole 2,3 dioxygenase DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.46
25	413554	AA319146	Hs.75426	socretogranin II (chromogranin C)	79.15	114.00
25	413573 413582	AI733859 AW295647	Hs.149089 Hs.71331	ESTs hypothetical protein MGC5350	1.00	1,00
	413582 413597	AVV200047 AW302885	Hs.117183	FSTs	1.00	1,00
	413690	BE157489	114.117100	gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
•	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
30	413719	BE439580	Hs.75498	small inducible cylokine subfamily A (Cy	2.88 144.10	9.52 108.00
	413753 413801	U17760 M62246	Hs.75517 Hs.35406	laminin, beta 3 (nicein (125kD), kafinin ESTs, Highly similar to unnamed protein	1.00	17,00
	413833	Z15005	Hs.75573	contromere protein E (312kD)	1.00	1.00
	413882	AA132973	Hs.184492	ESTs	64.24	148.00
35	413926	AA133338	Hs.54310	ESTs	1.00	67.00 42.00
	413943 413995	AW294416 BE048146	Hs.144687 Hs.75671	Homo sepiens cDNA FLJ12981 fis, done NT syntaxin 1A (brain)	43.42 1.23	1.11
	414035	Y00630	Hs.75716	serine (or cystolne) proteinase inhibito	2.02	2.51
	414142	AW368397	Hs.334485	Homo secions cDNA FLJ14438 fts, clone Ht.	1.00	102.00
40	414180	Al863304	Hs.120905	Homo sepiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein femily, member 1	1.00- 1.00	1.00 59.00
	414275 414317	AW970254 BE263280	Hs.889 Hs.75888	Charot-Leyden crystal protein phosphogluconate dehydrogenase	1,52	1.73
	414334	AAR24298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
45	414341	D80004	Hs.75909	KIAA0182 prolein	33.90	151.00
	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414418 414430	AW409985 AJ346201	Hs.76084 Hs.76118	hypothetical protein MGC2721 ubiquitin cerboxyl-terminal esterase L1	2.32 226.15	1.85 66.00
	414570	Y00285	Hs.76473	Insulin-like growth factor 2 receptor	1.64	1.98
50	414618	AI204800	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	Interleukin enhancer binding factor 1	1.51	1.39
	414683	S78296 AF002020	Hs.76888 Hs.78918	hypothetical protein MGC12702 Niemann-Pick disease, type C1	43.61 28.63	64.00 71.00
	414898 414711	AP002020 AI310440	Hs.288735	Homo saciens cDNA FLJ13522 fis, clone PL	14.86	42.00
55	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410978	Hs.77152	minichromosome maintenance deficient (S.	1.64	1.44
	414747	U30872 AU077228	Hs,77204	centromere protein F (350/400kD, mitosin enhancer of zeste (Drosophile) homolog 2	65.01 130.35	74.00 121.00
	414761 414774	X02419	Hs.77256 Hs.77274	plasminogen activator, urokinase	2.24	2.19
60	414306	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
	414309	Al434699	Hs,77356	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825 414839	X06370 X63692	Hs,77432 Hs,77462	epidermal growth factor receptor (avian	103.22 1.80	143.00 1.69
65	414883	AA926960	Na.//402	DNA (cytosine-5-)-methyltransferase 1 CDC28 protein kinase 1	14.29	10.06
05	414907	X90725	Hs.77597	polo (Drosonhia)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia tolangicclasio and Rad3 related	3.00	2.90
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
70	414972 415014	BE263782 AW954064	Hs.77695 Hs.24951	K/AA0008 gene product ESTs	1.42	2,84
70	415014	AL044872	Hs.77910	3-hydroxy-3-methylglularyl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
	415227	AW821113	Hs.72402	ESTs	1.87	49.00
75	415238	R37780 AA948033	Hs,21422 Hs,130853	ESTs ESTs	1.00	1.00
15	415263 415295	R41450	Hs.6546	ESTs	1.00	1.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	sprine (or cysteine) proteinase inhibito	30.84	63.00
80	415674	BE394784	Hs,78596	proteasome (prosome, macropain) subunit,	1.48 1.00	1.39
δU	415709 415735	AA649850 AA704162	Hs.278558 Hs.120811	ESTs ESTs, Weakly similar to 138022 hypotheti	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphalaso, receptor-t	24.30	1.00
0.5	415857	AA866115	Hs.127797	Home septens cDNA FLJ11381 fis, clone HE	32.51 78.89	35,00 1.00
85	415989	A1267700		ESTs	10.09	1.00

		O 02/086	443			
	416018	AW138239	Hs.78977	proprotein convertase sublifsin/koxin t	1.00	1.00
	416065 416111	BE267931 AA033813	Hs.78996 Hs.79018	proliferating cell nuclear antigen chromatin assembly factor 1, subunit A (3,35 39,03	2.32 3.00
	416177	AA174069	Hs.187607	ESTs	100	9.00
5	416178	AJ808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209 416239	AA 236776 AL 038450	Hs.79078 Hs.48948	MAD2 (mitotic arrest deficient, yeast, h ESTs	9.70 83.87	1.00 129.00
	416239	ALU38490 AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2,12
10	416322	BE019494	Hs.79217	pyrroline-5-carboxytele reductase 1	2.08	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448 416498	L13210 U33632	Hs.79339 Hs.79351	lectin, galactoside-binding, soluble, 3 potassium channel, subfamily K, member 1	1.26 27.29	1,54 67.00
	416658	1103272	Hs.79432	fortiin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
	416819 416936	U77735 N21352	Hs.80205 Hs.42987	pim-2 oncogene ESTs. Weakly similar to S21348 probable	1.59 1.00	1.84
	417034	NM_006183	Hs.80962	neumletsin	1.00	1.00
20	417061	AI675944	Hs.188691	Homo saplens cDNA FLJ12033 fis, clone HE	32.95	156.00
	417079	U65590	Hs.81134	interteukin 1 receptor antagonist	3.91	4.93
	417218	AA129547 W25005	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00 3.38	51.00 2.05
	417233 417308	W25005 H60720	Hs.24395 Hs.81892	small inducible cylokine subfamily B (Cy KIAA0101 gene product	3.36 82.94	25.36
25	417315	AI080042	Hs.180450	ribosomal protein S24	106,61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs,1076	small proline-rich protein 1B (comifin)	8,97	3.27
	417389 417428	BE260964 N87579	Hs.82045 Hs.278871	midkine (neurite growth-promoting factor gb:LL2030F Human fetal heart, Lambda ZAP	2.59 1.00	1.82 52.00
30	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprolein	304.75	173.0
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1,34
	417512	Al979168	Hs.344096	givcocrotein (transmembrane) nmb	2.14	5.50
	417515 417542	L24203 J04129	Hs.82237 Hs.82269	ataxia-telengiectasie group D-associated progestagen-associated endometrial prote	2.66 1.28	1.68
35	417576	AA339449	Hs.82285	phosphoribosylgtycinamide formyltransfer	42.76	51.00
55	417715	AW969587	Hs.86366	ESTs	6.35	2.75
	417720	AA205625	Hs.208067	ESTs	113.31	58.00
	417791 417830	AW965339 AW504786	Hs.111471 Hs.122579	ESTs hypothetical protein FLJ10461	39.98 2.61	16.00 31.00
40	417886	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	244
	417900	BE250127	Hs.82906	CDC20 (celt division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	trymidylate synthetase	4.74	2.55
	417944 417975	AU077196 AA641836	Hs.82985 Hs.30085	collagen, type V, alpha 2 hypothetical protein FLJ23186	3.61 12.49	5.21 38.00
45	417975	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	metrix metalloproteinase 1 (interstitial	187,59	1.00
	418054	NM_002318 NM_012151	Hs.83354 Hs.83363	lysyl oxidase-like 2 coagulation factor VIII-associated (intr	2.85 1.54	2.63 1.69
50	418057 418113	NM_012151 Al272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE813836 .	Hs.83551	microfibritar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207 418218	C14685 AA882240	Hs.34772 Hs.283099	ESTs	1.00 64.66	1.00 61.00
55	418236	AW994005	Hs.337534	AF15q14 protein ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (much 9	1.00	3.00
	418283 418300	S79895 A1433074	Hs.83942 Hs.86682	cathepsin K (pycnodysoslosis) Homo segiens cDNA: FLJ21578 fls, clone C	3.96 3.18	5.16 2.91
60	418300	AA284166	Hs.84113	cyclin-dependent kinase thribitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379 418397	AA218940 NM_001269	Hs.137516 Hs.84746	fidgetin-like 1	21.68 1.00	44,00 8.00
65	418403	D86978	Hs.84790	chromosome condensation 1 KIAA0225 protein	16.91	18.98
0.5	418462	BE001596	Hs.85266	Integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinese Inhibitor 2A (me	3.22	2.38
	418506 418526	AA084248 BE019020	Hs.85339 Hs.85838	G protein-coupled receptor 39	2.66 2.04	2.22
70	418526	BE244323	Hs.85838 Hs.85951	solute carrier family 16 (monocarboxylic exportin, IRNA (nuclear export receptor	1.33	37.00
, 0	418543	NM.005329	Hs.85962	hyaluronan synthase 3	1.04	1,23
	418574	N28754		M-phase phosphoprolein 9	48.60	85.00
	418592 418641	X99226 BE243136	Hs.284153 Hs.86947	Fanconi anomia, complementation group A a disinfegrin and metalloproteinase doma	18.24 1.19	26.00 1,41
75	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
, ,	418663	AK001100	Hs.41690	desmocotin 3	112.17	19,00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418686	Z36830	Hs.87268	annexin A8	1,54	1.98
80	418689 418712	AI360883 Z42183	Hs.274448	hypothetical protein FLJ11029 gb:HSC0BF041 normalized infant brain cDN	1.19 1.00	1.04 12.00
50	418727	AA227609	Hs,94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cetionic emino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
85	418830 418882	BE513731 NM_004996	Hs.88959 Hs.89433	hypothetical protein MGC4816 ATP-binding cassette, sub-family C (CFTR	20.97 57.09	23.00 35.00
05	+10002		10.004-03	among consens, one many o for 11		32,30

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		O 02/086				
	418971	AA360392	Hs.87113	ESTs	1.00 4.89	12.00 28.00
	418973 419078	AA233056 M93119	Hs.191518 Hs.89584	ESTs insulinoma-associated 1	1.00	10,00
	419079	AW014836	Hs.18844	ESTs	1.09	1.98
5	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
	419088	A1538323	Hs.52620	integrin, beta 8	15.60 1.11	51,00 1,83
	419092 419121	J05581 AA374372	Hs.89603 Hs.89626	mucin 1, transmembrane parathyroid hormone-like hormone	1.11	1.00
	419171	NM_002846	Hs.89655	protein tyrosine phosphalase, receptor t	1.10	1.14
10	419183	U60669	Hs.89663	cylochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256106	Hs.87507	ESTs	1.00	34.00
	419335	AW960146	Hs.284137 Hs.1252	hypothetical protein FLJ12888 apolipoprotein H (beta-2-glycoprotein I)	1.00 22.63	8.00 54.00
15	419354 419359	M62839 AL043202	Hs.1252 Hs.90073	chromosome segregation 1 (yeast homolog)	250	1,98
13	419423	D26488	Hs.90315	KIAA0007 protein	1,00	7.00
	419443	D62703		ab±HUM316G10B Clontech human aorta polyA	1.00	12.00
	419452	U33535	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
20	419474	AW968619	Hs.155849	ESTs	13,63	62.00
20	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4,27 3.66	2.26 3.63
	419488 419502	AA316241 AU076704	Hs.90691	nucleophosmin/nucleoplasmin 3 fibrinogen, A alpha polypeptide	13.05	115.00
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74,60	117.00
	419556	U29615	Hs.91093	chiltnase 1 (chilotriosidase)	1,47	4.98
25	419569	A1971651	Hs.91143	jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topolsomerase (DNA) II binding protein	94,30	94.00
	419703	AJ793257 NM 001650	Hs.128151 Hs.288650	ESTs aquaporin 4	15.26 1.00	50.00 191.00
	419721 419729	AA586442	Hs.288650 Hs.21411	gbgc53e03.s1 NCI_CGAP_SS1 Homo sapiens	1.00	59.00
30	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1,08
•	419745	AF042001	Hs.93005	stug (chicken homolog), zinc finger prot	1,00	1.00
	419752	AA249573	Hs.152618	ESTs. Moderately similar to ZN91 HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac gb;ol91d05,y5 NCI_CGAP_Kid5 Homo septens	50.99	214.00 1.00
35	419936	Al792788		gb;ol91d05,y5 NCI_CGAP_Rid5 Homo septens	1.00 1,64	2.47
33	419937 419983	AB040959 W55956	Hs.93836 Hs.94030	DKFZP434N014 protein Homo saplens mRNA; cDNA DKFZp585E1624 (f	15,72	94.00
	420005	AW271106	Hs.133294	ESTs	3.15	1.43
	420047	AM78658	Hs.94631	brefeldin A-inhibited quantine nucleotide	12.45	39.00
	420058	AK001423	Hs.94694	Homo sepiens cDNA FLJ10561 fis, clone NT	1.00	117.00
40	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35 0.77	3.23 1.15
	420259 420281	AF004884 Al623693	Hs.96253 Hs.323494	carcium channel, voltage-dependent, P/Q ESTs	45.04	54.00
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49,22	31,00
45	420332	NM 001756	Hs.1305	serine (or cysteine) proteinase inhibito	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420482	AF050147	Hs.97932	chondromodulin I precursor	1.00	1.00
	420520	AK001978	Hs,98510	similar to rab11-binding protein	49.74 94.65	133.00
50	420552 420580	AK000492 AW207748	Hs.98806 Hs.59115	hypothetical protein ESTs	1.00	17.00
50	420610	ANR3183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
	420759	T11832	Hs.127797	Homo sapiens cONA FLJ11381 fis, clone HE	1,00	48.00
55	420783 420900	Al659838 AL045833	Hs.99923 Hs.44269	lectin, galacioside-binding, schuble, 7 ESTs	3.04 2.24	1.25 7.00
	420900	ADJ40033 AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
	421027	AA781198	Hs.55254	ESTs	2.87	38,00
60	421037	A1684808	Hs.197653	ESTs	1,00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to 138022 hypot	1.00	98.00 1.46
	421073	NM_004689	Hs,101448	metastas's associated 1	1.34 119,47	427.00
	421110 421133	AJ250717 AA401369	Hs.1355 Hs.190721	cathepsin E FSTs	1.10	17.00
65	421150	AI913562	Hs,189902	ESTs	1.45	1.63
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1,37	1.10
	421316	AA287203	Hs,324728	SMA5	1.00	21.00
70	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92 5.89	3.94 14.00
70	421451 421474	AA291377 U76362	Hs.50831 Hs.104637	ESTs solute carrier family 1 (glutamate trans	1.46	1,76
	421506	BE302796	Hs,105097	thymidine kinese 1, soluble	1.56	1.08
	421508	NM 004833	Hs.105115	absent in melanoma 2	5,11	5.23
	421515	Y11339	Hs,105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
75	421524	AA312082	Hs.105445	GDNF family receptor alpha 1 DKFZP56400823 protein	263	10.58
	421526	AL080121 AF026692	Hs.105460	DKFZP56400823 protein secreted frizzled-related protein 4	1,46 30,21	1.88 50.32
	421552 421574	AF026692 AJ000152	Hs.105700 Hs.105924	defensin, beta 2	1.67	1.74
	421582	AJ910275	10.100324	trefoil factor 1 (breast cancer, estroge	1.23	1.00
80	421633	AF121860	Hs,106260	sorting nextn 10	1.00	116,00
-	421659	NM 014459	Hs,106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828 W69233	Hs,107911 Hs,112457	ATP-binding cassette, sub-family B (MDR/ ESTs	1.41 1.12	1.14
85	421773 421777	W69233 BE562088	Hs.112457 Hs.108196	HSPC037 protein	1,97	1.29
00	-21/1/	52000		1101 Ozor protes		

Action			O 02/086				
14/196 M-2023 M-5/1075 M-		421800	AA298151	Hs,222969	ESTs	1.03	1.30
\$\frac{4}{2}\frac{1}{2} \frac{4}{2} \frac{1}{2} \fra				Hs.100000 Hs 45107	FSTs		22.80
Activate	-	421928	AF013758	Hs.109643	polyadenylale binding protein-interactin	45.89	90.00
August 1.00	5		NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	
Comparison of							1.15
2029 A 1868/27 A 1979/25		422026	U80736	Hs.110826	trinucleotide repeat containing 9		52.00
\$1,000 \$	10				F-box only prolein 5		62.00
According Company Co	10	422095		Hs.282804 Hs 1473	nypotnescal protein PLI/22/04		
1.5 42316 AV179319 b 1.11210 elucibonidal difeozonal prodein L. 2.2 3 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0		422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
15 15 15 15 15 15 15 15		422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito		
2278 A-SS-6589 b. 11-1049 3100 c.	15				mitochononal ribosomal protein L42	41.59 2.37	1.10
2022	13	422168		Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
2028 AVX191307 ib.11.1510. 2029 AVX191307 ib.11.1510. 2029 AVX191307 ib.11.1510. 2029 AVX19130 i					frizzled (Drosophila) homolog 6		
201 AJ31672 i i i i i i i i i i i i i i i i i i i				Hs.114309	CDC45 (cull division curls 45, S coresis		
According Acco	20			Hs.98370	cylochrome P450, subfamily IIS, polypept	1.54	1.41
22364 APGS7801 bit.11551 Cybpic platform deponded, carbothyriane-bit. 3.39 6.00 color internating profess in color		422311		Hs.114948	cylokine receptor-tike factor 1		
25. 42466 AP02541 1.1.10200				Hs.115263	Characterism descented applications	1.00	112.0
2.2524 A169-631				Hs.116206	Con-interacting protein 5		53.00
2428F, AUTOMACO 11,1156 11,115	25	422424	Al186431	Hs,296638	prostate differentiation factor	1.71	
22311 AUSTRACE 111.17382 closure, https://doi.org/10.1738/10.17382 closure, https://doi.org/10.17382 closure, https://doi.org/10.17382 closure, https://doi.							32.00
2015 AVSQ-AVI 9 http://dx. 2016 AVSQ-AVI 9 http://dx. 2017 AVAIVES 11, 11, 11, 11, 11, 11, 11, 11, 11, 11		422487.	AJU10901 ALIO76442	Hs.196267	nucin 4, tracheopronomia colleges type XVIII aloba 1		
25.00		422515	AW500470	Hs.117950	multifunctional polynomide similar to S	4,68	2.92
2578 AA41787 https://doi.org/10.1009/11.3004 https://doi.org/1	30	422656	AI870435	Hs,1569	LIM homeohox protein 2		
2576 AVX69770 11.51578 20.0000000000000000000000000000000000		422737	M26939	Hs.119571	collagen, type III, elpha 1 (Enters-Dani	1.05	1.46
2309 A0001379 http://dx.doi.org/10.1001/10.100		422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
\$\frac{2238}{42586} \frac{845077}{42587} \frac{15275}{42587} \fr		422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99,58	53.00
Accessed Selection Accessed	35	422867	L32137	Hs.1584	cartilege oligomeric metrix protein (pse	1,69	
400 42861 A-64/9809 H-18/9071 September 1 2018 September 1 2018 A-64/9809 H-18/9072 September 1 2018 A-64/9809 H-18/9072 September 1 2018 A-64/9072 Septembe		422938	NM_001809	HS.1594 He 199570	ECT2 protein /Enithelial cell transformi	70,46 77,74	3.00
400 42861 A-64/9809 H-18/9071 September 1 2018 September 1 2018 A-64/9809 H-18/9072 September 1 2018 A-64/9809 H-18/9072 September 1 2018 A-64/9072 Septembe		422960	AW890487	Hs.63984	cedherin 13, H-cadherin (heart)	5.88	8.55
A	40			Hs.190721	ESTs		17.00
\$2086	40			Hs.1600	Cheperonin containing FCP1, subunit 5 (6	10.40	1,52 35.00
ACCOUNT ACCO		422901	AA319777	Hs.221974	ESTs		
4.50 (2008) AF282092 http://dx.doi.org/10.10.10.10.10.10.10.10.10.10.10.10.10.1		423034	AL119930		ob:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60,00
22194 N. M. Opt-Max 15.10	15	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H		
Access of the Company of the Compa	43	423081		Hs.123159	sperm associated arrigen 4		
50 42319		423217	NM_000094	Hs.1640	collagen, type Vii, alpha 1 (epidermolys	2.14	1.69
\$2,000 AW170005 Bit Art Color		423248	AA380177	Hs.125845	ribulose-5-phosphale-3-epimerase	7.18	
24345 AVX5077 H 13/2771 Complete C	50					1.00	1.00
August	-	423453	AW450737	Hs.128791	CGL09 aratela	55.52	66.00
\$2555 A2575 A257		423511			gonadotropin-releasing hormone 2	0.88	1.17
5.5 252564 M95016 ±±±1.074 plutamin-in-inclosed-phosphate transamin 1.00 50.0 4.2007. C1003.0 ±±±1.04 consolvante plutamin 3.00 70.0 4.2006. 4.2005.0 ±±1.00 ±±5.00 70.0 70.0 4.2007. 4.2002.0 ±±4.02 ±±5.00 ±±5.00 ±±5.00 ±±5.00 4.2007. ±±2.02 ±±5.02 ±±5.00		423518	AB007933	Hs.129/29	ngand of neuronal nanc oxide synthase		
ACCIDATE AUXISTRATE Miles ACCIDATE	55	423554	M90516	H\$.1674		1.00	50.00
\$2,023.4 AV(9)(2006) b.1-1.029 \$2,000 \$2,0		423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fls, clone HE		
\$\\ \frac{42562}{42071} \\ \frac{42562}{420		423624	AI807408	Hs.166368	ESTs	1.00	
\$\frac{2}{42778} \frac{1}{268000000000000000000000000000000000000				Hs.1690	hypothetical crotein MGC13204	19.14	58.00
August A	60	423662	AA642452	Hs.130681	B-cell CLLilymphoma 11A (zinc finger pro	3.61	13.57
22725 A(45196 18.15127 19		423673		Hs.1695	metrix metalloproleinase 12 (macrophage		
6.5 42771 N.M. (2019) 4 https://dx. colors.pine.colors					bypollysted protein LOC57822		
A				Hs.132576	paired box gene 9		1.00
A	65	423787		Hs.236204	nuclear pore complex protein	7.18	
A				U- 1707	hypothetical protein		
70 4238F AUSSECOV III https://dx.doi.org/10.1009/10.10					Homo saniens mRNA: cDNA DKFZc761J1324 (f		
A2936 AVX53154 https://doi.org/10.1096/https://doi.o	=-	423887	AL080207	Hs.134585	DKFZP434G232 protein		
August D1966 h 13946	70	423934		Hs.159234	forkhead box E1 (thyroid transcription f		
42012 AVX58377 Hs.137959 hrs. proposite 63 Novillet strong berindrag 234.02 65.07 75 42016 AVX58377 hs.13592 hrs. proposite 63 Proposit		423954	AW/53164 D13666	Hs 136348	osleobjast specific factor 2 /fascirdin		
75 42422 APSSSSSS https://doi.org/10.1009/10.100		424012	AW368377	Hs.137569	turnor protein 63 kDa with strong homolog		68.00
A2464 A797796 H. 113922 comine (or sphimle) professions inhibits 1,00 1	75	424016		Hs.6140	hypothetical prolein MGC15730	0.93	
4268.6 AUSS1010 h.s.102278 y.s.1022 y.s.1022 <td>13</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>1,00</td>	13						1,00
Acades AF77774 https://doi.org/10.1009/10.		424086	AI351010	Hs,102267	lysy oxidase	21.91	70.00
80 42455 WWS2504 http://doi.org/10.0079 10.00 10.00 34.00 42.005 WWS2504 http://doi.org/10.004 10.00 34.00 34.00 42.005 WWS2504 http://doi.org/10.004 10.00 34.00 34.00 42.005 WWS2504 http://doi.org/10.004 10.00		424098	AF077374	Hs.139322	small profine-rich protein 3	137,82	54.00
4/2/200 AA377271 gbtS71494 Endounteful tumor Homo sagie 13.06 45.07 (42.72 42.72) 123306 Hs. 171814 bytpstelm bytpstytes (hytophatin Smon 1.00 1.00 42.038 AM975531 Hs. 15/443 mithicromosome mehitreance deficient (S. 164.58 67.04 42.038 Nb. (14174) 14.4529 dishibicromosome mehitreance deficient (S. 3.72 30.0.	RΩ	424120		Hs,290270		1.00	1.00
424279 123906 Hs.171614 typlophen hydroxytase (hyptophen 5-mon 1.00 1.00 4.24308 AW975531 Hs.15443 minichromosom mehlenence dictiont (S. 164.58 87.0 42438 NM_014479 Hs.142266 dishtepsin protesse 53.72 302.	00		AN337221	HS.142255	ob:EST41944 Endometrial tumor Homo sanie	13.06	48.00
424326 NM_014479 Hs.145296 disintegrin protesse 53.72 302.1		424279	L29306		trypiophen hydroxytase (tryptophen 5-mon	1.00	1.00
			AW975531	Hs.154443	minictromosome maintenance deficient (S.	164.58	87.00
INFOOD EDITO	85			Hs.145296 Hs.7033	gisinggan protesse FSTs	0.88	
		-24540			2010		

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	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364 424381	AW383226 AA285249	Hs.201189 Hs.146329	ESTs, Weakly similar to G01763 atrophin- protein kinase Chk2	7.02 95,55	3.24 92.00
	424411	NM 005209	Hs.146549	crystalin, beta A2	1.63	3,25
5	424420	BE614743	Hs.146688	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82 1.00	1.29
	424502 424503	AF242388 X06256	Hs.149585 Hs.149609	lengsin integrin, alpha 5 (libronectin receptor,	1.02	2.24
	424513	BE385864	Hs.149894	milochondrial translational initiation f	1.00	17.00
10	424539	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
	424568 424602	AF005418 AK002055	Hs.150595 Hs.151046	cylochrome P450, subfamily XXVIA, polype	3.40 31.87	2.58 25.00
	424629	M90656	Hs.151393	hypothetical protein FLJ11193 glutamate-cysteine ligase, catalytic sub	3.58	2,37
	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1,00
15	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23 1.00
	424717 424834	AW992292 AK001432	Hs.152213 Hs.153408	wingless-type MMTV integration site fami Homo sagiens cDNA FLJ10570 fis, clone NT	1.00 56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. carevisiae, homo	2.65	1.30
20	424867	Al024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.23	1.05
20	424905	NM_002497 D87989	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35 1.36	1,00
	424979 424999	AW953120	Hs.154073	UDP-galactose transporter related gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11,00
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
25	425081 425118	X74794 AU076611	Hs.154443 Hs.154672	minictromos ome maintenence deficient (S. methylene letrahydrofolate dehydrogenase	2.52 4.84	3.82 4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphete synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Weakly similar to 138022 hypotheti	1.00	53.00
30	425234	AW152225	Hs.165909 Hs.155223	ESTs, Weakly similar to 138022 hypotheti stenniccelcin 2	100.77 3.30	44.00 2.90
30	425236 425245	AW067800 AI751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	metrix metalioproteinase 11 (strometysin	1.41	1,49
	425266	J00077	Hs.155421	e/pha-fetoprotein	1.00	68.00
35	425274 425322	BE281191 U63630	Hs.155462 Hs.155637	minichromosome maintenance deficient (mi protein kinase, DNA-activaled, catalytic	141,49	1.63 123.00
55	425349	AA425234	Hs.79886	ribose 5-phosphale isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesotheth	0.87	1.59
	425397 425420	J04088 BE536911	Hs.156346 Hs.234545	lopcisomerase (DNA) II alpha (170kD)	14.90	5.76 1.00
40	425424	NM_004954	Hs.157199	hypotheticel protein NUF2R ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Droscobila) homolo	1.74	1.40
	425588	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14 233.00
	425580 425650	L11144 NM_001944	Hs.1907 Hs.1925	galenin desmoglein 3 (pemphigus vulgaris entigen	53.29 33.45	1.00
45	425892	D90041	Hs.155958	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734 425776	AF056209 U25128	Hs.159396 Hs.159499	peptidylglycine alphe-amidaling monocxyg parathyroid hormone receptor 2	1.00 1.00	41.00 48.00
	425810	A/923627	Hs.31903	ESTs	27.39	98.00
50	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	A1077288	Hs.296323	serum/glucocorticold regulated kinase	71.16 1.35	3.42 1.34
	425852 426067	AK001504 AA401369	Hs.159651 Hs.190721	death receptor 6, TNF superfamily member ESTs	1.01	17.00
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
55	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227 426269	U67058 H15302	Hs.154299 Hs.168950	Human proteinase activated receptor-2 mR Homo saptens mRNA; cDNA DKFZp566A1046 (f	22.40 1.00	25.00 1.00
	426283	NM_003937	Hs.169139	kynureninese (L-kynurenine hydrolase)	91,39	229.00
	426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
60	426427	M86699	Hs.169840	TTK protein kinase	7.02	1.00 1.68
	426432 426440	AF001601 BE382756	Hs.169857 Hs.169902	peracxonase 2 solute carrier family 2 (facilitated glu	1.16 2.59	1,71
	426459	AF151812	Hs,169992	hypothetical 43,2 Kd protein	1.56	1.66
15	426471	M22440	Hs.170009	transforming growth factor, alpha	20,60	26.00
65	426496 426501	D31765 AA401369	Hs.170114 Hs.190721	KIAA0061 protein ESTs	9.81 19.23	22.00 17.00
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (coleogenic	103.74	41.00
	426536	Al949749	Hs,44441	ESTs	4.65	23,00
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00 8,00
70	426682 426691	AV660038 NM_006201	Hs.2056 Hs.171834	UDP glycosyltransferase 1 family, polype PCTAIRE protein kinase 1	160,06 1,51	1,35
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	2.13	1.63
	426752	X69490	Hs,172004	titin	0.02	5.14
75	426784 426807	U03749 AA385315	Hs,172216 Hs,156682	chromogranin A (parathyroid secretory pr FSTs	1.72 1.30	1.71 1.64
15	426812	AF105365	Hs.172613	solute carrier family 12 (potessium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocystoine hydrolase	1.51	1.25
80	426897 426925	AA401369 NM_001196	Hs.190721 Hs.315689	ESTs Homo saplens cDNA: FLJ22373 fis, clone H	141.56 32.61	17.00 38.00
80	426925 426935	NM_000196 NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	428964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	AM93134		scierostin	1.00	1.00
85	426991 427099	AK001536 AB032953	Hs,173560	Homo sapiens cDNA FLJ10674 fis, clone NT odd Oz/fen-m homolog 2 (Drosophila, mous	3.39 4,24	2.28 17.00
0.5	421039	M2002300	10,170000	one owner, in nomon's a forced-such sugge	7.67	11.00

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	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848	Hs.102869	gb:se70b06.s1 Strategene schizo brain S1 ESTs	1.34	1.60 66.00
	427281 427335	AA906147 AA448542	Hs.251677	Ganijoen 7B	51,83	4.00
5	427354	T57896	Hs.191095	ESTs	1.17	1,95
	427356	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383 427427	NM_005411 AF077345	Hs.177582 Hs.177936	surfactant, pulmonary-associated protein lectin, superfamily member 1 (cartilage-	0.42 1.00	1.32
10	427441	AA412505	Hs.343879	SPANX family, member C	1.00	1.00
10	427445	X80818	Hs.178078	glutamate receptor, metabolropic 4	0.97	1.03
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
15	427528 427546	AU077143 AA188763	Hs.179565 Hs.36793	minichromosome maixtenance deficient (S. hypothetical protein FLJ23188	97.45 1.50	92.00 3.24
13	427562	R56424	Hs.26534	FSTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427660	Al741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49,00
20	427666	AI791495	Hs.180142	calmodulin-like skin protein	1.37	1.88
20	427663	AA298760	Hs.180191	hypothetical protein FLJ14904	29,55 3,52	67.00 2,63
	427677 427701	NM_007045 AA411101	Hs.180296 Hs.243886	FGFR1 oncogene partner nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (milochondrial	15.84	70.00
	427719	AJ393122	Hs.134726	ESTs	7.03	4.52
25	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
	427747	AW411425	Hs.180655 Hs.181097	serine/threonine kinase 12	1,76 9,63	1.26 59.00
	427912 427961	AU022310 AW293165	Hs.143134	tumor necros's factor (ligand) superfami ESTs	41.97	118.0
	428004	AA449563	Hs.151393	glutamete-cysteine ligase, catalytic sub	23.82	1.00
30	428023	AL038843		Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
	428046	AW812795	Hs.337534	ESTs, Moderately similar to \$38022 hypot	96.28	167.0
	428093	AW594506	Hs.104830	ESTs	1.25 1.86	1.29
	428098 428129	AU077258 AI244311	Hs.182429 Hs.26912	protein disulfide isomerase-related prot ESTs	1.00	42.00
35	428169	AJ928984	Hs.182793	goigi phosphoprotein 2	2,76	2,11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1,00	1.00
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	85.59	181.0
	428242 428330	H55709 1.22524	Hs.2250 Hs.2256	leukemia inhibitory factor (cholinergic matrix metalloproteinase 7 (matrilysin,	8.57 7.77	21.64 15.90
40	428330	A1909935	Hs.65551	Homo sapions, Similar to DNA segment, Ch	0.58	1.43
40	428450	NM 014791	Hs.184339	KIAA0175 gene product	237,53	204.0
	428471	X57348	Hs.184510	stratifin	8,00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	56.54	16.00
45	428484 428505	AF104032 AL035461	Hs.184601 Hs.2281	sclute carrier family 7 (cationic amino chromogranin B (secretogranin 1)	3.53 1.00	2.15 1.00
73	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017/2054 diltydro	1.00	16.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
50	428698	AA852773	Hs.334838	KIAA1336 protein	187.37 47.24	255,0 80,00
30	428728 428748	NM_016625 AW593206	Hs.191381 Hs.98785	hypothetical protein Ksp37 protein	1,00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	428771	AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
	428801	AW277121	Hs.254881	ESTs	1.67	6.15
55	428810	AF068236	Hs.193788	nitric code synthese 2A (inducible, hep	1.03	1.27 43.00
	428839 428845	Al767756 AL157579	Hs.82302 Hs.153610	Homo sapiens cENA FL/14814 fis, clone NT KIAA0751 gene product	124.17 1.00	1.00
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	15.16	27.00
	428969	AF120274	Hs.194689	artemin	1.36	1.24
60	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065	A/753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT ESTs	6.82 19.08	16.47 67.00
	429164 429170	Al688663 NM_001394	Hs.116586 Hs.2359	dual specificity phosphalase 4	16.18	105.0
	429183	AB014604	Hs.197955	KiAA0704 prolein	79.72	104,0
65	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.33	1.09
	429220	AW207206		ESTs ESTs	1.00 39.47	7.00 29.25
	429228 429259	AI553633 AA420450	Hs.326447 Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
70	429263	AA019004	Hs,198396	ATP-binding cassette, sub-family A (ABC1	1.07	1,00
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.70	142.0
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1,94
	429412 429413	NM_006235 NM_014058	Hs.2407 Hs.201877	POU domain, class 2, associating factor DESC1 protein	94.09 41.91	86,00 10,00
75	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
, ,	429504	X99133	Hs.204238	Epocatin 2 (oncogene 24p3)	1.61	1.06
	429538	BE182592	Hs.11261	smail proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17,00
80	429551 429563	AW450624 BE619413	Hs.220931 Hs.2437	ESTs eukaryotic translation initiation factor	2.89 1.49	65.00 1.37
00	429593	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.0
	429610	AB024937	Hs.211092	LUNX protein: PLUNC (palate tung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
85	429616 429656	AI982722 X05608	Hs.120845	ESTs	1.00 1.00	1.00 4.00
0.5	429656	V09908	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

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	429663	M68874	Hs.211587	phospholipase A2, group NA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212680	turnor necrosis factor receptor superfami	1.25	1.21
	429782	NM_005754	Hs.220689	Res-GTPase-activating protein SH3-domein	1.00	7.00
5	429903 429918	AL134197 AW873986	Hs.93597 Hs.119383	cyclin-dependent kinase 5, regulatory su FSTs	11.80 1.00	1.00 78.00
,	429978	AA249027	FIG. 115500	ribosomat protein S6	1,98	3.09
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59,00
10	430114	AA847744 BE380149	Hs.99640 Hs.105223	ESTs ESTs, Weakly similar to T33188 hypotheti	1.00	1.00 51,00
10	430134 430147	RE0704	Hs. 234434	hairy/enhancer-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEUS_HUMAN LEUKE	1.00	127.00
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
15	430300	U60805	Hs.238648	oncostatin M receptor	1.00 92.31	35.00 28.00
15	430315 430337	NM_004293 M36707	Hs.239147 Hs.239600	guanine deaminase calmodulin-like 3	1,18	1.08
	430378	229572	Hs.2556	tumor necrosis factor receptor superfami	5,28	66,00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
20	430393	BE185030	Hs.241305	estragen-responsive B box protein	1,63	1.50
20	430439 430451	AL133561 AA836472	Hs.297939	DKFZP434B061 protein cathepsin B	1.64	2,12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), thete	2,47	1.91
0.5	430481	AA479678	Hs,203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
25	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam ESTs	12.28 4.75	41,00 7,27
	430508 430533	Al015435 AA480895	Hs.104637 He.57749	ESTs, Weakly similer to T17288 hypotheti	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
	430677	Z26317	Hs.94560	desmoglein 2	1,72	1.30
30	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686 430788	NM_001942 Al742925	Hs.2633 Hs.7179	desmoglein 1 ESTs, Weakly similar to 2004399A chromos	1.00 1.62	1.00 1.84
	430690	X54232	Hs.2699	glypicen 1	1,58	1.40
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
35	430965	AA490232	Hs.27323	ESTs, Weakly similar to 178885 serine/th	0.94	1.28
	431009 431069	BE149762 BE041395	Hs.48956	gap junction protein, beta 6 (connexin 3 ESTs, Weakly stmiler to unknown protein	60.25 23.32	28.00 941.00
	431009	Al332764	Hs.125757	ESTs Vicenty singer to unknown protein	13.46	63.00
	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43	82,00
40	431164	AA493650	Hs.94367	Homo sepiens cDNA: FLJ23494 fis, clone L	0.44	2.20
	431211	M86849	Hs.323733	gep junction protein, beta 2, 26kD (conn	182.26 4.15	101.00
	431221 431277	AW207837 AA501806	Hs.286145 Hs.345824	SRB7 (suppressor of RNA polymerase B, ye ESTs	1.00	86.00
	431322	AW970622	FIG.040024	gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
45	431342	AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94 1.30	1,14
	431462 431494	AW583672 AA991355	Hs.256311 Hs.298312	granin-like neuroendoorine pepiide precu hypothetical protein DKFZp434A1315	3.90	26.00
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
50	431548	A1834273	Hs.9711	novet protein	5.66	15.00
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	0.99	1,44 3,51
	431745 431770	AW972448 BE221880	Hs.163425 Hs.268555	ESTs 5'-3' exoribonuclease 2	67.12	91.00
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3,36	4.71
55	431848	BE019924	Hs.271580	uronlakin 1B	4.49	2.51
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 suburi	2.20	3.32
	431934 431958	AB031481 X63629	Hs.272214 Hs.2877	STG protein cadherin 3, type 1, P-cadherin (placenta	1.01 51.17	1,04 46.35
	431956	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
60	432023	R43020	Hs.236223	EST	0.94	47.00
	432201	AJ538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210 432226	AI567421 AW182766	Hs.273330 Hs.273558	Homo sapiens, clone IMAGE:3544662, mRNA, phosphate cylidylytransferase 1, cholin	1.42	1.45 1.00
	432220	X81334	Hs.2936	matrix metalloproleinase 13 (collagenase	18,67	1.00
65	432265	BE382679	Hs.285753	SCG10-tike-protein	1.09	1.21
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
	432365 432374	AK001105 W68815	Hs.274419 Hs.301885	hypothetical protein FLJ10244 Homo sapiens cDNA FLJ11346 fis, clone PL	1.00 157.34	214.00 37.00
	432374	W68815 BE536069	Hs.301885 Hs.2962	S100 calcium-binding protein P	1.65	1.06
70	432407	AA221036	Hateson	qb:zr03f12.r1 Stratagene NT2 neuronal pr	73.71	75.00
	432441	AW292425	Hs.163484	ESTs	56.35	72,00
	432489	AJ804855	Hs.207530	ESTs	1.00 137.72	24.00 98,00
	432543 432552	AA552690 AJ537170	Hs.152423 Hs.173725	Homo sapiens cDNA: FLJ21274 fls, clone C ESTs, Weakly cimilar to ALUS_HUMAN ALU S	1,00	31.00
75	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	AJ243596	Hs.94830	ESTs. Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	1.92	5.29 48.00
80	432677 432715	NM_004482 AA247152	Hs.278611 Hs.200483	UDP-N-acetyl-alpha-D-galactosamine:potyp ESTs, Wealth similar to KIAA1074 protein	45.13	31.00
	432753	NM_014075	Hs.336938	Homo sacions PRC0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sagiens cDNA: FLJ23117 ffs, done L	2.69	3.67
	432842 432867	AW674093 AW016936	Hs.334822 Hs.233364	hypothetical protein MGC4485 ESTs	1.22	1.34
85	432867	NM_014125	Hs.241517	PRO0327 protein	10.25	6,62
	.56511	314120				

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Autonome		w	O 02/086	443			
\$\frac{43023}{5}\$ \tag{4000}\$ \tag{4000}		432920	U37689	Hs,3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
\$\frac{43092}{24393} \times \frac{43092}{24222} \times \frac{43092}{24393} \times \frac{43092}{24222} \times \frac{43092}{24393} \times \frac{43092}{24223} \times \frac{43092}{24393} \times \frac{43092}{24233} \times \frac{43092}{242333} \times \frac{43092}{2423333} \times \frac{43092}{2423333} \times \frac{43092}{2423333} \times \frac{43092}{2423333} \times \frac{43092}{24233333} \times \frac{43092}{24233333} \times \frac{43092}{24233333} \times \frac{43092}{24233333} \times \frac{43092}{24233333} \times \frac{43092}{24233333} \times \frac{43092}{242333333} \times \frac{43092}{242333333} \times \frac{43092}{2423333333} \times \frac{43092}{2423333333} \times \frac{43092}{2423333333} \times \frac{43092}{2423333333} \times \frac{43092}{24233333333} \times \frac{43092}{2423333333333333333333333333333333333			AF217513 AW864703	Hs.279905 He 87409			100.0
\$\ \text{5.50}{\text{9.17}} \text{ \$\text{2.529}{\text{9.17}} \t					Homo saplens cDNA FLJ11660 fis, clone HE		10.00
10	- 5	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
ASSISTANCE ASS		433159		Hs.150587	kinesin-like protein 2		
10 43490 AC78802 H-2585 1.2585 1.2586 1.25					ESTs. Weakly similar to ALUB HUMAN IIII	1,00	1,25
Additional Content of the Content		433409	AI278802	Hs.25551	ESTs		117.0
15 1439	10	433437	U20536	Hs.3280	caspase 6, apoptosts-related cysteine pr	70.39	105.0
1.5 43555 105277 11.5 1500 11.5			AH93075				
15 43555 MS521 https://doi.org/10.1001						25.16	83.00
\$2.00		433555	W55321	Hs.111490	calcium/calmodulin-dependent protein kin	1.00	19.00
ASSIST	15					20.30	49.00
Assisted		433558	L03578	Hs.155110	timmunoglobulin kappa constant tuno tuno Logil mombrano secorished olu	2.92	
2.5 2.5		433600	AW511097	Hs.112785	ESTs		8.00
Acides A. Art 19677		433862	D86960	Hs.3610	KIAA0205 gone product		104.0
Addisorption Addi	20				phosphoserine aminotransferase		47.00
\$\frac{4.4016}{4.4027}\$		434088	AF1166//		hypothetical protein PRO1000 hypothetical archite PRO2012		
2.5 46379 AVX1479 In 2.23385 Sept. 1 1549 Sept. 1 142		434105	AW952124	Hs.13094	presentins associated rhomboid-like pro	1.22	1,23
Add Add 15	0.5	434217	AW014795	Hs.23349	ESTs	14.11	57.00
Add	25		Al193043	Hs.128685		2.10	
Add		434300	A1798375	Ha. 130/21			
\$4,000 \$		434424	AJ811202		Home sariens cDNA: FLJ23523 fs. done L	1.00	64.00
A-822 A-22 694 H-33511 E-32	20			Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	
Add	30					1.00	
A-5769		434599	AA643587	Hs.149425	Homo saniens cDNA FLJ11980 fis, clone HE	1.00	23.00
\$4.772		434759	AA548884	Hs.134278	Home sepiens cDNA FLJ12675 fis, clone NT	7.08	56.00
Add	25	434792	AA649253	Hs.132458	ESTs		44.00
Addition	22		AF155108		nhorted 12 marietate 13 costate inchesed	11.33	1.00
Asker		434876	AF160477	Hs.61460	ig superfamily receptor LNIR	1.25	1.29
4.00 4501 919122 h. h. 11002 54502 54503 92517 0 h. 4717 45505 54502 54503 925		434891	AA814309	Hs.123583	ESTs		6.00
\$4,000 \$2,000 \$1,000 \$	40	434928	AW015595	Hs.4257	Homo sopiens clones 24714 and 24715 mRNA	1.00	1.00
Assert	40	435058				1.69	1.37
45 45009 A589879 in 11599 Simmuno() belief british bloom british 20 pt 1 10 10 10 10 10 10 10 10 10 10 10 10 1		435087	AW975241	Hs.23557	ESTs	1.00	1.00
4.55		435099		Hs.4756		2.90	1.93
14,000	45	435159	AA888879 VE1125	Hs.115549		1.00	1.00
145304 110709	73		NM 001262		cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
\$\\ \frac{45555}{45595} \frac{\text{AVSP}}{45697} \frac{1}{160} \frac{1}{160} \frac{1}{160} \frac{1}{160} \frac{1}{160} \frac{1}{160} \frac{1}{160} \frac{1}{160} \frac{1}{160} \frac{1}{160} \qua			H10709		ESTs	27.58	139.0
50		435313	AI759400				
1.00	50	435500		He 181015		1.00	1.00
ASSESS AUZ-MASS M.224695 H.3246971 H.3246971 H.3246971 H.3246971 H.3246971 H.3246971 H.3246971 J.324671 J.324671 J.324671 J.324671 H.3246971 H.3246971 H.426981 L.3246971 J.324671 J.32	50	435525	AJ831297	Hs.123310	ESTs	1.00	55.00
55 459726 APZ17915 bt 285522 bt 28578 APZ17915 bt 285522 bt 28578 APZ17915 bt 285522 bt 28578 APZ17915 bt 28552 bt 28578 APZ17915 aPZ		435532			Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
55		435550	AI224455	Hs.324507	H.Sapiens polyA site UNA Homographics and home morrow protein RM03		
ASSPR A ABSYRT H-4989 ASSET AS	55				ESTs	1.00	28.00
AST AVACASS In 14-122 AVACASS AVACAS		435793	AB037734	Hs.4993	KIAA1313 protein		42.00
60 4321 A26521						1.00	58.00
ASS211 ASS2512 bit 71472 byto-brited ajrotich F14/0774 (NATO) 142 131		436770	AW450381 AK001581	Hs.14529 He 334838	hypothetical protein FL J10719: KIAA1794		22.00
ASS21 TSS205 the 10.77 the 10.75	60	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KlAA1709	1.42	1.27
Access BEST-5056 best-20565 best-205		436217	T53925	Hs.107	fibrinogen-like 1	67.97	
50.259 18.508.54 18.503.53 18.508.54 18.503.53 18.508.54 18.503.				Hs.301724	hypothetical protein FLJ11301	2.51	1./1
\$5.500		436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
\$25414 \$252,6423 \$15,14583 \$10 popular formani 4	65	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
C5419 A948928 Hs.771595 E571 0.95 1.32		436396	AW992292	Hs.152213	wingless-type MMTV Integration site fami	50.01	
25444 AV158211 https://doi.org/10.1009/10.10		430414		MS.143036	WD repeat domain 4	0.95	1.33
10		436443		Hs.128746	ESTs	1.12	9.26
Sisses Avi 1222 https://doi.org/10.1009/10	70		AJ270693	Hs.199687		1.00	1.00
43551 A771282 16,291502 ESTs 15,76 144 75 43555 17,3799 1,1112 1		436481	AA379597	Hs.5199	HSPC150 protein similar to utiquitin-con	3.28	
75 48555 X57890 http://dx.doi.org/10.1001/20.1						15.75	14.00
36999 A-529890 A-529890 A-529890 A-529890 A-529890 A-529890 A-529890 A-52999 A		436553	X57809	Hs.181125	mmunoolobulin lambda locus	1.08	1.74
A00907 A0090183 http://doi.org/10.1009 115	75	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr		9.75
48777 AVST988F 1b.202979 ESTs 1.00 104		436608	AA528980 AA025183	He 127680	down syndronie chiical region protein US	0.89	1.19
43839 AA01399 Hs.190721 ESTs 43894 AV075817 Hs.19272 hypothetical protein DK72p547D185 1.05 11.5 43894 AV075814 Hs.580 ESTs 1.00 11.5 43891 AV075814 Hs.580 ESTs 25.1 43891 AV075814 Hs.580 ESTs 25.1 43891 AV075814 Hs.5874 ESTs 25.1 43891 AV075814 Hs.5894 data 3 15.9 14.2 437016 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 437016 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581 Hs.5594 data 3 custom condoctochide swiftbytuse 2.25 17.7 43891 AV07581		438771				1.00	10.00
436961 AW375974 Hs.156704 ESTs 20.13 20.1 436972 AA284679 Hs.25640 claudin 3 1.59 1.44 437016 AU075916 Hs.5398 quarine monotosobale synthetase 2.35 1.71	00	436839	AA401369	Hs.190721		1.00	17.00
436961 AW375974 Hs.156704 ESTs 20.13 20.1 436972 AA284679 Hs.25640 claudin 3 1.59 1.44 437016 AU075916 Hs.5398 quarine monotosobale synthetase 2.35 1.71	80	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155		
435972 AA284679 Hs.25640 claudin 3 1.59 1.44 437016 AU075916 Hs.5398 quaning monohosohale synthetase 2.35 1.71				Hs 158704	FSTs	25.13	25.0
85 437016 AU075916 Hs.5398 guaraine morephosphale synthetase 2.35 1.76 437044 AL035864 Hs.69517 CONA for differentiality expressed CO16 g 1.34 1.15		436972	AA284679	Hs.25640	claudin 3	1.59	1.46
OU 43/044 ALUSO004 HS.05517 CUNA for directed employ expressed CU16 g 1.34 1.15	05			Hs.5398	guarine monphosphale synthetase	2.35	1.78
	03	43/044	ALU35864	rts.69517	CUTAN IO: Unterementy expressed CO16 g	1.34	1.13

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	w	O 02/086	443			
	437181	Al306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17,00
	437204	AL110216	Hs.22826	ESTs. Weakly similar to 155214 salivary	40.55	82.00
	437205 437259	AL110232 AI377755	Hs.279243 Hs.120695	Homo sapiens mRNA; cDNA DKFZp564D2071 (f ESTs	1.00	112.00 205.00
5	437259	R18087	Hs.323769	cispiatin resistance related protein CRR	1.66	1.54
-	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1,82 1,35	4.57 1.75
	437390 437412	Al125859 BE069288	Hs.112607 Hs.34744	ESTs Homo sagiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
10	437435	Al306152	Hs.27027	hypothetical prolein DKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1,00	39.00
	437568	A1954795 D63880	Hs.156135 Hs.5719	ESTs chromosome condensation-related SMC-asso	1.00 1.95	19.00 1,57
	437623 437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
15	437814	Al088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852 437879	BE001836 BE262082	Hs.256897 Hs.5894	ESTs, Weakly similar to dJ365012.1 [H.sa hypothetical protein FLJ10305	1.68 1.87	3.26 2.52
	437915	AI637993	Hs.202312	Homo sapions clone N11 NTera2D1 teratoca	74.05	35.00
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
	437937	Ai917222	Hs.121655	ESTs	1,00 12,28	1.00
	437942 438091	Al888256 AW373062	Hs.307526	ESTs nuclear receptor subfamily 1, group I, m	1.53	31.00 10.85
	438113	AI467908	Hs.8882	ESTs	1.80	2.39
25	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22,67	36.90
	438274	Al918906	Hs.55080 Hs.86434	ESTs	1.00 38.92	1.00 38.00
	438378 438403	AW970529 AA806607	Hs.292206	hypothetical prolein FLJ21816 ESTs	1.00	1.00
	438494	AA908678	Hs.130183	ESTs	2.05	80.00
30	438546	AW297204	Hs.125811	ESTs	1.00	131.00
	438552 438702	AJ245820 AI879064	Hs.6314 Hs.54618	type I transmembrane receptor (seizure-r ESTs	1.43	1.45 34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
	438746	Al885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1,59
35	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00 2.03	18.00 2.57
	438821 438885	AA826425 Al886558	Hs.192375 Hs.184987	ESTs ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
40	438915	AA280174	Hs.285681	Williams-Bouren syndromo dixomosome regi	1.00	1.00
40	438958	W00847 AW979121	Hs.135056	Human DNA sequence from clone RPS-850E9 gb:EST391231 MAGE resequences, MAGP Homo	2.20 2.78	1.88 4.81
	439000 439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R96698	Hs.35598	ESTs	1.00	28.00
45	439128	A/949371	Hs.153089	ESTs	1.00	67.00 1.41
45	439146	AW138909 AW238299	Hs.156110 Hs.250818	immunoglobulin kappa constant UL 16 binding protein 2	1.38	1.64
	439285	AL133916	1102230010	hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2,00	2.20
50	439343 439394	AF086181 AA401369	Hs.114811 Hs.190721	hypothetical protein FLJ11808 ESTs	6.10 3.39	7.37 17.00
50	439384	AA632012	Hs.188746	ESTS	1,83	3.07
	439451	AF086270	Hs.278554	helerochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs,57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76 2.78	122.00 1.58
55	439453 439477	BE264974 W69813	Hs.6566 Hs.58042	lhyroid hormone receptor interactor 13 ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
-	439492	AF086310	Hs,103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592 439606	AF086413 W79123	Hs,58399 Hs,58561	ESTs G protein-coupled receptor 87	1.00 33.61	1.00
60	439870	AF088078	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706 439738	AW872527 BE246502	Hs.59761 Hs.9598	ESTs, Weakly similar to DAP1_HUMAN DEATH sema domain, immunoslobulin domain (lg).	86.55 2.36	11.00 1.88
	439738	AL359053	Hs.57664	Homo sapiens mRNA full length Insert cDN	2.02	6.08
65	439759	AL359055	Hs.67709	Homo sepions mRNA full length insert cDN	1.00	21.00
	439780	AL109688		gb:Homo sapiens mRNA full length insert	7.27	25.00 1.00
	439840 439926	AW449211 AW014875	Hs.105445 Hs.137007	GDNF family receptor alpha 1 ESTs	32.58	71.00
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
70	439979	AW600291	Hs.6823	hypothetical grotein FLJ10430	68.83	61,00
	440006 440028	AK000517 AW473675	Hs.6844 Hs.125843	hypothetical protein FLJ20510 ESTs, Weakly similar to T17227 hypotheti	1.83	4.02 2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	5200
75	440273	Al805392	Hs.325335	Homo sapieus cDNA: FLJ23523 fis, clone L FSTs	3.21 38.63	4.72 113.00
	440289	AW450991 NM_003812	Hs.192071 Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp5473036	2.35	3.62
90	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57,00 2,37
80	440659 440704	AF134160 M69241	Hs.7327 Hs.162	claudin 1 insulin-like growth factor binding prote	3.18 2.89	2.09
	440943	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1.41
	440994	Ai160011	Hs.272068	ESTs	1.29	1.14
85	441020 441031	AA401369 AI110684	Hs.190721 Hs.7645	ESTs fibrinogen, B beta polypeptide	142.99 1.41	17.00 99.00
0.5	441001		.10.7043	managem, a nom paypapara		

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	W	O 02/086	443			
	441128	AA570256 W27501	Hs.89605	ESTs, Weakly similar to T23273 hypotheti	4.13 1.00	3.50 1.00
	441290 441352	W2/501 BE614410	Hs.23044	cholinergic receptor, nicotinic, alpha p RADS1 (S. cerevisiae) homolog (E coll Re	130,23	43.00
_	441377	BE218239	Hs.202656	ESTs	22.03	1.00
5	441390	A1692560	Hs.131175	ESTs	3.65 1.00	7.70 1.00
	441497 441525	R51064 AW241867	Hs.23172 Hs.127728	ESTs ESTs	1.53	1.42
	441553	AA281219	Hs.121296	ESTs	1.89	1.57
10	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	1.47 216.22	2.11
10	441633 441636	AW958544 AA081846	Hs.112242 Hs.7921	normal mucosa of esophagus specific 1 Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2,31	2.05
	441737	X79449	Hs.7957	adenosine dearninase, RNA-specific	1.30	1.49
	441790	AA401369	Hs.190721	ESTs	44.15	17.00
15	441801 441919	AW242799 Al553802	Hs,86366 Hs,128121	ESTs ESTs	1.00 1.00	1.00 122.00
13	441937	R41782	Hs.22279	ESTS	0.86	1,37
	441954	A)744935	Hs.8047	Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	Hs.11810	CDA11 protein	1.00 9.92	46.00 45.00
20	442029 442072	AW966698 Al740832	Hs.14456 Hs.12311	neural procursor cell expressed, develop Homo seriens clone 23570 mRNA sequence	25.05	77.00
20	442108	AW452649	Hs.166314	ESTs	3.61	3.14
	442117	AW664964	Hs.128899	ESTs	3.00	5.49
	442137 442159	AA977235 AW163390	Hs.128830 Hs.278554	ESTs, Weekly similar to Z192_HUMAN ZINC heterochromatin-like protein 1	1.00	1.00 1.66
25	442179	AA983842	Hs.333555	chromosoma 2 open reading frame 2	27.22	50.00
	442328	A1952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3,42 76,00
	442432 442530	BE093589 Al580830	Hs.38178 Hs.176508	hypothetical protein FLJ23468 Homo sapiers cDNA FLJ14712 fis, clone NT	181.59 10.59	144.00
	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98,00
30	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
	442619	AA447492	Hs.20183	ESTs, Weekly similar to AF164793 1 prote	29.02 1.00	50.00 19.00
	442710 442717	Al015631 R88362	Hs.23210 Hs.180591	ESTs Weakly similar to T23976 hypotheti	1.00	5.00
	442875	BE623003	Hs.23625	Homo saplens clone TCCCTA00142 mRNA sequ	22.85	50.00
35	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	25.33	82.00
	442932 442942	AA457211 AW167087	Hs.8858 Hs.131562	bromodomain edjacent to zinc linger doma ESTs	3.18 8.45	4,41 64.00
	442942	AV167067 Al188710	MS. 13 1002	ESTS	1.00	27.00
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
40	443211	Al128388	Hs.143655	ESTs	12,42 128,84	2.00 96.00
	443247 443324	BE814387 R44013	Hs.333893 Hs.164225	e-Myc largel JPO1 ESTs	0.02	4.59
	443383	Al792453	Hs.166507	ESTs	1.00	47.00
	443400	R28424	Hs.250648	ESTs	18.52	61.00
45	443426 443572	AF098158 AA025610	Hs.9329 Hs.9605	chromosome 20 open reading frame 1 cleavage end polyadenyletion specific fa	4.02 2.98	1.75 2.57
	443575	AAU20010 A1078022	Hs.269636	ESTS, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16,00
50	443833	AL031290	Hs.9654	similar to pregnancy-associated plasma p FSTs	1.00 39.81	39.00 70.00
30	443648 443715	Al085377 Al583187	Hs.143610 Hs.9700	extin E1	48,74	7.00
	443723	Al144442	Hs.157144	syntaxin 6	1.29	1.30
	443802	AW904924	Hs.9805	K/AA1291 prolein	1.75	1.61
55	443859 443892	NM_013409 AA401369	Hs.9914 Hs.190721	follistatin ESTs	1.35 1.00	1.13 17.00
55	443947	W24187	110.100721	gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
	443991	NM_002250	Hs.10082	polassium intermediate/small conductance	5.71	6.87
	444006 444009	BE395085 Al380792	Hs.10086 Hs.135104	type I transmembrane protein Fn14 ESTs	1.47 1.00	1.92 77.00
60	444009	U04840	Hs.214	neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	Hs.13281	ESTs	1.00	29.00
	444129	AW294292	Hs.256212	ESTs	1.00 0.60	1.00 7.80
	444279 444371	U62432 BE540274	Hs,89605 Hs,239	cholinergic receptor, nicofinic, alphe p forkhead box M1	2,91	1.14
65	444378	R41339	Hs.12569	ESTs	1.00	1.00
	444381	BE387335	Hs.283713	ESTs, Weekly similar to S64054 hypotheti	469.00	556.00
	444461 444471	R53734 AB020684	Hs.25978 Hs.11217	ESTs, Weakly similar to 2109260A B cell KIAA0877 protein	12.88 24.91	105.00 90.00
	444489	AI151010	Hs.157774	ESTs	1.00	111.00
70	444619	BE538082	Hs.8172	ESTs, Moderately Similar to A46010 X-lin	1.00	70.00
	444665	BE613126 AH88613	Hs.47783 Hs.41690	B aggressive lymphoma gene desmocollin 3	30.56 1,00	139.00 1,00
	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	77.02	90.00
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.57	1.31
75	444783	AK001468	Hs.62180	analin (Drosophila Scraps homolog), acl	77.55	2.00
	445236 446258	AK001676 AI635931	Hs.12457 Hs.147613	hypothetical protein FLJ10814 ESTs	1.00 1.00	27.00 73.00
	445413	AA151342	Hs.12677	CGI-147 protein	28.14	50.00
90	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
80	445443 445462	AV653838 AA378776	Hs.322971 Hs.288649	ESTs hypothetical protein MGC3077	1.00 2.09	1.00 1.70
	445462 445617	AA3/8//6 AF208855	Hs.288649 Hs.12830	hypothetical protein	1.87	70.00
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.71	2.72
85	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog Brioredoxin reductase 1	1.52	1.34
03	445654	X91247	Hs.13046	BIRDFORMAII (EDDCISSE 1	1.01	1.04

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	445669	A1570830	Hs.174870	ESTs	10.95 1.00	11.45 1.00
	445818 445873	BE045321 AA250970	Hs.136017 Hs.251946	ESTs poly(A)-binding protein, cytoplasmic 1-1	1.00 49.42	54.00
	445885	AA250970 A1734009	Hs.127699	KIAA1603 protein	1.00	132.0
5	445898	AF070623	Hs.13423	Homo sagless clone 24468 mRNA sequence	1.00	1.00
	445903	A1347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41 1.60	2.88 1.35
	445982 446078	BE410233 Al339982	Hs.13501 Hs.156061	pescadillo (zebralish) homolog 1, contai ESTs	1.00	42.00
10	446102	AW168067	Hs,317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fts, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73,01	48.00
	446292 446293	AF081497	Hs.279682 Hs.149722	Rh type C glycoprotein ESTs	1.55 1.00	1.26
15	446423	Al420213 AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AWQ82270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	AI377320	Hs.150058	ESTs	1.00	5.00
	446528 446574	AU076640 AI310135	Hs.15243 Hs.335933	nucleolar protein 1 (120kD) ESTs	1.36 3.89	1.31 72.00
20	446619	AU076643	Hs.330933	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
20	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4,19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	milotic spindle colled-coll related prot	110.28	28.00 2.94
25	446849 446856	AU076617 AI814373	Hs.16251 Hs.164175	cleavage and polyadenylation specific fa ESTs	6.38	11.30
20	446872	X97058	Hs.16362	ovimidheraic recentor P2Y, G-protein c	1.98	2.03
	446880	AI811807	Hs.108646	pyrimidinergic receptor P2Y, G-protein c Homo sapiens cDNA FLJ14934 fls, clone PL	94.90	113.0
	446921	AB012113	Hs.16530	smell inducible cytokine subtamily A (Cy	1.67	3.90
30	446989	AK001898	Hs.16740	hypothetical protein FLJ11036 ESTs	2.82 1.00	3.12 170.0
30	447022 447033	AW291223 AJ357412	Hs.157573 Hs.157601	ESTs	7,15	107.0
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447081	Y13895	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
25	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	0.97	1.48
35	447149 447153	BE299857 AA805202	Hs.326 Hs.315562	TAR (HIV) RNA-binding protein 2 ESTs	1.24	1.26 54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
	447178	AW594641	Hs.192417	ESTs	3.42	50.00
40	447250	AJ878909	Hs.17883	protein phosphalase 1G (formerly 2C), ma	1,60	1.52
40	447289 447342	AW247017	Hs.36978 Hs.19322	melanoma antigen, family A, 3 Homo saplens, Similar to RIKEN cDNA 2010	1.00 28.63	1.00
	447343	Al199268 AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146,62	51.00
	447350	Al375572	Hs.172634	ESTs	1.00	12.00
4.5	447377	N27687	Hs,334334	Iranscription factor AP-2 alpha (actival ESTs, Weakly similar to KF3B_HUMAN KINES	2.55	63.00
45	447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91 1.00	1.13 35.00
	447425 447519	Al983747 U46258	Hs.18573 Hs.339665	scylphosphatase 1, erythrocyle (common) ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
	447534	AA401369	Hs.190721	ESTs	1.00	17.00
50	447636	Y10043	11 40000	high-mobility group (nonhistone chromoso	1.41	1,11
	447688 447733	N87079 AF157482	Hs.19236 Hs.19400	Target CAT MAD2 (mitolic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo saplens cDNA FLJ14597 fis, clone NT	6.47	5,95
	447802	AW593432	Hs.161455	ESTs	0.73	2.34
55	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.0
	447924	Al817226 AB011169	Hs.313413 Hs.20141	ESTs, Weakly similar to T23110 hypotheti similar to S. cerevisiae SSM4	1.00 3.50	4.27
	447973 448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.0
	448105	AJ538613	Hs.298241	Transmembrane protesse, serine 3	1.15	2.24
60	448243	AW389771	Hs.52820	integrin, beta 8	15.84	1.00
	448278 448290	W07369	Hs.11782 Hs.20843	ESTs Homo sepians cDNA FLJ11245 fis, clone PL	0.97 1.00	1.90 1.00
	448296	AK002107 BE622756	Hs.10949	Homo sapiens cDNA FLU14162 fis, clone NT	2.42	2.17
	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
65	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63 1.84	2.49 2.53
	448569 448663	BE382657 BE614599	Hs.21486 Hs.106823	signal transducer and activator of trans hypothetical protein MGC14797	3.29	46.00
	448672	A/955511	Hs.225106	ESTs	1.00	21.00
70	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48 23.53	1.92 20.00
	448757 448775	Al366784 AB025237	Hs.48820 Hs.388	TATA box binding protein (TBP)-associate nudix (nucleoside diphosphate linked moi	23.53	1.97
	448826	A1580252	Hs.293246	ESTs, Weakly similar to putative p150 (H	74.07	62.67
75	448830	AL031658	Hs.22181	hypothetical protein dJ310O13.3	1.37	1.31
	448844	A1581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto KIAA0144 gene product	1,84	1,95 1,49
	448993 449003	Al471630 X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1,00
80	449029	N28989	Hs,22891	solute carrier family 7 (callonic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048 449053	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc ESTs	27.13 8.33	90.00 44.00
	449053 449054	AI625777 AF148848	Hs.344766 Hs.22934	myoneurin	73.85	104,0
85	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

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	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleopovin 156kD	2.36	1.56 1.15
	449228	AJ403107 BE613348	Hs.148590 Hs.211579	protein related with psoriasis metanoma cell'adhesion molecule	1.15	151.00
5	449305	A1638293	FIS.2 10/8	gb:ti09b07.x1 NCI_CGAP_GC6 Homo sepiens	17.28	45.00
-	449318	AW235021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467 449523	AW205006	Hs.197042 Hs.54443	ESTs	1.00	1.00 216.86
10	449722	NM_000579 BE280074	Hs.23960	chemokine (C-C molif) receptor 5 cyclin B1	150.03	1.00
10	449978	H06350	Hs.135056	Haman DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	1.17	1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
15	450101 450149	AV649989 AW969781	Hs.24365 Hs.132863	Human hbc647 mRNA sequence Zic family member 2 (odd-paired Drosophi	1.00 1.00	69.00 1.00
13	450193	AV969761 AI916071	Hs.15807	Homo sapiens Fanconi enemia complementat	29.85	34.00
	450221	AA328102	Hs.24641	cyloskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs	1.00	1.00
20	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	51.26	93.00
20	450447 450568	AF212223	Hs.25010 Hs.25159	typotherical protein P15-2 Homo sapiens cDNA FLJ 10784 fis, clone NT	123.20	181.00 19.00
	450589	AL050078 AI701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	Interleukin 1 receptor, type II	1.00	100.00
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.89	1.55
25	450705	U90304	Hs.25351	iroquals homeobox protein 2A (IRX-2A) (1.00	45.00
	450832 450937	AA401369 R49131	Hs.190721 Hs.26267	ESTs ATP-dependent interferon response proteil	25.17 90.92	17.00 90.00
	450963	AA305384	Hs.25740	ERO1 (S. cerevisiae) like	3.33	1,70
	451105	A1761324	110.23740	ab:wi50b11.x1 NCL CGAP Co16 Home sapiens	15.02	124.00
30	451110	A1955040	Hs.265398	ESTs, Weekly similar to transformation-r	1.00	143.00
	451253	H48299	Hs.26126	claudin 10	3.02	2,29
	451291	R39288	Hs.6702	ESTS	1.00	1,00 18,00
	451320 451380	AW498974 H09280	Hs.13234	diacylglycarol kinese, zete (104kD) ESTs	6.90	6.67
35	451386	AB029006	Hs.26334	spastic paraplegie 4 (autosomal dominant hypothetical protein FLJ11071	35.75	72.00
	451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524 451541	AK001466 BE279383	Hs.26516	hypothetical protein FLJ10604	1.13 1.88	1.07 1.33
40	451692	ARC6416	Hs.26557 Hs.213897	ptakophilin 3 ESTs	1.00	1.00
	451635	AA018899	Hs.127179	cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854 AJ821005	Hs.118599	hypothetical protein FLJ23293 similar to ESTs	1,55 1,81	35.00 2.53
45	451871 451952	AL120173	Hs.301663	ESTS	1.00	22.00
	452012	AA307703	Hs.279766	kinesin femily member 4A	3.43	2.26
	452048	AB018345	Hs.27657	KIAA0802 protein	56.59	19.00
50	452194	Al694413	Hs.332649	offactory receptor, family 2, subfamily	1.67 9.31	4.09 63.00
30	452206 452240	AW340281 AA401389	Hs.33074 Hs.190721	Homo sepiens, clone IMAGE: 3606519, mRNA, ESTs	13.42	17.00
	452240	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo segiens cDNA FLJ11041 fis, clone PL	153.01	340.00
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	1.95	23.00
55	452296	BE379936	Hs.28866 Hs.61311	programmed cell death 10	42.33 1,17	61.00 2.14
	452304 452340	AA025386 NM_002202	H8.51311 Hs.505	ESTs, Weakly similar to \$10590 cysteine ISL1 transcription factor, LiM/homeodoma	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
60	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	32.00
	452410 452481	AL133619 N78223	Hs.108105	Homo saplens mRNA; cDNA DKFZp434E2321 (f	1.26 24.47	1.99 35.00
	452571	W31518	Hs.34665	transcription factor ESTs	54.61	102.00
	452613	AA461599	Hs.23459	ESTs	1.39	1.32
65	452699	AW295390	Hs.213062	ESTs	1.00	26.00
	452705	H49805	Hs.246005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	lg superfemily receptor LNIR	112,87	1.29 · 1.00
	452787 452795	AW294022 AW392555	Hs.222707 Hs.18878	KIAA 1718 protein hypothetical protein FLJ21620	1.00	1.00
70	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
	452833	BE559681	Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	174.35	1.00
	452962 452965	AA401369 AW173720	Hs.190721 Hs.345805	ESTS	98.26 1.55	17.00 1.00
75	452934	AW173720 AA581322	Hs.4213	ESTs, Weakly similar to A47582 B-cell gr hypothetical protein MGC16207	1.73	1.19
15	452946	X95425	Hs.31092	EphA5	1.00	1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
80	453095	AW295660	Hs.252756	ESTs	0.77 1.00	1.50
80	453102 453103	NM_007197 A\301052	Hs.31664 Hs.153444	frizzled (Drosophila) homolog 10 ESTs	1.00	1.00
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
0.5	453160	A1263307	Hs.239884	H2B histone family, member L	1.00	30.00
85	453197	Al916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00

	w	O 02/086	443				PCT/	US02/12476
		AL133161	Hs.32360	hypothetical protein FLJ 10867	1.69	1.93		
	453240		Hs.166254	hypothetical protein DKFZp666i133	1.00	1.00		
	453317		Hs.41696	keratin, hair, acidic,1	1.19	1,27		
_		AF034102	Hs.32961	solute carrier family 29 (nucleoside tra	4.90	4.11		
5		A1240665	Hs.8850	ESTs	199.42	340.00		
		U23752	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00		
	453431	AP094754	Hs.32973	glycine receptor, beta	1.00	1.00		
	453439		Hs.32976	guarrine nucleotide binding protein 4	3.44	5.17		
10	453459	BE047032	Hs.257789	E8Ts	2.84	5.58		
10	453563			Hs.181163		protein MGC5629	4.58	90.00
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775		Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830		Hs.20953	ESTs	24.92	25.00		
1.5	453857		Hs.35861	DKFZP586E1621 prolitin	167,59	66,00		
15	453867	A1929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39,00		
	453883	A)638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63,89	20.00		
	453900		Hs.226414	ESTs, Weakly shriter to ALUS_HUMAN ALU S	20.41	16.00		
20	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
20	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00		
	453964		Hs.12744	ESTs	1.00	1.00		
	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06 3.02	1.81		
	453976	BE463830	Hs.163714	ESTs	1.00	131.00 131.00		
25	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.23	1.02		
23	454034	NM_000691	Hs.575	aldehyde dohydrogenase 3 family, member	30.63	171.00		
	454042 454059	T19228 NM 003154	Hs.172572 Hs.37048	hypothetical protein FLJ20093 statherin	1,00	1,00		
	454066	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	Hs.37058	calcitorin/calcitonin-related polypeptid	1.01	1.45		
	454098		Hs.292911	ESTs, Highly similar to S60712 bend-6-pr	1.26	1.11		
30	454241	W27953	HS.292911	ab: CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
30	454417	BE144666 Al244459	Hs.110826	irinucleofide reseat containing 9	4.30	7.82		
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00		
	455175	AW993247	FIS. 154020	gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
	455601	AVV980247 A/368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00		
35	456237	AA203682	ns,010	gb:zx52e07.r1 Soares, fetal liver_soleen_	1.00	1.00		
55	456321	NM_001327	Hs.87225	cancentests arigen	1.14	1.10		
	456475	NM_000144	Hs.95998	Friedreich etaxia	1.00	48.00		
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189,00		
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80		
40	456736	AW248217	Hs.1619	scheete-scule complex (Drosophila) homol	1.15	1.94		
-10	458759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00	1.00		
	466990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	Ihyroid transcription factor 1	0.57	1.76		
	457234	AW968360	Hs.14355	Homo sapiers cDNA FLJ 13207 fis, clone NT	2.71	4.15		
45	457466	AW301344	Hs.122908	DNA replication factor	46.37	47.00		
	457489	A)693815	Hs.127179	cryptic gene	1.12	1.35		
	457646	AA725650	Hs.112948	ESTs	1.55	2.51		
	457733	AW974812	Hs.291971	FSTs	1.00	55.00		
	457819	AA057484	Hs.35408	ESTs, Highly similar to unnamed protein	4.36	3.18		
50	458092	BE545684	Hs.343566	KIAA0251 projein	1.00	1.32		
	458098	BE550224		metallothlonein 1E (functional)	1.00	22.00		
	458207	T28472	Hs.7855	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242	BE299588	Hs-28465	Homo sapiens cDNA; FLJ21869 fis, clone H	1.00	1.00		
	458247	R14439	Hs.209194	ESTs	7.00	9.85		
55	458879	AW975480	Hs.142913	ESTs	1.00	3.00		
	458778	AW451034	Hs.326525	arvisulfatase D	1.31	2.01		
	458933	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71		
	459352	AW810383	Hs.208828	ESTs	12.60	63.00		
	469670	F01020	Hs.172004	ätin	1.00	1.00		
60	459702	Al204996		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		

TABLE 9B

65 Pkey: Unique Eos probeset identifier number CAT number: Gene diuster number Accession: Genbank accession numbers

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70	Pkey 407746	CAT Number 10125_1	Accession ANO 1962 REACHS BE-664005 AACHSRIPS AMSSZDS AALHGIUTS AADSSDS AWXZSSZDS AWXZZSSZDS AWXZZSSZDS AWXZSSZDS AWXZSSZDS AWXZSSZDS AWXZSSZDS AWXZSSZDS AWXSSSZD AZSZDS AWXZSSZD AZSZDS AWXZSSZD AZSZDS AWXZSSZD AZSZDS AWXZSSZD AZSZDS AZSZDS AWXZSSZD AZSZDS
	408070	1036688 1	AW148852 RE350895
	408660	107294 1	AA525775 AA056342 AI538978 AW976281 AA664986
75	409522	113735 1	AA075382 AA075431
	409866	1156522 1	AW502152 H41202 H29772
	410032	1170435 1	BE065985 BE065944 BE066008 BE066093 BE066093
	411089	123172_1	AA456454 AA7 137 30 AA091294 AA584921 N86077 AW836781 AA601031 AA579876 AA551106 AA633188 AW905577 AI955808 AI679386 AI679805 AA514764 AA654862 AI082382 AA595822 AA551351 AA566369 AA666384 AA188934 AA666388 AA551297 AA565188
80	411152	1234028_1	BE060199 AW938012 AW877466 AW819782 AW835798 AW835546 AW936042 BE069121 AW835625 AW877536 AW835885 BE069202 AW870119 AW836837 RF160180 AW836946 RF0069101 BE069125 AW877527 BF160316 BE160398 AW935794 AW835701 AW835704
	412537	1304_1	ALG31778 XSS711 NML 072505 MS6079 AB370439 A464259 AVIG60401 AA405050 AA435123 BE174516 AA412861 A4405114 AA43024 T29403 BE079412 BE079422 N00202 AB370439 A464258 AVIG60416793 AH167658 AI862075 AB376230 AP128445 AVI235763 AL044113 A842557 AVIG60516 AA6727516 AA682863 BE00004 AVIG6056 AVIG30605 AVIG60603 AVIG60610 AA4725472 AB69422 AU04114 AI864577 AB05685

WO 02/086443 PCT/US02/12476 A4T8773 A1160445 AI674630 N69088 AW665529 M9278 A129239 AM57890 AI621264 AW297152 A1268215 A4907787 A1286170 A017982 A963341 A1469807 AI669363 BE552356 N66509 AA736741 AA382555 AW078911 AW292026 412811 1320/3 1 H06382 AW357730 AA332014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AH24991 AI693507 AI863108 AA599060 A091148 AA598699 R39687 AA813482 AW016452 H06363 R41807 Al364269 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 5 AA121202 R17734 413690 1383256 1 RF157489 RF157580 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H63186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 414883 15024 1 ANGECCIO PARTICIO NA PIGE NO PER WORLD IN VELICIA AND THE DECENTION INCIDENTAL RESIDENCE PROPERTY AND THE DECENCION AND 10 AA872039 W72385 T99630 A1422691 H98460 N31428 BE265916 H03265 Al657576 AA776920 AA910644 AA489522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA676046 AVY613002 AA527373 AW972459 AIB31360 AA621337 AA100926 AA772418 AA594628 AIB33892 W95996 AIG34317 AA598727 AIG85031 N95210 A459432 AI041437 AA932124 AA627684 AA693829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA578045 AA643280 W44561 A1991988 A1537692 A1090262 AA740817 A1312104 A1911822 AA416871 A1185409 AA129784 AA701623 A1075239 15 A138549 AA633648 A339996 A335680 AA386239 A078706 A085351 A382835 A346618 A146955 A1989380 A1346243 N92832 A7765850 A494330 A1278837 A4962596 A492600 W80435 AA001979 F87424 A1129015 N24127 AA157451 AA235549 AA459292 AA037114 AA 129785 A 494211 AW059601 AW866710 R92790 N59755 A381126 AW589407 H47725 H97534 H48076 H48460 T99631 AW300758 H03431 R76789 A 485434 H77575 R9823 AM67100 N29245 H48088 L48088 B2520698 B252015 H98525 AA701524 H74175 R5414 H78520 H78520 H03266 B2531919 AA706933 AA490310 A/507454 A470688 A202372 AW10472 W2591 H38980 HX551 3 T7598 B99156 20 W95095 R97470 AA702275 T77551 AA911962 H82956 NB3673 AA283672 415989 156454 1 Al267700 Al720344 AA191424 Al023543 Al469633 AA172056 AW958465 AA172236 AW953397 AA355086 417324 166714 1 AVI265494 AA456904 AA195677 AW265432 AW991605 AA456370 17690 1 N28754 N28747 AL568 M6 AIG79539 AA322671 AA322672 AW955043 AIG90326 AA776406 AIG16250 AA843678 AW451882 N23137 N23129 W70051 Al038748 AA831327 Al925845 AW94589 25 418712 1784125 1 Z42183 T31621 T97478 184788_1 410443 D62703 AA24296 D79798 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T66781 T67845 T67593 T73952 T67864 T60 630 419502 18535 1 T88387 T68401 T53939 T72360 T72099 160377 T58961 T71712 T72821 T64738 T74945 T72037 T65888 T72063 T73288 T72288 T84242 TISSUE TISSUED TISSUED TISSUED TISSUED TISSUED TITLY TIZZE TISSUED TIS 30 35 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 Al111192 H61463 H72060 AA344503 H38639 AI277511 AV661106 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72458 AV649539 AV653476 T72957 T72300 T69906 T71457 T70494 T72956 T70495 T8267 T74407 T36978 AA344726 T27854 T74467 T74601 T73696 T71516 T72504 AA348853 T7399 T87070 T72056 H7219 T73495 T73459 X466958 R92293 T74475 T84751 A344441 A434673 A434732 A434738 A141659 A76460 A760351 T64696 T8651 T72222 T66907 T67635 R29500 40 T72517 R02292 T80599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72067 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 Al064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T6437 5 AA345234 T67598 AA011414 T68036 H45262 A1207557 T68219 W69031 T69061 T64232 P30196 T62136 AV650539 H67469 T72978 AA344583 T60362 H58121 T95711 T72803 T68955 T71715 R29036 T72793 T69122 T64695 T62898 T69139 T68291 T64852 T67971 T46962 45 AA883592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H50426 AA342489 T73986 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56066 189181_1 419936 Al792788 BE142230 AA252019 421582 2041 1 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314625 AI571948 AA507595 AA614579 AA587613 R63618 50 AA568312 AA614/09 AA507576 AI625552 AW660155 AI610083 M12075 BED74052 AW004668 AA578674 AA62064 BED74053 BED7410 AA51776 AA586034 BED74652 AW601669 AW005690 AA86276 R5339 BED74654 AW601651 AW00570 AW750216 AA61 4539 BED74054 AW601651 AW60176 AW601760 AW750216 AA61 4539 BED74054 AW60176 AW601760 AW601765 AW601765 AW601760 AW60 422128 211994 1 AWBB1145 AA490718 MB5637 AA304575 T06067 AA331991 423034 224122 1 AL119930 AA320696 AW752565 55 423816 23234_1 236596 1 AL031985 AL137241 Al792386 Al733664 Al857654 Al049911 424200 AA337221 AA336756 AW966196 424999 245835 1 AW953120 R56325 AA349562 AM93124 A193629 AM94935 A198457 A1768408 A1783624 A1383985 A1580267 D79813 AA393768 AK001536 AA191092 AW510354 A1564256 A1353908 AA134266 426966 273896_1 27415_1 426991 60 42726 276598_1 AA663848 AA400100 AA401424 428023 28589 2 AL038843 AA161338 BE268213 AA425597 N67306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831 AISSISSE WESSES MESSA48 AIZ78611 AIZ8SSST AI824306 AIV338655 AVV150899 AA87514 N47393 NIZ9855 AA973469 AIQ3934 AIZ92064 AIQ34339 AIV674593 NIZ156 AIQ79733 AIQ38683 AIZ91616 AA491599 AA993675 AA837380 BE006554 BE006473 AIQ87090 T33044 AAS52043 AI203503 AA553359 W35263 AI129926 Z41844 AW020925 AW575848 AI684503 AA453297 AI140689 AI277175 AA426444 65 AISG2767 W02632 BE396786 R37261 429220 301384_1 AW207206 AW341473 AA448195 AI951341 429978 31150_1 AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA690585 AA375688 AA301092 AA298454 W057 62 AMMOTIVES 161568 DISCRED INACED BEZINEET AMMOTIVET DELET AMMOTIVES I AACCEPACE AMOTITIES ALSSAMLE AMAZIZEZ REZINEET AMMOTIVES ALSSAMLE AMAZIZEZ REZINEET AMOTIVES ALSSAMLE AMAZIZEZ REZINEET AMBOTIVES ALSSAMLE AMAZISEZ REZINEET AMOTIVES ALSSAMLE AMBOTIVES AMOTIVES ALSSAMLE AMBOTIVES AMOTIVES ALSSAMLE AMBOTIVES AMOTIVES ALSSAMLE AMBOTIVES AMBOTIVE 70 31808.1 AWAGGUIG MIGRIFUM WILIBOOSO WILIDO 3 MAI GUIGO GEOUZISSO WILIBOOT A WAGGUIT S AL 133561 ALO41090 AL117481 AL122089 AW4659292 A1968826 AW072916 A 184013 AA489155 AW465994 AW465044 HYSSO A1819642 A1280239 AI220572 AA788302 AI473611 AW541126 D80537 430439 430935 325772 1 431089 327825 BE041395 AA491826 AA621946 AA715980 AA666102 75 AW970622 AA503009 AA502998 AA502989 AA502806 T92188 431322 331543_1 NW31/M22 / NG30303 PAGGESS PAGGESS PAGGESS PAGGESS PAGGES 432407 34624 1 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 434414 38585_1 A798376 S46400 AW811617 AW811616 W00567 BE142245 AW858232 AW96185 LAW358362 AA232351 AA218567 AA055556 AW858231 80 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA082174 T61139 AA149776 AA699829 AW679188 AW613567 AW813538 Al267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705

AW817705 AW817703 AW817659 BE081531 H59570

AA628980 AI126603 BE504035

85 436608 42361_3

AA157730 AA157715 AA033524 AW849581 AW849581 AW854566 C00254 AW862636 T92637 AV892621 AA206593 AA209204 EE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60009 AA149726 AV/195620 EE081333 BE073424 AW817692

		O 02/08		PCT/US02/12476 w373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616
	438091	44964_1	A	A709126 AW898628 AW896544 AA947932 AW896625 AW896622 A1276125 A1185720 AW510696 AA967230 T52522 BE467708 AW243400
			A	W/M3642 AI28R245 AI18R342 DE2864 DE5017 DE2715 DE2477 DE3933 DE4679 AI298739 AI146984 AI222204 N98343 BE174213 AA845571
5			Á	.1813854 A1214518 A1635262 A1139455 A1707807 A1698085 AW884628 A1024788 A1004723 AW087420 A1565133 N34964 A1269399 W513280 A1061126 A1435618 A1869106 A1360606 A1024767 AA513019 AA757598 X56196 AA302959 A1334784 A1803794 AA010207
-			A	W890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI966295 AA780994
	439000	467716_1	· ·	1965913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 A4045713 R79750 N76096 W979121 AA847986 AA829098
	439285	47065_1	A	L133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014832
10	439780	47673 1	A	A775552 N62351 N9253 A4626243 AI341407 BE175639 A4456968 AI358918 AA457077 L109688 R23965 R26578
	439780	51021_2	â	L10968 R2306 R26978 A570256 ANO14761 AA573721 AA73237 A022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE325850 A1148171
		_	Α.	1359627 A1005068 A1356567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923
15	443068 443947	558874_1 586160_1	A	.11887 (D.A.1032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390 (24187 W24194 R17789
15	447636	7301_1		10049 NM 005342 L05095 AL03450 RF614226 AW749053 AA379173 AA248230 RE514634 AA334622 R70656 AA367593 AA214649
				A380318 AV/957081 R05760 AA039903 A1896597 AW630122 AA906264 AA041527 R01145 A1086668 BE463637 AA395795 A1354883 I/768938 A1569996 A462952 A1168562 A1168569 A066670 AW262560 AW613854 AA662639 AA435840 AA670197 A1024032 A1990659
			Ä	1990389 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595
20	448993	4	A	A095002 NB3992 I471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 A1656234 A1636283 A1567265
	440333	79225_1	A	W340858 BE207794 AA053065 R69173 AA292343 AA454906 AA293504 Al659741 Al927478 AA399460 Al760441 AA346416 BE047245
			A	A730390 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D20284 AI221458 BED48537 AI263048 AA346417
25	449305	804424_1	2	A911497 BE537702 J638293 AW813981
	451105	859083_1		1761324 AW880941 AW880937
	451320	86576_1	^	W118072 AIB31982 T15734 AA224195 AI701456 W20198 F26326 AA890570 N90562 AW071907 AI671352 AI375892 T03517 R88265 J124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205636 AA63/364 T03515 T33230
				A017131 AAAA3303 T33623 A0222566 T33511 T33785 A0419606 D55612
30	451807	8865_1	Y	NS2894 ALT17600 BE208116 BE208432 BE206239 BE062291 ANYSS423 AA351619 BE190648 BE140560 W60090 AA865478 N90291 W450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827526 AA904789 AA380381 AA880045 AA774409 BE003229 Z41756
	452410	9163_1		I 133610 AMAGRITR AM3R306A AM764A7 T09430 AIG73758 AA524895 AIGRI345 AI300600 AW498812 AA29616Z AIS69724 AI685732
			A	TABO2400 AA906453 AIZ04995 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AW272454 AIZ15594 AA622747 874039 N35031 AIB04126 AW513621 AA868351 AID26026 AI493386 AA614641 W61604 AI557060 AIZ14351 AA730140 AI125754 AIZ00813
35			Δ.	J 269603 ALS65082 AIB07095 AL476629 AA506909 AL368449 AL686077 AL582930 AW085038 AA757863 AA730154 AL767072 AA468316
	454241	1067807_	. A	U734130 AI734136 AA426284 AA433997 AI741241 AW043663 AI732741 AI732734 AA437369 AA425320 AA664046 R74130 IE144666 BE164942 AW238414 BE184946
	455175	1257335	1 A	W993247 AW861464
40	456237	168730_1	A	A203682 R11958 RE550224 AA832519 N45402 AW865857 N29245 BE465409 W07677 AW970089 A1299731 AA482971 BE503548 H18151 W79223 AF088393
40	458098	47395_1	Ā	A461301 W74510 R34182 A1090689 N46003 BE071550 R28075 AW134982 A1240204 Al138906 AW026179 A1572316 BE466182 A1206395
			A	V276154 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407
				8E467534 BE218421 BE467767 AA989054 BE467063 AI797130 BE327781
45	TABLE 90			•
	I ABLE 90	-		
	Pkey:	Unique	rumber oor	responding to an Eos probesel The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham i. et al." refers to the publication entitled "The DNA.
50	Ref:	sequenc	e of humai	n chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand	Indicates	DNA stra	nd from which exons were predicted.
	Nt_postfic	in: Indicate	nucleotic	e positions of prodicted exons.
55	Pkey	Ref	Strand	Nt_position
33	400512 400517	9796593 9796888	Minus Minus	1439-1615 49908-50346
	400560	9643598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
	400664 400685	8118496 8118496	Plus	13558-13721,13942-14090,14554-14679 16879-17023
60	400666	8118496	Plus	17962-18115,20297-20456
	400749 400783	7331445 8131618	Minus	9162-9293 35537-35784
	401027	7230983	Minus	70407-70554,71060-71160
65	401093 401203	8516137 9743387	Minus Minus	22335-23166 172961-173056.173968-173928
05	401212	9658406	Plus	87839-89028
	401411 401435	7799787 8217934	Minus Minus	144144-146329 54508-55238
	401464	6682291	Minus	170688-170834
70	401714	6715702	Plus	96484-96691
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131886- 131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83290.85320-85540,94719-95287
75	401780 401781	7249190 7249190	Minus Minus	28397-28617,26920-29045,29135-29296,29411-29567,29705-29787,30224-30573 83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
, 5	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167459,169634-168942
	401797	6730720 4581193	Plus Minus	6973-7118 124054-124209
	401961 401985	2580474	Plus	61542-61750
80	401961 401985 401994	2580474 4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
80	401961 401985 401994 402075 402260	2580474 4153858 8117407 3399665	Minus Plus Minus	42904-43124, 42211-43338,44607-44763,45199-45281,46337-46732 121907-122035,122804-122921,124019-124161,124455-124610,125672-125076 113765-113910,115655-115765,119006-116904
80	401985 401985 401994 402075 402260 402265	2580474 4153858 8117407 3399665 3287673	Minus Plus Minus Plus	42904-43124,42214-4358,44607-44763,45919-45281,46537-46732 12100-712055,722004-12201,72019-124161,124455-124610,125672-126076 13765-13910,156653-115765,116006-116940
80 85	401961 401985 401994 402075 402260	2580474 4153858 8117407 3399665	Minus Plus Minus	42904-43124, 42211-43338,44607-44763,45199-45281,46337-46732 121907-122035,122804-122921,124019-124161,124455-124610,125672-125076 113765-113910,115655-115765,118006-1186940

	w	O 02/08	6443		PCT/US02/12476
	402420	9796339	Pius	129750-129919	
	402674	8077108	Minus	39290-39502	
	402802	3287156	Minus	53242-53432	
	402994	2996643	Mittus	4727-4969	
5	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337	
	403306	8099945	Plus	127100-127251	
	403329	8516120	Plus	96450-96598	
	403381	9438267	Mittus	26009-26178	
	403478	9958258	Plus	116458-116564	
10	403485	9966528	Plus	2888-3001,3198-3532,3655-4117	
	403627	8569879	Minus	23868-24342	
	403715	7239669	Plus	85128-85292	
	404044	9558573	Minus	225757-225939	
1.5	404076	9931752	Minus	3848-3967	
15	404101	8076925	Minus	125742-125997	
	404140	9843520	Plus	37761-38147	
	404165	9926489	Minus	69025-69128	
	404185 404210	4572584 5006246	Minus Plus	129171-129327 169926-170121	
20	404210	9367202	Minus	109920-170121 55675-56055	
20	404253	2326514	Plus	53134-53281	
	404297	9944263	Minus	73591-73723	
	404347	9838195	Plus	73493-74829	
	404440	7528051	Plus	80430-81581	
25	404721	9856648	Minus	173763-174294	
20	404794	4826439	Plus	101619-101898	
	404854	7143420	Plus	14260-14537	
	404877	1519284	Pius	1095-2107	
	404927	7342002	Plus	68690-69563	
30	404996	6007890	Plus	37999-38145.38652-38996.39727-39872.40557-40674.42351-42450	
	405449	7622497	Plus	42236-42570	
	405568	6006906	Plus	35912-36065	
	405572	3800891	Plus	85230-85938	
	405646	4914350	Plus	741-969	
35	405676	4557087	Plus	73195-73917	
	405770	2735037	Flus	61057-62075	
	405932	7767812	Minus	123525-123713	
	406137	9165422	Minus	30487-31058	
40	406360	9256107	Minus	7513-7673	
40	406399	9256288	Minus	63448-63554	
	406467	9795551	Plus	182212-182958	

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Caroor and Non-malignant Lung Disease
Table 2A shows about 307 geness up-regulated in non-malignant lung disease neither to lung is unuses and normal body sesses entire of several regulated in lung tumors relative to
committed upon and normalignant lung disease. These geness were selected from about 5690 protected on the EnchAfgment's Mail Gamerinip array. 45

Table 108 show the accession numbers for those Play's lacking lakeling lakeling of No table No. For each problem is well have failed the garte design number from which have designed. Gets and calleng some completed lakeling seasons comment from 100 for 1 50

Table 10C show the generate positioning for those Pikey's leading Unigene ID's and accession numbers in table 10A. For each predicted exon, we have listed the general sequence source used for prediction. Nucleotide locations of each predicted exon are also listed. 55

			a may be a market to the second of the secon						
			number, Genbank accession number						
		Inigene number							
60	Unigene Title:	Inigene gene fille							
			ors (including squemous cell caroinomas, edence	arcinomas, small o	ell carcinomas, granulomalous	and carcinoid lumors) divided by the			
		everage of normal b	ing samples						
	R2:	verage of non-mai	gnant lung disease samples (including bronchilis,	emphysema, fibro	sis, alelectasis, asthma) divider	t by the average of normal tung samples			
65	Pkey ExAccr	UnigeneID	Unigene Title	Rt	R2				
	404394		ENSP00000241075:TRRAP PROTEIN.	0.79	3.10				
	404916		Target Exon	1.00	159.00				
	405257		Target Exon	1.00	422.00				
	407228 M2507	Hs,156376	hemoglobin, beta	0.47	2.33				
70	407568 AA740		ESTs	1.00	123.00				
	408562 Al4363		Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00				
	409031 AA376		ESTs	1.00	128.00				
	410434 AF051		toll-like receptor 2	39.65	149.00				
	410467 AF1025		dachshund (Drosophila) homolog	1.00	109.00				
75	410808 T40326			1.14	13.14				
	412351 AL1359		T-cell acute lymphocylic leukemia 1	0.37	2.27				
	412372 R65998	Hs.285243	hypothetical projein FLJ22029	1.00	173,00				
	413795 AL0401	78 Hs.142003	ESTs	0.10	11.90				
	414154 AW205	314 Hs.323060	ESTs	0.62	2.09				
80	414214 D49951	Hs.75819	givoporotein MGA	0.03	4.55				
	414998 NM_00	2543 Hs.77729	oxidised low density Ropprotein (lectin	0.64	2.97				
	415122 D60708		ESTs	0.07	8.97				
	415765 NM_00		tyrosine kinase with immunoplobulin and	0.67	1.65				
	415775 H00747		ESTs. Weakly similar to 138022 hypotheti	0.29	2.64				

Hs.78824 tyrosine kinase with immunoglobulin and Hs.29792 ESTs, Weakly similar to 138022 hypotheti Hs.78913 chemokine (C-X3-C) receptor 1

Unique Eos probeset identifier number

85

415910 U20350

	W	O 02/086	443			
	416319	AJ815801	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
5	417421	AL138201 AL049176	Hs.82120 Hs.82223	nuclear receptor subfamily 4, group A, m chardin-like	36,30 1.00	357.00 179.00
,	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87860	nmiele hymotine phospholase, non-recent	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Wealdy similar to S41044 chromosom	0.44	1,90
	418883	BE387036	Hs.1211	acid phosphalase 5, tartrate resistant	0.96	2.04
10	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrimin	1.48	5.13 336.00
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55 0.80	3.65
15	420556	AA278300	Hs.124292 Hs.187636	Homo sapiens cDNA: FLJ23123 fis, clone I. ESTs	1.65	8.07
13	420656 420729	AA279098 AW964897	Hs 290825	ESTs	2.99	25,82
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
	422060	R20693	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156,00
	422426	W79117	Hs.58559	ESTs	0.03	7.44
20	422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA464340	Hs.131987	ESTs	1.00	167.00 3.01
25	424711 424973	NM_005795 X92521	Hs.152175 Hs.154057	calcitorin receptor-like	0.43	19.45
23	425023	AW956889	Hs.15405/ Hs.154210	matrix metalloproleinase 19 endothelial differentiation, sphingolipi	0.14	3.35
	425023	A3006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1,42
	426657	NM_015865	Hs.171731	solule cerrier family 14 (urea transport	0.03	3.74
30	426753	T89832	Hs.170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
	427963	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25 3.82
35	428927	AA441837	Hs.90250	ESTs	0.01 1.00	3.82 138.00
33	429496	AA453800	Hs.192793	ESTs anglopoietin-like 1	1.00	132.00
	430468 431385	NM_004673 BE178536	Hs.241519 Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
	431728	NM_007351	Hs.268107	multimerin	1.00	157.00
	431848	A1378857	Hs.126758	ESTs, Highly similar to AF175283 1 zine	0.34	2.24
40	432128	AA127221	Hs.117037	ESTs	0.00	1.15
	432519	AJ221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433903	A1823593	Hs.27633	ESTs	1.00	105.00
45	434730	AA644669	Hs.193042	ESTs	1.05	3.15
43	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid gb:nv54h12.r1 NCL_CGAP_Ew1 Homo saplens	0.83 1.00	1.94 218.00
	436532 437119	AA721522 Al379921	Hs.177043	ESTs CONFIGNORS SPIES	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
50	437980	A1669586	Hs.222194	ESTs	1.00	147.00
	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	Al302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875	AA827840	Hs.189059	ESTs	23.32	370.00
55	441043	AA913488	Hs.192102	ESTs ESTs	0.77 3.43	8.50 16.36
33	441188 441499	AW292830 AW298235	Hs.255609 Hs.101889	ESTS	1.00	167.00
	444513	AL120214	Hs,7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM 005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
60	445279	R41900	Hs,22245	ESTs	0.60	141.00
	446017	N98238	Hs,55185	ESTs	0.18	2.39
	446934	AB020722	Hs.16714	Rho guanine exchange factor (GEP) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53 2.64
65	447357	Al375922	Hs.159367 Hs.171941	ESTs ESTs	18,05	2,64
03	448106 448253	Al800470 H25899	Hs.171941 Hs.201591	ESTS	1.00	141.00
	449275	AW450848	Hs.205457	periavin	0.56	1.38
	450400	AI694722	Hs.279744	ESTS	0.88	4.33
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
70	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497	H83294	Hs.284122	Writ inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530	serum deprivation response (phosphalidy)	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
75	458332	AI000341	Hs.220491	ESTs	1.00 0.20	192,00 2,98
13	459590 400269	AA022888	Hs.176065	ESTs Eos Control	0.40	2.40
	400269			NM_016369":Homo sapiens claudin 18 (CLDN	0.53	1.77
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
	412295	AW088826	Hs 117176	poly(A)-binding protein, nuclear 1	0.56	1,74
80	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	0.64	1.50
	417204	N81037	Hs.1074	surfactan), pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T26499	Hs.89485	carbonic anhydrase IV	0.20	1.28
85	421502 421798	AF111856 N74880	Hs.105039 Hs.29677	solute carrier family 34 (sodium phospha N-acylsphingosine amidohydrolase (acid c	0.78 0.59	1.90 1.54
03	421798	N/488U	ris.296/7	rv-асугорны довны агтионум маве (400 c	403	1.09

		O 02/086	443	and the second continue descendent while	0.59	1.55
	423354 423738	AB011130 AB002134	Hs.127436 Hs.132195	calcium channel, voltage-dependent, alph arway trypsin-like prolease	10.14	1.50 51.00
	423738	M18667	Hs.132190 Hs.1867	progestricsin (pepsinogen C)	0.35	1,62
	425438	T62216	Hs.270840	ESTs	0.23	9.45
5	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732	Hs.173233	hypothetical protein FLJ 10970	0.01	1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26 2.43
	430280 431433	AA361258 X65018	Hs.237868 Hs.253495	interleukin 7 receptor surfactant, pulmonary-associated protein	0.46 0.57	1,59
10	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.37	1.80
	432965	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
	442275	AW449457	Hs.54795	ESTs	0.55	1.78
1.5	443709	AI082692	Hs.134662	ESTs	0.00	3.02 2.49
15	444325 450954	AW152618 At904740	Hs.16757 Hs.25691	ESTs receptor (calcitonin) activity modifying	0.32 0.46	1.74
	451558	NM 001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	sotule carrier family 6 (neurotransmitte	0.00	3.30
	456855	AF035528	Hs.153863	MAD (mothers agains) decapentaplogic, Dr	0.01	2.31
20	444342	NM_014398	Hs.10887	similar to tysosome associated membrane	0.66	2.20
	400754			Target Exon	1.00	297.00
	401045			C11001883*:gij6753278 ref NP_033938.1 c	1.00 0.89	109.00 1,39
	401083			NM_016582* Homo sapiens peptide transpor	1.45	4.47
2.5	402474			NM_004079:Homo sapiens cathepsin S (CTSS ENSP00000235229:SEMB.	1.00	1.87
20	403021			C21000030:gij9955960jref[NP_063957.1] AT	1.00	149.00
	403438			NM 031419* Homo saniens molecule nossess	1.06	2.96
	403687			NM_007037*:Homo saplens a disinlegrin-li	0.04	4.89
20	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.0
30	404277 404288			NM_019111*:Homo sapiens major histocompa NM_002944*:Homo sapiens v-ros avian UR2	0.97 1.00	1.93 68.00
	404288	AI815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83
	405106	MIDIOUVI		C11001637*:gi;5032241 reliNP_005732.1 z	1.00	235.0
	406381			Target Exon	1.00	93.00
35	406387			Target Exon	1.37	6.02
	406646	M33600		major histocompatibility complex, class	0.88	2.46
	406714	AI219304	Hs.266959	hemoglobin, gemma G annoxin A2	0.01 1.00	3.19 147.0
	408753 406973	AA505665 M34996	Hs.217493 Hs.198253	major histocompatibility complex, class	1.03	204
40	407248	U82275	Hs.94498	leukocyle immunoglobulin-like receptor,	1.00	64.00
40	407510	U96191	110.04400	gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.0
40	408045	AW136959	Hs.245123	ESTs	1.00	70.00
45	408074	F20723		ESTs	1.00	112.0 10.17
	406374 409064	AW025430 AA062954	Hs.155591 Hs.141883	forkhead box F1 ESTs	0.07	2.31
	409083	AF060083	Hs.673	interieukin 12A (natural killer cell sti	1.00	96.00
	409153	W03754	Hs.50813	hypothesical protein FLJ20022	0.01	4.56
50	409203	AA780473	Hs,687	cylochrome P450, subfamily IVB, potypept	0.01	3.72
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo saplens mRNA, chromosome 1 specific	0.14	27.35
	409718	D66640	Hs.56045	src homology three (SH3) and cysteine ri gb:PM3-HT0605-270200-001-a02 HT0606 Homo	1.00 0.64	113.00 2.47
55	410798 411020	BE178622 NM 006770	Hs.16291 Hs.67726	macrophage receptor with collagenous str	0.55	2.40
55	411667	BE160198	FIG.07720	gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.0
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
60	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07 1.72
	412869 412870	AA290712 N22788	Hs.82407 Hs.82407	CXC chemokine ligand 16 CXC chemokine ligand 18	0.93	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
	413533	BE145973	114.040	gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1,50
65	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232,0
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	At129238	Hs.192235	ESTs	1.00	85.00 213.0
	413902	AW964490	Hs.32241	ESTs, Weakly similar to 965657 alpha-1C-	1.00 0.02	3,93
70	413829	NM_001872 BE393856	Hs.75572 Hs.66915	carboxypeptidase B2 (plasma) ESTs, Weakly similar to 16.7Kd protein (1.00	115.0
/0	414376 414577	AI058548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1,94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.263091	found in inflammatory zone 3	0.86	1.95
75	415120	N64464	Hs.34950	ESTs	1.00	120.0
75	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (66kD, chr	0.60	2.48 95.00
	415335	AA847758	Hs.111030	ESTs Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	95.00 136.0
	415582 416030	W92445 H15261	Hs.165195 Hs.21948	ESTs	0.02	8.07
	416427	EE244050	Hs.79307	Rac/Cdc42 guarine exchange factor (GEF)	1.00	73.00
80	416464	NM 000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00 0.85	114.0 1,30
85	417370 417573	T28651 T87281	Hs.82030 Hs.16355	tryptophanyl-IFNA synthetase ESTs	0.85	1.30
0.0	41/0/3	107201	18.10300	Lois	J. 10	14.54

	u	O 02/086	443			
	418067	Al127958	Hs.83393	cyslatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprolein D1 polyp	1.00	60.00
5	418832	X04011	Hs.88974	cytochrome b-245, bela polypeptide (chro	2.40 0.67	14.74
3	418945 419261	BE246762 X07876	Hs.89499 Hs.89791	arachidonate 5-lipoxygenase wingless-type MMTV integration site famil	1.00	73.00
	419564	LIGRARA	Hs 91139	solute carrier family 1 (neuronal/lepithe	1.00	192.0
	419574	AK001989	Hs.91165	hypothelical protein	1.00	94.00
	419968	X04430	Hs.93913	interioukin 6 (interferon, bota 2)	61.16	500.0
10	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420235	AA258124	Hs.293878 Hs.186649	ESTs, Moderalely similar to ZN91_HUMAN Z	1.00	172.0 97.00
	420577 421262	AA278436 AA286746	Hs.186649 Hs.9343	ESTs Homo sepiens cDNA FLJ14265 fis, clone PL	1.00	64.00
	421445	AA913059	Hs.104433	Homo sepiens, clone IMAGE:4054868, mRNA	0.88	1.51
15	421470	R27496	Hs.1378	annexin A3	0.05	11.26
	421478	Al683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105906	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50 1.00	31,57 129,0
20	421855 421913	F06504 Al934365	Hs.27384 Hs.109439	ESTs, Moderately similar to ALU4_HUMAN A osleoglycin (osleoinductive factor, mime	1.00	129.0
20	421913	AA300900	Hs 98849	ESTs, Moderately similar to AF161511 1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.0
	422385	AF105374	Hs.115830	heparan sulfate (olucosamine) 3-O-sulfol	1.40	3.98
	423168	R34385	Hs.124940	GTP-binding prolein	0.34	3.59
25	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09 1.00	2.13 141.0
	423424 423456	AF150241 AL110151	Hs.128433 Hs.128797	prosteglandin D2 synthese, hemalopoletic DKFZP586D0824 protein	1.00	66.00
	423696	Z92546	Fig. 120731	Sushi domain (SCR repeat) containing	0.73	1.27
30	424027	AW337575	Hs-201591	ESTs	0.54	2.58
	424212	NM_005814	Hs.143131	glycoprotein A33 (fransmombrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.98
35	425771 426486	BE561776 BE178285	Hs.159494 Hs.170056	Bruton agammaglobulinemia tyrosine kinas Homo sapiens mRNA; cDNA DKFZp59680220 (f	1.18	2.56 76.00
22	427507	AF240467	Hs.179152	toll-like receptor 7	1.00	83.00
	427618	NM_000760	Hs.2175	colony simulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
40	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.0
40	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00 2.55
	428769 428780	AW207175 AJ478578	Hs.106771 Hs.50636	ESTs ESTs	0.09 1.00	98.00
	428833	A1928355	Ha.185806	ESTS ESTS	1.00	113.0
	429657	D13626	Hs.2465	KIAA0001 gene product; gutative G-protei	1.00	52.00
45	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	1.00	132.0
	430226	BE245562	Hs.2551	adrenergic, bela-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.0 6.96
	430414 430858	AW365665 AA482900	Hs.120388 Hs.162080	ESTs ESTs	1.00	70.00
50	430843	AI734149	Hs.119514	ESTS	1.00	90.00
50	430998	AF128847	Hs.204038	indolelhylamine N-melhyltransferase	0.29	1.84
	431217	NM_013427	Hs,250630	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
55	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63 76.00
22	432203	AA305746	Hs,49	macrophage scavenger receptor 1 CLST 11240 protein	1.00 0.46	1.46
	432231 432485	AA339977 N90866	Hs.274127 Hs.276770	CDW52 antigon (CAMPATH-1 antigon)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
	432596	AJ224741	Hs.278461	metriin 3	0.04	5.79
60	432850	X87723	Hs.3110	angiolensin receptor 2	1.00	167.0
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	A1732637	Hs.277901	ESTS FSTs	1.00 120.16	91,00 315,0
	434445	AI056872 AI349306	Hs.133386 Hs.11782	ESTS	0.60	1.84
65	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.0
05	435974	L/29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.0
	436061	A1248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
70	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.0 71.00
/0	437311	AA370041 H29796	Hs.9456 Hs.269622	SWI/SNF related, matrix associated, acti ESTs	1.00	115.0
	437439 438199	AW016531	Hs.122147	ESTS	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
	440515	AJ131245	Hs.7239	SEC24 (S. cerevisioe) related gene famil	1.00	77.00
75	440887	Al799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384 441735	AA447849 AI738675	Hs.288660 Hs.127346	Homo sapiens cDNA: FLJ22182 fis, clone H ESTs	0.79 1.00	1.89 75.00
	441735	AV590572	Hs.235768	ESTs	0.78	5.83
80	442832	AW206560	Hs.253569	ESTs	0.03	10.88
-	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443262	T47764	Hs.132917	ESTs	1.00	197.0
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.0 2.09
85	443951 444330	F13272 Al597655	Hs.111334 Hs.49265	femilin, light polypaptide ESTs	0.55 1.00	90.00
ری	114330	MIDS/ 000	115,48260	Edia	1.00	50,00

	we	02/086	443				PCT/US02/12476
		W204908	Hs.169979	ESTs	1.00	84.00 4.38	
		1741471 13580	Hs.23666 Hs.13436	ESTs Homo sapiens clone 24425 mRNA sequence	1.00	97.00	
		E397753	Hs.14623	interferon, gamma-inducible protein 30	0.93	1.69	
5	446917 A	1347863	Hs.156672	ESTs	1.00	106.00	
	447261 N	M_006691	Hs.17917 Hs.301957	extracelfular link domain-containing 1 nudix (nucleoside diphosphate linked moi	0.40 1.00	47.20 100.00	
		W958473 B033059	Hs. 18705	KIAA1233 protein	0.05	8.21	
- 0	447997 H	00656	Hs.29792	ESTs, Weakly similar to 138022 hypotheti	0.02	5.42	
10		A497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00 1.56	
		L050295 IM_005859	Hs.22039 Hs.29117	KIAA0758 protein purine-rich element binding protein A	0.42	11.33	
	450684 A	AQ40403	Hs.60371	ESTs	1.00	94.00	
1.5		W450461	Hs.203965	ESTs	1.00	91.00 152.00	
15		1266484 152804	Hs.31570 Hs.25956	ESTs, Weakly similar to KIAA1324 protein DKFZP564D206 protein	1.00	152.00 86.00	
		F124251	Hs.26064	novel SH2-containing protein 3	0.60	1.30	
		43948	Hs.326444	cartilage acidic protein 1	0.54	1.91	
20	452197 A	W023595 A596509	Hs.232048 Hs.29117	ESTs purine-rich element binding protein A	1.00 4.53	67.00 11.07	
20		18825	Hs.29191	epithelial membrane protein 2	0.72	224	
	453049 E	E537217	Hs.30343	ESTs	1.00	68.00	
		IM_016113	Hs.279746	vanifold receptor-like protein 1 Homo sapiens cDNA FLJ11422 fis, clone HE	0.83 1.00	1.70 132.00	
25		W295374 A862496	Hs.31412 Hs.28482	ESTs	1.00	72.00	
	453531 A	A417940		ESTs, Wealdy similar to JC5795 CDEP prot	1.00	68.00	
		E154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89 82.00	
		A287827 K002016	Hs.284205 Hs.114727	up-regulated by BCG-CWS Homo sapiens, clone MGC:16327, mRNA, com	1.00 0.79	1.96	
30		F032906	Hs.252549	calhepsin Z	1.03	3.25	
		18572	Hs-22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00	
	459696 F	03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00	
	TABLE 10B						
35	Pkey:	Holono Gor	s probeset ide	offer number			
	CAT numbe	r: Gene clust	er number				
	Accession:	Genbank a	ocession num	bers			
40	Pkov	CAT Numb	er Access	due.			
+0	406074	103684_1	R2072	3 AA263003 AA333976 AA334725 AA334151 AW96	5490 AA3105	13 A/810530 D31302 AW1	34897 AA830127 AA046953 Al668930
				4 AW104534			
	411667 413533	1253334_1 1375344_1	BE160	198 AW935898 T11520 AW935930 AW656073 AW6 973 BE146972 BE147042 BE147018 BE146783 BE	161034 147030 DC14	e701 DE147010 DE146766	DE1/17/021 DE1/6062 RE1/67/67 RE1/17/04/
45	410000	1070044_1	DE146	707 DE146776 DE146085 RE146703 RE146768 RE-	146771 RE14	8954 RF146780 RF147048	RF147025 RF147030
	423387	22779_1	AJ012	374 U11087 L13288 X75299 L20295 AW630780 H14	1880 T28037 .	A/872991 R72136 AW4498	339 T81622 T79697 T29519 R94105 T83923
			R7330	0 Al797007 R73390 AA961010 H74168 Al689932 BI 115 R50647 R73210 H45098 R46451 AW166269 T7	045543 AIBU	18418 A1606912 A1606673 /	AW884084 AW872978 AW872985 AA500055
			T7961	2 R73145 R50549 A1094557 A1668793 R72302 A156	4366 W01956	AA418962 W32571 R728	40 H45409 R72085 R46356 R48758
50			80244	RAS AAA1R79R TR3751 R94072 T161R2 AA92R7R5 A	AA903896		
	423696	23112_1	Z9254	3 AA330586 AI570588 AW341487 AI827050 AW298 175 AI206100 AA912444 AI289365 AI640254 AW772	668 AI792189	9 AND 15693 AT 733599 AND 73	2251 Alb/2468 AW193262 Al244/16 8/77 A 4998000
	430212	314437_1	AA489	153 AI718503 AA469225	.400)/ 33/	0 70102100411103147050	DHI / PACCULUS
	436532	421802_1	AA721	522 AW975443 T93070			
55	453531	97026_1	AA417	940 AA036735 T07025			
	454741	1232559_1	BE154	396 AW817959 BE154393			
60	TABLE 100						
	Pkey:	Unique nur	mber correspo	nding to an Eos probeset			
	Ref:			digit numbers in this column are Genbank Identifier inceome 22." Dunham I. et al., Nature (1999) 402:4		, "Dunham Let al." recers	to the publication entitled . I lie DMA
	Strand:	Indicates D	NA strand fro	m which exons were predicted.	U3*45U.		
65	Nt_position	indicates n	ucleotide posi	tions of predicted exons.			
	Pkey	Ref	Strand	Nt_position			
	400754	7331445	Plus	144559-144684			
70	401045	8117619	Plus	90044-90184,91111-91345			
70	401083 402474	3242744 7547175	Plus	33192-33360 53526-53628,55755-55920,57530-57757		*	
	402808	6456148	Minus	114964-115136,115461-115585,115931-116047	,117666-1177	771,118004-118102	
	403021	7547270	Plus	120799-120966			
75	403421 403438	9665041 9719679	Minus Plus	126609-126773,139986-140205 90792-90938			
, 5	403436	7387384	Plus	9009-9634			
	403764	7717106	Minus	118692-118853			
	404277 404288	1834458 2769644	Minus Plus	91665-91946 3512-3691			
80	404288	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-	41593,41773	41919	
	404518	8151988	Plus	84494-84603			
	404916 405106	7341826 8079395	Plus Minus	91057-91188 80877-81418			
	405106 405257	8079395 7329310	Minus	73121-73273			
85	405381	6006920	Minus	7638-8054			

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116229-116371,117512-117651

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TABLE 11A: Genes Disfinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows elect 84 genes uproplished in larg edenocacionemas rolative to other larg lamces, non-malignant larg disease, and normal lung. These genes were selected from about 99680 probesets on the Ecoloffymetric Hud

Table 10 locus the accession numbers for these finely hassing LitipsosDin for table 11s. For each probabative hower finels the grant cluster number from which the object-includes was obegined. Discus clusters recreaged using responses desent from referenced EST and enfilled. These objectives recreaged under proposes desent from referenced EST and enfilled. These objectives recreaged under proposes desent from referenced EST and enfilled. These objectives recreaged under proposes comprising each cluster are titled in the Accession's cluster.

Accession courts.

Table 11C show the genomic positioning for those Pkey's lacking Uniques ID's and accession numbers in table 11A. For each predicted exon, we have fished the genomic sequence source used for prediction. Notice lists locations of each producted count are also failed.

15	Pkey: ExAcon: UnigenelD: Unigene Title:	injug Eag probated Idealfiller number ment probated from number Genberk accomption number riginary counter. gjenne grunner gjenner g	
	R1:	verage of lung turnors (including squemous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid turnors) divided by the	
20	R2:	erage of normal lung samples erage of non-maignant lung disease samples (including bronchibs, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung sample	:\$
	Distr. EvA	University Universe Title R1 R2	

	Ploty	ExAcon	Unigenei/D	Unigene Title	R1	R2
	403329			Terget Exon	1.00	61.00
	406399			NM_003122*Homo sepiens serine protease	1.00	39.00
25	406690	M29540	Hs. 220529	carcinoembryonic antigen-related cell ad	226.37	350.00
	407869	A1827976	Hs-24391	hypothetical protein FLJ13612	0.77	1.18
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	409103	AF251237	Hs.112206	XAGE-1 protein	80.44	40.00
30	409187	AF154830	Hs.50966	carbamcyl-phosphete synthetase 1, miloch	1.00	1.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs-279727	Homo seplens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
35	411908	L27943	Hs.72924	cyticine deaminase	1.00	1.00
	412612	NM_000047	Hs.74131	arylsuffatese E (chondrodysplasia puncta	1.02	1.03
	414075	U11862	Hs.75741	emiloride binding protein 1 (amine oxida	0.84	1.07
	416206	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
40	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419502	AU076704		fibrinogen, A alphe polypeptide	13.05	115.00
	419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
	420931	AF044197	Hs.100431	smell inducible cytokine B subfamily (Cy	1.00	8.00
4.5	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
45	421190	U95031	Hs.102482	mucin 5, aubtype B, tracheobronchiał	1.17	1.55
	421474	U76362	Hs.104637	solute cerrier family 1 (glutamate trans	1.46	1.76
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyttransferase I, I	1.00	3.00
	421582	AI910275		trefoli factor 1 (breast cancer, estroge	1.23	1.00
50	422026	U90736	Hs.110626	trinuclectide repeat containing 9	1.00	52.00
50	422095	A1888872	Hs-282804	hypothetical protein FLJ22704	4.37	2.34
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1,15	1,78
	422867	L32137	Hs.1584	cartilage oligomeric metrix protein (pse	1.69	3,17
	423472	AF041260	Hs.129057	breast cardinoma amplified sequence 1	48.13	72.00
55	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00 1.00
22	424502	AF242388	Hs.149585	lengsin		59.00
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci NIMA (never in mitosis gene a)-related k	1.00 21.35	1.00
	424905	NM_002497	Hs.153704		1.00	1.00
	424960	BE245380 AB007948	Hs.153952 Hs.158244	5' nucleofidase (CD73)	1.00	35.00
60	425523 426230		Hs.241395	KIAA0479 protein protesse, serine, 1 (trypsin 1)	1.00	83.00
00	426230	AA367019 AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
65	429263	AAD19004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1,07	1.00
00	429610	AB024937	Hs.211092	LUNX protein: PLUNC (palate tung end nas	1.59	1.69
	430508	A)015435	Hs.104637	ESTs	4.75	7.27
	430985	AA490232	Hs.27323	ESTs, Weakly similar to 178885 serine/th	0.94	1.28
	431548	AI834273	Hs.9711	novel protein	5.66	15.00
70	431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
	431986	AA536130	Hs.149018	Novel human gene mapping to chomosome 20	1,19	1.47
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432677	NM 004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19,00
75	433819	AW511097	Hs.112765	ESTs	3.71	8.00
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29,31	72.00
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fls, clone L	1.00	64,00
	434792	AA649253	Hs.132458	ESTs	8.52	44.00
	436217	T53925	Hs,107	fibrinogen-like 1	57.97	31.00
80	436749	AA584890	Hs,5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
	437866	AA156781		metallothionein 1E (functional)	3.62	101.00
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
0.5	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
85	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

	W(D 02/086	443 Hs.67709	Homo sapiens mRNA full length insert cDN	1,00	21.00	PCT/US02/12476
	441031	Al110684 BE218239	Hs.7645 Hs.202656	fbringen, B beta polypeptide ESTs	1.41	99.00 1.00	
5	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00 1.99	
,	443991	AA876372 NM_002250	Hs.93961 Hs.10082	Homo saplens mRNA; cDNA DKFZp667D095 (fr potassium intermediate/small conductance	1.20 5.71	6.87	
	444931	H58373 AV652066	Hs.332938 Hs.75113	hypothetical protein MGC5370 general transcription factor IIIA	1.98 1.00	38.00 54.00	
10	446102 446163	AW168067 AA026880	Hs.317694 Hs.25252	ESTs Homo sepiens cDNA FLJ13603 fis, clone PL	1.00	1.00 36.00	
		BE094848 AW630534	Hs.15113 Hs.76277	homogentisate 1,2-dioxygenase (homogenti Homo sapiens, clone MGC:9381, mRNA, como	1.00 1.24	11.00 1,16	
	447532	AK000614 AW369771	Hs.18791 Hs.52620	hypothetical protein FLI20607 integrin, beta 8	1.23	1,63 1,00	
15	448844	AI581519 AW818436	Hs.177164 Hs.23590	ESTs solute carrier family 16 (monocarboxylic	1,00	31.00 83.00	
	451807	W52854		hypothetical protein FLI23293 similar to	1.55	35.00 1.44	
20	453392	F33868 U23762	Hs.284176 Hs.32964	transferrin SRY (sex determining region Y)-box 11	1.00	16.00	
20		A1884911 A1066629	Hs.32989 Hs.125073	receptor (calcitonin) activity modifying ESTs	1.55 1.01	2.45 1.30	
	TABLE 118	В					
25	Pkey:			ntifier number			
	CAT numb Accession:	er: Gene clust Genbank a	er number occession num	bers			
30	Pkey 410399	CAT Number 11995_1	BE068	889 BE068882 AF044311 AF017256 NM_003087 A	F037207 AF010	1126 AA 633976 AA	.872836 BE298825 BE299889 Al016464 Al684600
		_	Al9365 AA410	27 AA804675 AA394097 AH39933 AA946606 BE1 737 H49348 AA486472 AA411094 AA236594 AA40	71313 AA72240 2624 AA443638	7 AA293803 A1468 3 AW452137 AA42	1480 AA056035 AA055968 AW796957 Al637713 1708 AW265211 Al493266 AA365132 AW969044
	419502	18535_1	AU076	704 T74854 T74860 T72098 T73265 T73873 T6918 7 T68401 T53959 T72360 T72099 T60377 T58961 `	0 T74658 T587	86 T60385 T73410 T64738 T74645 T7	T68781 T67845 T67593 T73952 T67864 T60630
35			T68229	T74673 T71800 T68355 T61227 T62738 T69317	F53850 T64692	T73768 T73962 T7	73382 T68914 T70975 T73400 T60631 T73277 22 T67736 T68716 T67755 T74765 T73819 T58719
			T74756	5 T60477 T74863 T61109 T68329 T58850 T71857 T 5 T73787 T56036 T64425 T71870 T60476 T61376	73425 T53736	T68607 T58898 T6	34309 T72031 T72079 T64305 T71908 T68107
40			H4835	3 T71914 T53939 T64121 AA693996 T72525 T6777 4 AA344542 AW605054 Al207457 T61743 AA0267:	9 T68078 AA01	1465 AA345378 A	V654847 AV654272 AV656001 Al064740 T82897
40			AA312	919 T40156 H66239 AV652989 H38728 R98521 AV	4655200 R9579	0 W03250 W00913	AA344136 AV660126 R97923 AA343596
			AA235	1774 AV651296 N54417 AA812862 AW182929 Al11 252 T27853 T47778 R95746 H70620 AA701463 AV	V827166 R9847	5 C20925 AV65728	87 T71959 T71313 T73920 T73333 T61618 T69293
45			AA344	3 T73931 T72178 T72456 AV645639 AV653476 T7 726 T27854 T74485 T74101 T73868 T71518 T7230	M AA343853 T7	3909 T63070 T720	065 H72149 T73493 T73495 AV645993 R02293
			T72517	5 T64751 AA344441 AA343657 AA345732 AA3443 7 R02292 T60599 T69206 T70452 T74677 R29366	T61277 T74914	T60352 R29675 T	74843 AV545792 AA344408 T69197 T72057
			T6936	3 T69358 T88258 AV650429 T73341 T61702 T7455 7 T72042 T62764 Al064899 AA343060 T67832 T72	18 T 40095 K022 440 T71770 T68	72 T40106 AA3430 1091 T69108 T724	045 AA341908 AA341907 AA342807 AA341964 49 T69 167 T71289 T68251 AV654844 T64375
50			AA345	234 T 67598 AA011414 T 68036 H 48262 AI 207557 T 583 T 60362 H 58121 T 95711 T 72803 T 68055 T 717	68219 W86031	T69081 T64232 R	93196 T62136 AV650539 H67459 T72978
			AA693	592 AJ248502 R29454 T64764 T67001 T73052 T71 7 T73317 T74273 T69420 T68245 T74380 T67862 T	429 T51176 T58	3866 AV655414 HS	90426 AA342489 T73666 T67848 T72512 T53835
55	421582	2041_1	Al9102	75 X00474 X52003 X05030 NM_003225 AA314326 312 AA614409 AA307578 AI925552 AIV950155 AIS	AA308400 AA5	06787 AA314825	A 571948 AA507595 AA814579 AA587613 R83818
33			BE074	140 AA514776 AA588034 BE074051 BE074068 AV	/009769 AW050	1690 AA858276 R5	5389 Al001051 AW050700 AW750216 AA614539
	437866	44433_2	AA156	045 Al307407 AW602303 BE073575 Al202532 AA5 781 AW253839 U52054 AA024963 AA778446 BE07	73977 AW44490	4 AW602574 BE16	64040 BE164012 BE163972 BE163974 BE163992
60			AA812	481 AW468444 BE185091 AW468002 AA687333 A 489 AW874142 AI471883 W84421 AA156850			
	451807	8865_1	W5285 AW450	4 AL117600 BE208116 BE206432 BE206239 BE06 652 AW449519 AA993634 AI806539 AA351618 AV	12291 AW95342 V449522 AI8276	3 AA351619 BE18 326 AA904788 AA3	0648 BE140560 W60080 AA865478 N90291 380381 AA886045 AA774409 BE003229 Z41756
65	TABLE 110	c					
	Pkev:		nher correspo	nding to an Eos probetet			
	Ref:	Sequence	source. The I	digit numbers in this column are Genbank Identifier mosome 22." Dunham I. et al., Nature (1999) 4024	r (GI) numbers. 89.495	"Dunham I, et al." i	refers to the publication entitled "The DNA
70	Strand; Nt_position	Indicates D	NA strand fro	m which exons were predicted.			
	Pkey	Ref	Strand	Nt_position			
75	403329 406399	8516120 9256288	Plus Minus	96450-96598 63448-63554			

PCT/US02/12476

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TABLE 12A: Genes Distinguishing Squemous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell cardinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were solected from about 99580 probeseds on the EoslAftymetrix Hu03 Genechip array.

Table 129 show the accession numbers for those Play's lacking UnigeneID's for table 124. For each probered we have listed the gene cluster number from which for oligonaccides were designed. Gene clusters were compiled using sequences defined from Genhark ESTs and nRPMs. Those sequences ware dustried based on sequence many clustered based on sequence many clustered based on sequence and name of the complete sequences were consistent sequences. The complete sequences were consistent sequences are not included to the complete sequences are not included in the 10 "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also foliat.

15												
	Pkey:	Unique 8	Eos probaset is	denlifier number								
	Exacon:	Exempla	ar Accession no	umber, Genbank accession number								
	UnigenelD: Unigene r											
	Unigene Title: Unigene gene tille											
20	R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatious end cercinoid tumors) divided by the											
20	Average of normal lung samples											
	arreage of non-metig carriers R2: Average of non-metig carriers in great in the same process and the same process are samples. (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples.											
	na.	Atologo	or non-margin	on thing around outspice (moderning thousand) ampily	oomoj merome, e							
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2						
25		X07820	Hs.2258	metrix metelloproteinase 10 (stromolysin	132,45	4.00						
2.5	400266	N01020	H8-2200	NM_002425:Homo sepiens matrix metallopro	3.26	3.22						
	401780			NM_005557*:Homo sapiens karain 16 (foca	26.47	10.50						
	401781			Target Exon	10.33	4.61						
	401785			NM_002275*:Homo sapiens keralin 15 (KRT1	4.13	2.70						
30				Target Exon	61.84	47.00						
50	401994			ENSP00000251056*Plasma membrane caldium	1.00	1,00						
	402075				1.00	1.00						
	404996		11- 404500	Target Exon ESTs	173.91	108.00						
		AA045144	Hs.161566		151.17	8.00						
35		L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1.96	1.24						
30		AI541214	Hs.45320	Smell proline-rich protein SPRK [human,	10.04	1.00						
		BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	1.00	30.00						
		AL044872	Hs.77910	3-hydroxy-3-melhylglutaryl-Coenzyme A sy		1.00						
		U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30							
40	416668	U03272	Hs.79432	fibrilin 2 (congenital contractural ara	53.29	51.00						
40		NM_005183	Hs.80952	neurotensin	1.00	1.00						
		BE185289	Hs.1076	small proline-rich protein 1B (comifn)	8.97	3.27						
		AK001100	Hs.41690	desmocoffin 3	112.17	19.00						
		NM_001327	Hs.87225	cencer/lestis antigen	1.18	1.10						
4.5		AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00						
45		A1659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25						
		W69233	Hs.112457	ESTs	1.12	1.14						
		L42583	Hs.334309	keratin 6A	51.83	20.25						
	421978	AJ243662	Hs.110195	NICE-1 protein	1.01	0.91						
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10						
50		NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32,00						
		AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00						
		AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00						
		AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00						
		AW368377	Hs.137569	turnor protein 63 kDs with strong homolog	233,42	68,00						
55		AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00						
		AF077374	Hs.139322	small proline-rich protein 3	137,82	54.00						
		AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56,19	12.00						
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris anligen	33.45	1.00						
	427099	AB032953	Hs.173550	odd Oz/ten-m homolog 2 (Drosophila, mous	4,24	17.00						
60	427335	AA448542	Hs.251677	G antigen 7B	51.83	4,00						
	428182	BE385042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00						
	428845	AA431400	Hs.98729	ESTs, Weakly similar to 2017/205A dihydro	1.00	16,00						
	428748	AW593205	Hs,98785	Ksp37 protein	1,00	87.00						
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18						
65		BE182592	Hs.11261	small profine-rich protein 2A	4,43	2.90						
		AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00						
		BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00						
		X54232	Hs.2699	alvoican 1	1,58	1.40						
		BE149762	Hs.48966	gap function protein, beta 6 (connexin 3	60.25	28.00						
70		BE019924	Hs.271580	uroptakin 1B	4,49	2.51						
		Y12642	Hs,3185	lymphocyte antigen 6 complex, locus D	1.20	1.09						
		AW015415	Hs.127780	ESTs	40.98	27.00						
		U02388	Hs.101	cylochrome P450, subfamily IVF, polypept	1.00	1.00						
		AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00						
75		AB037734	Hs.4993	KIAA1313 protein	23.58	42.00						
80		AA721252	Hs.291502	EST\$	16.76	14.00						
		AA806607	Hs.292206	ESTs	1.00	1,00						
	439285	AL133916	110.252200	hypothetical prolein FLJ20093	46.23	139.00						
	439280	W79123	Hs,58561	G protein-coupled receptor 87	33.61	1.00						
		AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00						
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00						
		NM_003612	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00						
		AW241867	Hs.127728	ESTs	1.53	1.42						
	443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00						
85		R41339	Hs,12569	ESTs	1.00	1.00						
05	*****	rve 1038	110, 12000	LOIV	1.00							

		02/086		W. 0.1	1.55	1.26	PCT/US02/12476				
5	447078 447342 44903 449101 450832 452240	AF081497 AW885727 AI199268 X76342 AA205847 AW970602 AI591147 NM 002277	Hs.279682 Hs.9914 Hs.19322 Hs.389 Hs.23016 Hs.105421 Hs.61232 Hs.41696	Rh type C glycoprolein EST Homo sepieres, Similar to RIKEN cDNA 2010 alcohol dehydrogenese 7 (class IV), rau o G protein-coupled receptor ESTs ESTs ESTs keratin, hais, actidic, 1	1,56 47,24 28,63 1,00 2,58 25,17 13,42 1,19	1.29 24.00 1.00 1.00 27.00 36.00 1.00					
10	453830 454098	AA534296 W27953 AI368680	Hs.20963 Hs.292911 Hs.816	ESTs	24.92 1.26 206.11	25.00 1,11 1,00					
	TABLE 12B										
15	Pkgy: Unique Eos probasel idonifior namber CAT number Gene clusier number Anosasion: Genetik accussion numbers										
20		CAT Number Accession AL 1986 to 1791 13 AFGB510 N/GF21 ANGERES AASH013 A W059584 ADSB31 H S67245 NS4784 A5555270 A421279 AW014882 A37155023 NS2521 NS5253 AASZ6543 A354407 BE175639 AAS5965 A3558918 AA457017									
2.5	TABLE 12C										
25	Pkgr. Unique number corresponding to an Eos probeset. Ref: Sequence source. The 7 digit numbers in this column are Gambank klentifier (GI) numbers. "Durshem L. et al." refless to the publication entitled "The DNA sequence for Junan characterizer 22. Turshem et al., Mature (1959) 402-469-455.										
30	Strand: NLposition:	Indicates DNA strand from which exons were predicted.									
35	Page										
40	404996	6007890	Plus	3/999-30140,30002-30990,39/27-390/2,4000/	00/4,4230144240						

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TABLE 13A: Genes Distinguishing Non-Melignant Lung Disease from Lung Tumors and Normal lung

- Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59690 probesets on the Eos/Attymetrix Hu03 Genechip array. 5
- Table 138 abow the accession numbers for those Pkey's lacking UnigeneiO's for table 134. For each probests we have listed the gene cluster number from which the objourniceOise were designed. Given clusters were compiled using sequences derived from Centeral EST's and mRNMs. These seconds were clustered based on sequence similarly using Custaring and Adjament Foot Chedel-levial, Calded Celifornia, The General excellent accession manness for sequences comprising each Custaring as feed in the "Accession" column. 10
- Table 13C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15	Pkey: ExAcon:	Unique Ece probeset identifier number Exemplar Accession number, Genbank accession number

Unigene number Unigene gene fille

Average of lung lumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the

20 average of normal lung samples
Average of normal lung disease samples (including bronchitis, emphysema, fibrosis, alchoctasis, asthma) divided by the average of normal lung samples R2:

	Pkey	ExApon	UnigenelD	Unigene TWe	R1	HZ.
	408562	A1436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein.	1.00	230.00
25	409031	AA376836	Hs.76728	ESTs	1.00	128.00
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
30	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
	424585	AA464840	Hs.131987	ESTs	1.00	167.00
	426753	T89832	Hs.170278	ESTs	1.00	141.00
	429496	AA4538C0	Hs.192793	ESTs	1.00	138.00
	430719	AA488968	Hs.293796	ESTs	1.00	133.00
35	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
	431728	NM 007351	Hs.268107	multimenin	1.00	157.00
	436532	AA721522		gbow54h12.r1 NCL_CGAP_Ew1 Homo sapiens	1.00	218.00
	437960	A1669586	Hs.222194	ESTs .	1.00	147.00
40	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs-7117	clutamate receptor, lonotropic, AMPA 1	1.00	151.00
	448253	H25899	Hs 201591	ESTs	1.00	141.00
	453636	R67837	Hs.169872	ESTs	1.00	116.00
45	458332	A1000341	Hs.220491	ESTs	1.00	192.00
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00

TABLE 13B

50 Pkey: Unique Eos probeset identifier CAT number: Gene cluster number Accession: Genbenk accession numbers Unique Eos probeset identifier number

CAT Number Accession 327825_1 BE041395 AA491826 AA621946 AA715960 AA696102 421802_1 AA721522 AW975443 T93070 55 436532

TABLE 13C 60

Pkey: Unique number corresponding to an Eos probesel

Sequence source. The 7 digit numbers in this column are Genbank Identifier (0) numbers. "Dunharm L et al." refers to the publication smilled "The DNA sequence of human chromosom 22." Dunharm L et al., Notare (1999) 402-489-455.
Indicates DNA straff from which sows even predicted. Ref:

Strand NL position: Indicates nucleotide positions of predicted exons. 65

Pkey Strand

121907-122035.122804-122921.124019-124161.124455-124610.125672-126076 402075 8117407 Plus 70

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TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

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Table 14A shows the subclubial localization and proternol utility for the genne appearing in Tables 9A and 10A. m/No symbolizes monoclonal antibody, diag symbolizes of alignostic, an symbolizes small molecular, and CTL symbolizes of closic hymphosytic figural. These genes were solected from 59600 probesets on the Ecs1A65/metrix Hu03 5 Genneby are

Table 18, then the accession number for these Play is builty Lidgeost?s for table 14.5. For each probased are been field the goes desire number from which the appropriate properties of the pro

Table 14C show the genomic positioning for those Pixey's tacking Unigene ID's and accession numbers in table 14A. For each predicted exert, we have fished the genomic sequence source used for prediction, Nucleotide locations of each gredicted exen are also fisted.

15

Pksy: Unique Eos probeset identifer number
ExAcor: Examplar Accession number, Genbank accession number
Uniques number

20 Unigene Title: Unigene gene title
Pref.Utility: Proferred Utility
Pred.Loc: Predicted suborblular localization

	Heurico	Previousu	SUUCHILIA IOCAI	ZBJOII		
	Pkey	ExAcon	UnigenelD	Unigena Title	Pref Utility	Prod. Loc
	400289	X07820	Hs.2258	matrix metalloproleinase 10 (stromelysin	mAb & diag & s.m.	extracellular
25	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
	402075			ENSP00000251056*:Plasma membrana calcium	mAb & diag	secreted
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	dlag	secreted
	408243	Y00787	Hs.624	Interleukin 8	diag	secreted
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
30	408908	BE295227	Hs.250622	serine/threonina kinase 15	s.m.	cylociasm
-	409041	AB033025	Hs.50061	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
	409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
	409420	Z15008	Hs.54451	taminin, gamma 2 (nicein (100kD), kalini	diag	secreted
	409632	W74001	Hs.55279	sarine (or cysteina) proteinase inhibito	diag	secreted
35	409757	NM 001898	Hs.123114	cystatin SN	diag	extracellular
	409693	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nudear
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	diag	axtracellular
	410001	AB041036	Hs.57771	kalikrein 11	diag	extracelular
	410407	X66839	Hs.63287	carbonic anhydrase tX	mAb & s.m.	plasma membrane
40	410418	D31382	Hs.63325	Iransmembrane professe, serine 4	mAb & diag & s.m.	plasma membrana
-10	412140	AA219891	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	promo memo er o
	412719	AW016610	Hs.816	ESTs	s.m.	nudear
	414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracallular
	414883	AA928980	110.77274	CDC28 protein kinasa 1	s.m.	evir diversion
45	415138	C18356	Hs.295944	lissue factor pathway inhibitor 2	CTL & diag	extracellular
73	415669	NM .005025	Hs.78589	serina (or cysteine) proteinase inhibito	mAb & diag & s.m.	accreted
	415817	U88987	Hs,78867	projein tyrosing phosphalase, receptor-l	mAb & s.m.	plasma membrane
	416658	U03272	Hs.79432	fibrilin 2 (conganital contractural ara	diag	extracellular
	417034	NM .006183	Hs.80962	neurolensin	diac	extracellular
50	417079	U65590	Hs,81134	Intertaukin 1 receptor antagonist	diac	extracellular
50				KIAA0101 gane product	s.m.	mitochondriai
	417308 417389	H60720	Hs.81892	midkine (neurile growth-promoting factor	mAb & diag	secreted
	417433	BE260964 BE270266	Hs.82045 Hs.82128	5T4 oncofetal trophoblast alycografia	mAb	plasma membrane
				thymidylate synthetasa	s.m.	endoplasmic reficulur
55	417933 418478	X02308 U38945	Hs.82962 Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cyloplasm
22	418506		Hs.85339		mAb & s.m.	plasma mambrane
		AA084248		G protein-coupled receptor 39	CTL	cyloplasmic
	418678	NM_001327	Hs.167379	cancar/lestis antigan (NY-ESO-1)	diac	secretad
	419121	AA374372	Hs.89626	parallyroid hormone-like hormone	mAb & s.m.	olasma mambrana
60	419171 419183	NM_002846	Hs.89655	protein tyrosine phosphalase, receptor t	CTL & s.m.	mitochondrial
UU		U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin		secreted
	419216	AU076718	Hs.164021	small inducible cylokine subfamily B (Cy	diag	nlasma membrane
	419235	AW470411	Hs.288433	neurotrimin	mAb & diag	plasma membrana
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	extracellular*
65	419556	U29615	Hs.91093	chitinasa 1 (chitotriosidase)	mAb & diag	
0.5	420610	Al583183	Hs.99348	distal-less homeo box 5	CTL	nuclear extracellular
	421110	AJ250717	Hs.1355	calhepsin E	sm & diag	secreted
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	oliag mAh&s.m.	plasma membrane
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans		presma memorane secroled
70	421552	AF026692	Hs.105700	secrated frizzled-related protein 4	offag mAh & s.m.	plasma membrane
70	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/		plasma membrane plasma membrane
	421817	AF146074	Hs.108650	ATP-binding cassalte, sub-family C (CFTR	mAb & s.m. diao	secreted
	422109	S73265	Hs.1473	gasinn-releasing peptide		secreted
	422158	L10343	Hs.112341	protesse inhibitor 3, skin-derived (SKAL	diag	secreted
75	422282	AF019225	Hs.114309	apolipoprolein L	diag	
13	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.ocrevis	s.m.	nuclear
	422424	Al185431	Hs.296638	prostate differentiation factor	diag	extracellular
	422765	AW409701	Hs.1578	baculoviral IAP repeal-containing 5 (sur	s.m.	cytoplasm
	422609	AK001379	Hs.121026	hypothalical protein FLJ 10549	s.m.	nuclear
0.0	422867	L32137	Hs.1584	cartfage oligomeric matrix protein (pse	diag	extraoslular
80	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transform)	CTL & s.m.	
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
	423961	D13666	Hs.136348	periostin (OSF-20s)	mAb & diag	extracefular
85	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	diag	secreted
83	424381	AA285249	Hs.146329	protein kinase Clrk2	s.m.	nuclear

	W	O 02/086	443			
	424502	AF242388	Hs.149585	lengsin	s.m.	cytopiasmic
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687 425247	J05070 NM 005940	Hs.151738 Hs.155324	matrix metalloproteinase 9 (gelatinase B matrix metalloproteinase 11 (stromeivsin	diag mAb & diag & s.m.	extracellular secreted
5	4253247	NM_005940 U63630	Hs. 155637	prolein kinase, DNA-activated, catalytic	S.M.	cytoplasmic
,	425650	NM_001944	Hs. 1925	dosmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.159396	pepfidylighycine alpha-amidaling monooxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
10	425852 426215	AK001504 AW963419	Hs.159651 Hs.155223	death receptor 6, TNF superfamily member stenniocatcin 2	mAb & s.m. mAb & dian	plasma membrane secreted
10	426427	W86668	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251677	G antigen 7B	CTL	cytoplasmic
15	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m. diag	cytoplasmic
15	428242 428330	H55709 L22524	Hs.2250 Hs.2256	leukemia inhibitory factor (cholinergic matrix metallooroteinase 7 (matritysin.	mAb & diag & s.m.	extracellular
	428450	NM 014791	Hs.184339	KIAA0175 gene product	S.M.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic arrino	mAb & s.m.	plasma membrane
20	428664	AK001666	Hs.189095	similar lo SALL1 (sel (Drosophila)-like	CTL & s.m. mAb	nuclear
	428698 428748	AA852773 AW593206	Hs.334838 Hs.98785	KIAA1866 prolein Ksp37 prolein	dag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	dag	milochodria*
	428969	AF120274	Hs.194689	artemin	ɗag	extracellular
25	429211	AF052693	Hs.198249	gap Junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263 429547	AA019004 AW009166	Hs.198396 Hs.99376	ATP-binding cassette, sub-family A (ABC1 ESTs	mAb&s.m. diaq	plasma membrane secreted
	429610	AW009100 AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
30	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extraceltular plasma membrane
	431515 431848	NM_012152 BE019924	Hs.258583 Hs.271580	endothelial differentiation, lysophospha uroplakin 1B	mAb & s.m. mAb & diag	plasma membrane
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
35	432201	AJ538613	Hs.298241	Transmembrane protesse, serine 3	mAb & dlag & s.m.	plasma membrane
	433001	AF217513	Hs-279905	clone HQ0310 PR00310p1	s.m.	nuclear
	435505 436481	AF200492	Hs.211238	interleukin-1 homolog 1	diag s.m.	secreted
	437016	AA379597 AU076918	Hs.5199 Hs.5398	HSPC150 protein similar to ubiquitin-con quanine monphosphate synthetase	s.m.	cyloplasm
40	437044	AL035864	Hs.69617	differentially expressed in Fanconi's an	CTL	ER
	437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001838	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	mAb & s.m.	plasma membrane
	439223 439477	AW238299 W89813	Hs.250618 Hs.58042	UL16 binding protein 2 ESTs, Moderalely similar to GFR3_HUMAN G	mAb mAb & s.m.	plasma membrane
45	439606	W79123	Hs.58561	G prolein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (ig),	mAb & s.m.	plasma membrane
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (É coli Re	s.m. mAb & s.m.	plasma membrane
50	442117 443247	AW664964 BE614387	Hs.128899 Hs.333893	ESTs; hypothetical protein for IMAGE:447 c-Myc larget JPO1	CTL	extreodiular*
50	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
	443859	NM_013409	Hs.9914	folislain	diag	extrecellular
	444006	BE395085	Hs.10066	type I transmembrane protein Fn14	mAb s.m.	plesma membrane nuclear
55	444371 444381	BE540274 BE387335	Hs.239 Hs.283713	forkhead box M1 ESTs, Weakly similar to S64054 hypotheli	dag	secreted
55	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted extracollular
60	446921 447033	AB012113 Al357412	Hs.18530 Hs.157601	small inducible cytokine subfamily A (Oy FSTs	diag CTL & diag	secreted
00	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	boatowe
	448243	AW369771	Hs.52620	Integrin, bela 8	mAb&s.m	plasma membrane
	448844	Al581519	Hs.177164	ESTs	mAb & s.m.	
65	449048	Z45051	Hs.22920	similar to \$68401 (cattle) glucese induc	mAb	plasma membrano cytopiasm
03	449722 450001	BE280074 NM_001044	Hs.23960 Hs.406	cyclin B1 solute carrier family 6 (neurotransmitte	s.m. mAb & s.m.	plasma membrane
	450375	AA009647	110.400	a disinjegrin and metalloproleinase doma	mAb & diag & s.m.	plasma membrane
	450701	H39960	Hs.288467	hypolhetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
70	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
70	451668 452281	Z43948 T93500	Hs.326444 Hs.28792	cartflage acidic protein 1 Homo saplens cDNA FLJ11041 fis, clone PL	mAb & diag diag	plasma membrane
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	dag	extracellular
	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	mAb	plasma membrane
76	452638	U65011	Hs.30743	preferentially expressed antigen in mela	CTL	nuclear
75	453968 457489	AA847843 AI693815	Hs.62711 Hs.127179	High mobility group (nonhistone chromoso cryptic gene	CTL & s.m. diag	nuclear secreted
	401409	nives010	110-12/119	cijhte Acio	ung	3011000
	TABLE 1	4B				

TABLE 14B

80 Pikey: Unique Eos probeset identifier number CAT number: Gene duster number Accession: Genbank accession numbers

Pkey CAT Number Accession

	wo	02/08644	3	PCT/US02/12476								
	414883	15024_1	AA08243	O AA928959 W76521 W24270 W21525 AA037172 BE267636 H83186 AA469900 N86396 AA001348 DE535736 AA01745 BE566745 6 H72525 H77575 N4976 W60056 H78746 BE56908 W04339 R6912 T75283 BE279277 AW050034 T2881 2 AA4776573 EE297387 3 A4777048 MM 001826 X54941 BE344966 AA926783 A/1719075 BE270172 BE268919 AA889955 A204630 W25243 N363150								
5			AA87203 R75953 A AW61300 N95210 A	3 AT / 1/10/9 RIL UPI (80.5 PER) HEAVINGO AND AND AN IT YELD SEZENTI / ZE ZESHIS PARABOSE AND								
10			AI139549 AI494230 AI494211 AA95434	V VAMADO IN SINSINS ANSINS AND								
15	450375	83327_1	W95095 I AA00964	PRIFYER AND AND ZET TYPES I AME 1982 HEEDER INSUST AND ZESTEY TO ASSISTED AND ZET TYPES I AME 1982 HEEDER INSUST AND ZESTEY 3 HIS 2231 HIS SEGES HOTI 642 AMES ZET RANTI 3758 AMES ZESTEY AND 158 EE ESTAFF EE 15780 I HOUSAU WAS ZET ANNES SET A HOUZT HO I 532 3 HIS 2231 HIS SEGES HOTI 642 AMES ZET RANTI 3758 AMES ZESTEY AND ZESTEY								
20	TABLE 14C											
20	Pkey: Ref:	Sequence sou	que number corresponding to an Eos probeset que nos source. The 7 digit numbers in this oclumn are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entified "The DNA									
25	Strand: Nt_position:	Indicates DNA	juence of human chromosome 22" Dunham I to al., Nature (1999) 402-489-495. ioasso DNA strand from which exons were proficted. ioasso musecide positions of proficted drones.									
	Pkey	Ref	Strand	NL position								
30	402075	8117407	Plus	121907-122005,122804-122921,124019-124161,124455-124610,125672-120076								

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TABLE 15A: Information for all sequences in Table 16

PCT/US02/12476

Table 15A shows the Seq ID No, Pkey, ExAcon, UnigeneID, and Unigene Title for all of the sequences in Table 16.

- Table 198 show the accession numbers for those Pkey's lacking UrigenedID's for table 194. For each probased we have 194d the gare cluster number from which the oligonactionides were designed. Gene clusters were complete using sequence defined from Genthal CE17s and mRIVAs. These sequences were obtained no expectors. The contracting value of sequences are relatively using Collections and Adjustment Central Counter for the Central Centr "Accession" column.
- Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exent, we have itsied the genomic sequence source used for prediction. Nucleatile locations of each predicted exent are also listed. 10

		ID number			
15	Pkey: Unique Ed	s probeset i	dentifer number		
	ExAcon: Exemplar	Accession n	umber, Genbank	accession number	
	UnigenelD: Unigene n	umber			
	Unigene Title: Unigene g	ene title			
20	A 17 M	Diver	Fuhren	Helessel	Unigene Title
20	Seq ID No:	Pkey	ExAgen	UnigeneID	Ungere tite
	Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
	Sea ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
	Sea ID No; 5 & 6	417034	NM_006183	Hs.80962	neurolensin
25	Seg ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 9 & 10	407788	EE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 11 & 12	407788	EE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No. 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
20	Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
30	Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
	Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, bela 3 (nicein (125kD), kalinin
	Seq ID No: 21 & 22	120486	AW368377	Hs.137569 Hs.1925	turnor protein 63 kD a with strong homolog
	Seq ID No: 23 & 24	425650	NM_001944	Hs.1920 Hs.73625	desmoglein 3 (pemphigus vulgaris antigen RABS Interacting, kinesin-like (rabkines
35	Seq ID No: 25 & 26	412140 423673	AA219691 BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
33	Seq ID No: 27 & 28	452838	U65011	Hs.30743	preferentially expressed antigen in mela
	Seq ID No: 29 & 30 Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
	Seg ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito
40	Soa ID No: 37 & 38	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
10	Sea ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Sea ID No: 41 & 42	431846	BE019924	Hs.271580	uroclakin 1B
	Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
	Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
45	Seq ID No: 47 & 48	443648	AI085377	Hs. 143610	ESTs
	Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD_HUMAN NKG2
	Seq ID No: 50 & 51	408522	Al541214	Hs.46320	Small proline-rich protein SPRK [human,
	Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
50	Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
30	Seq ID No: 58 & 57	417386	BE185289	Hs.1076 Hs.2877	smell proline-rich protein 1B (comitin) cadherin 3, lyge 1, P-cadherin (clacenta
	Seq ID No: 58 & 59	431958 441020	X63629 W79283	Hs.35962	ESTs
	Seq ID No: 60 & 61	423217	NM 000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
	Seq ID No: 82 & 83 Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small profine-rich protein 2A
55	Seq iD No: 66 & 67	448733	NM_005629	Hs. 187958	solute carrier family 6 (neurotransmitte
55	Seg ID No: 88 & 89	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
	Seg ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 74 & 75	422188	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
60	Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psonas
	Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Ptakophilin
	Seq iD No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
	Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
65	Seq iD No: 84 & 85	423662	AK001035	Hs.130881 Hs.184601	B-cell CLL/lymphoma 11A (zinc finger pro solute carrier family 7 (cationic amino
03	Seq ID No: 86 & 87	428484	AF104032 AF052693	Hs.198249	oap junction protein, beta 5 (connexin 3
	Seq ID No: 88 & 89 Seg ID No: 90 & 91	429211 417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seg ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
	Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
70	Seg ID No. 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
, 0	Seg ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
	Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
	Seg ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
75	Seq ID No: 106 8 107	417542	J04129	Hs.82269	progestagen-associated endometrial prote
	Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratifin
	Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
	Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
00	Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
80	Seq ID No: 116	447343	AA256641	Hs.236894 Hs.5398	ESTs, Highly similar to S02392 alpha-2-m
	Seq ID No: 117 & 118	437016	AU076916 BE613348	Hs.211579	guanine monphosphale synthetase melanoma cell adhesion molecule
	Seq ID No: 119 & 120	449230 446989	BE613348 AK001898	Hs.211579 Hs.16740	hypothetical protein FLJ11036
	Seq ID No: 121 & 122 Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
85	Seq ID No: 125 & 126	424687	J05070	Hs. 15 1738	matrix metalloproteinase 9 (gelatinase B
05	Guy ID MU. 120 & 120	424001	20000		

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	WO 02/086				
	Seq ID No: 127 & 128	414430	AJ346201	Hs.76118	ubiquitn carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462 100668	BE001596 L05424	Hs.85296 Hs.169610	integrin, beta 4 CD44 antigen (homing function and Indian
	Seq ID No: 131 & 132 Seq ID No: 133 & 134	458933	AJ638429	Hs.24763	RAN binding protein 1
5	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 141 & 142 Sea ID No: 143 & 144	418478 446269	U38945 AW263155	Hs.1174 Hs.14559	cyclin-dependent kinase inhibitor 2A (me hypothetical protein FLJ10540
10	Seq ID No: 145 & 146	422766	AW409701	Hs.1578	begulovirat IAP repeat-containing 5 (sur
	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
	Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disinlegnin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561 Hs.36232	G protein-coupled receptor 87 KIAA0186 gene product
15	Seq ID No: 153 & 154 Seq ID No: 155 & 156	453884 453884	AA355925 AA355925	Hs.36232 Hs.36232	KIAA0186 gene product
13	Seg ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
20	Seq ID No: 163 & 164	413129 413281	AF292100 AA861271	Hs.104613 Hs.222024	RP42 homolog transcription factor BMAL2
20	Seq ID No: 165 & 166 Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Sea ID No: 169 & 170	416819	U77735	Hs.80205	pim-2 oncogene
	Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
25	Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
23	Seq ID No: 175 & 176 Seq ID No: 177 & 178	454034 425397	NM_000691 J04088	Hs.575 Hs.156346	aldehyde dehydrogen ase 3 family, member topolsomerase (DNA) II alpha (170kD)
	Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein lyrosine phosphalase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
-	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
30	Seq ID No: 185 & 186	415817	U88967	Hs.78867 Hs.78867	protein tyrosine phosphalase, receptor-t
	Seq ID No: 187 & 188 Seq ID No: 189 & 190	415817 419121	U88967 AA374372	Hs.89626	protein lyrosine phosphatase, receptor-t parathyroid hormone-like hormone
	Seg ID No: 191 & 192	448993	AH71630	Hs.8127	KIAA0144 gene product
	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
35	Seq 1D No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
	Seq ID No: 197 & 198	425057 420462	AA826434 AF050147	Hs.1619 Hs.97932	achaele-scute complex (Diosophile) homol chondromodulin t precursor
	Seq ID No: 199 & 200 Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
	Seq ID No: 203 & 204	100578	X00366	Hs.37058	calcitonin/calcitonin-related polypeptid
40	Sen ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	Seq ID No: 207 & 208	429038	AL023513	Hs.194766 Hs.167379	seizure related gene 6 (mouse)-like canceritestis antigen (NY-ESO-1)
	Seq ID No: 209 & 210 Seq ID No: 211 & 212	418678 418678	NM_001327 NM_001327	Hs.167379 Hs.167379	cancerlesis anigen (NY-ESO-1)
	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecodor: lissencenhaly, X-linked (d.
45	Seq ID No: 215 & 218	428182	BE386042	Hs 293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
	Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G anligen 78
	Seq ID No: 219 & 220 Seq ID No: 221 & 222	409420 114348	. Z15008 AL137256	Hs.54451 Hs.130489	laminin, gemma 2 (nicein (100kD), kalini ATPase, aminophospholipid trensporter-li
	Seq ID No: 223 8 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9
50	Sea ID No: 225 & 226	404440			NM_021048:Homo sapiens melanome entigen,
	Seg ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito
	Seq ID No: 229 & 230	103312 320843	Y12642 BE089288	Hs.3185 Hs.34744	lysosomal Homo sapiens mRNA; cDNA DKFZp547C136 (fr
	Seq ID No: 231 & 232 Seq ID No: 233	429065	Al753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
55	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	FSTs
	Seq ID No: 233 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
	Seq ID No: 238	413573	Al733859	Hs.149089 Hs.334562	ESTs celt division cycle 2, G1 to S and G2 to
	Seq ID No: 239 & 240 Seq ID No: 241 & 242	428479 428479	Y00272 Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
	Sea ID No: 245	437915	Al637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teretoce
	Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
	Seq ID No: 248 & 249 Seq ID No: 250 & 251	331692 429413	A1683487 NM 014068	Hs.152213 Hs.201877	wingless-type MMTV integration site fami DESC1 protein
65	Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
•••	Sea ID No: 254 & 255	448357	N20169	Hs,108923	RAB38, member RAS oncogene family
	Sea ID No: 256 8 257	446292	AF081497	Hs.279682	Rh type C glycoprotein
	Seq ID No: 258 & 259	416209	AA235776 AE053306	Hs.79078 Hs.36708	MAD2 (milotic arrest deficient, yeast, h budding uninhibited by benzimidazoles 1
70	Seq ID No: 260 & 261 Seq ID No: 262 & 263	453922 424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito
70	Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
	Sea ID No: 266 & 267	429228	Al553633	Hs.326447	ESTs
	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cyclelin SN
75	Seq ID No: 270 & 271 Seq ID No: 272 & 273	411089 436511	AA456454 AA721252	Hs.214291 Hs.291502	cell division cycle 2-like 1 (PITSLRE pr ESTs
15	Seq ID No: 274 & 275	428969	AF120274	Hs. 194689	artemin
	Seg ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seg ID No: 278 & 279	428969	AF120274	Hs 194689	artemin
80	Seq ID No: 280 & 281	428969 407137	AF120274 T97307	Hs.194689	artomin gb:ye53h05.s1 Soares felal liver spicen
50	Seq ID No: 282 Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seg ID No: 285 & 286	450701	H39980	Hs.288467	hypothetical protein XP_098151 (leucine-
	Sea ID No: 287 & 288	405770			NM_002362:Horno sapiens melanoma antigen,
85	Seq ID No: 289 & 290	439453	BE264974	Hs.6566 Hs.77274	thyroid hormone receptor interactor 13 plasminogen activator, prokingse
63	Seq ID No: 291 & 292	414774	X02419	HB.//2/4	presentingen activator, urokirese

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	WO 02/086	112			
	Seq ID No: 293 & 294	424629	M90656	Hs.151393	giulamate-cysteine ligase, catalytic sub
	Sea ID No: 295 & 295	437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 297 & 298	437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheli
5	Seq ID No: 299 & 300	437789 437789	Al581344 Al581344	Hs.127812 Hs.127812	ESTs, Weakly similar to T17330 hypotheli ESTs, Weakly similar to T17330 hypotheli
,	Seq ID No: 301 & 302 Seq ID No: 303 & 304	437789	AI581344 AI581344	Hs. 127812	ESTs, Weakly similar to T17330 hypotheti
	Sea ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromogo
	Seq ID No: 307 & 308	403478		Hs.127728	NM_022342:Homo sapiens kinesin protein 9
10	Seq ID No: 309 Seq ID No: 310 & 311	434105	AW241867 AW952124	Hs.127728 Hs.13094	ESTs presentins associated rhombold-like pro
10	Seg ID No: 312 & 313	428810	AF068236	Hs.193788	nitric code synthase 2A finducible, hen
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317 Seq ID No: 318 & 319	423934 409228	U89996 R16811	Hs.159234 Hs.22010	forkheed box E1 (thyroid transcription f ESTs, Weakly similar to 2109260A B celt
15	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	paptidylglycine alpha-amidaling monoxyg
	Seg ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
	Seq ID No: 326 & 327 Seq ID No: 328 & 329	403329 409693	AW247090	Hs.57101	unnamed protein product (Homo sapiens) minichromosome maintenance deficient (S.
20	Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets ervityoblastosis virus E26 onconen
	Sea ID No: 332 & 333	113196	H83265	Hs.8881	ESTs, Wealdy similar to S41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552 NM 005795	Hs.83381 Hs.152175	guanine nucleotide binding protein 11 calcitonin receptor-tike
	Seq ID No: 336 & 337 Seq ID No: 338 & 339	101345 103280	NM_005795 U84722	Hs.76206	cachorin 5, type 2, VE-cacherin (vascula
25	Seg ID No: 340 & 341	102012	BE 259035	Hs.118400	singed (Drosophila) like (sea urchin fas
	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Home sapiers HSPC285 mRNA, partial eds
	Seq ID No: 344 & 345 Seq ID No: 346 & 347	134299 412719	AW580939 AW016610	Hs.97199 Hs.816	complement component C1q receptor ESTs
	Seq ID No: 348 & 349	422158	L10343	Hs.112341	nrotogeg Inhibitor 3 skin derived (SKA)
30	Sea ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
	Seq ID No: 352 & 353	100486	T19005	Hs.10842	RAN, member RAS cricogene family
	Seq ID No: 354 & 355 Seq ID No: 356 & 357	419121 409459	AA374372 D86407	Hs.89626 Hs.54481	perathyroid hormone-like hormone low density lipoprotein receptor-retated
	Seq ID No: 358 & 359	330493	M27826	1021101	endogenous retroviral professe
35	Seq ID No: 360 & 361	417866	AW057903	Hs.82772	collagen, type XI, alpha 1
	Seq ID No: 362 & 363 Seq ID No: 364 & 365	418113 437016	AJ272141 AU076916	Hs.83484 Hs.5398	SRY (sex determining region Y)-box 4 guarante monphosphate synthetase
	Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary turnor-transforming 1
	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
40	Seq ID No: 370 & 371	431221	AA449015 AF161470	Hs.286145 Hs.260622	SRB7 (suppressor of RNA polymerase B, ye butyrate-induced transcript 1
	Seq ID No: 372 & 373 Seq ID No: 374 & 375	431565 431565	AF161470 AF161470	Hs.260622	butyrate-induced transcript 1 butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich projein 1B (cornifin)
45	Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
45	Seq ID No: 380 & 381	103788 417512	AF086009 X76534	Hs.296398 Hs.82226	gb:Homo sapiens full length insert cDNA glycoprotein (transmembrane) nmb
	Seq ID No: 382 & 383 Seq ID No: 384 & 385	425266	300077	Hs.155421	alpha-fetoprotein
	Sea ID No: 386 & 387	424503	NM_002205	Hs.149609	Inlegrin, alpha 5 (fibronectin receptor,
50	Seq ID No: 388 & 389	400289 418007	X07820 M13509	Hs.2258 Hs.83169	matrix metalloproteinase 10 (strometysln matrix metalloproteinase 1 (interstitial
30	Seq ID No: 390 & 391 Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalicoroteinase 1 (interstital
	Seg ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic emino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathwey inhibitor 2
55	Seq ID No: 398 & 399 Seq ID No: 400 & 401	418506 423961	AA084248 D13666	Hs.85339 Hs.136348	G protein-coupled receptor 39
33	Seq ID No: 402 & 403	414812	X72755	Hs.77367	periostin (OSF-20s) monokine induced by gamma interferon
	Seg ID No: 404 & 405	417433	BE270266	Hs.82128	514 Oncoteial trophoblast glycoptolein .
	Seq ID No: 406 & 407	417433 422867	BE270266 132137	Hs.82128 Hs.1584	5T4 oncofetal trophoblast glycoprotein cartilege oligomeric metrix protein (pse
60	Seq ID No: 408 & 409 Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similer to S64054 hypotheti
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated Adlican
	Seq ID No: 416 & 417 Seq ID No: 418 & 419	411789 428698	AF245505 AA852773	Hs.72157 Hs.334838	KIAA1866 protein
65	Seg ID No: 420 & 421	450098	W27249	He 8109	hypothetical protein F1.121080
	Seg ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425 Seq ID No: 426 & 427	452747 450375	BE153856 AA009647	Hs.61460	tg superfamily receptor LNIR a disintegrin and metalloproteinase doma
	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stamiocalcin 2
70	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
	Seq ID No: 432 & 433	432201	AI538613	Hs.296241	Transmembrane professe, serine 3
	Seq ID No: 434 & 435 Seq ID No: 436 & 437	427585 442117	D31152 AW664964	Hs.179729 Hs.128899	collegen, type X, alpha 1 (Schmid metaph ESTs; hypothetical protein for IMAGE: 447
	Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
75	Sen ID No: 440 & 441	447033	AJ357412	Hs.157601	ESTs
	Seq ID No: 442 & 443	447033 447033	AJ357412 AJ357412	Hs.157601 Hs.157601	ESTs ESTs
	Seq ID No: 444 & 445 Seq ID No: 446 & 447	115522	AJ357412 BE614387	Hs.333893	c-Myc target JPO1
	Sea ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protesse, serine 4
80	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 452 & 453 Seq ID No: 454 & 455	409041 452461	AB033025 N78223	Hs.50081 Hs.108106	Hypothelical protein, XP_051860 (KIAA119 transcription factor
	Seg ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
0.5	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrilin 2 (congenital contractural ara
85	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon

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	WO 02/08	5443			
	Seg ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Wealthy similer to dJ365012.1 [H.sa
	Seg ID No: 464 & 465	402075	DEGOTOGO		ENSP00000251056*:Plasma membrane calcium
	Sec ID No: 466 & 467	421110	AJ250717	Hs.1355	cathepsin E
5	Seq ID No: 468 & 489	451668 451668	Z43948 Z43948	Hs.326444 Hs.326444	cartilage acidic protein 1 cartilage acidic protein 1
,	Seq ID No: 470 & 471 Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartiage acidic protein 1
	Seg ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
10	Seq ID No: 478 & 479	439738 427747	BE246502 AW411425	Hs.9598 Hs.180655	sema domain, immunoglobulin domain (Ig), serine/threorine kinase 12
10	Seq ID No: 480 & 481 Seq ID No: 482 & 483	420281	A)623693	Hs.323494	Predicted cation effux pump
	Seq ID No: 484 & 485	405932	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		C15000305:gij3806122 gb AAC69198.1 (AF0
	Seq ID No: 485 & 487	405932			C15000305;ql3806122/qb(AAC69198.1) (AFU
15	Seq ID No: 488 & 489	444342 421379	NM_014398 Y15221	Hs.10687 Hs.103982	simitar to lysosome-associated membrane smatl inducible cytokine subfamity B (Cy
13	Seq ID No: 490 & 491 Seq ID No: 492 & 493	421379	U65590	Hs.81134	interleukin 1 receptor antagonist
	Sec ID No: 494 & 495	430890	X54232	Hs.2599	ctypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471 413063	AB020684 AL035737	Hs.11217 Hs.75184	KIAA0677 protein chitinase 3-like 1 (cartilage glycoprote
20	Seq ID No: 500 & 501 Seq ID No: 502 & 503	433800	AL036737 AI034361	Hs.135150	lung type-I cell membrane-associated gly
	Sea ID No: 504 & 505	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced pro
	Seq ID No: 505 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
25	Seg ID No: 508 & 509	450001	NM_001044 X66839	Hs.406 Hs.63287	solute carrier family 6 (neurotransmitte carbonic anhydrase IX
25	Seq ID No: 510 & 511 Seq ID No: 512 & 513	410407	AW341683	HS.03207	gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_005183	Hs.80962	neurolensin
20	Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam Iaminin, beta 3 (nicein (125kD), kalinin
30	Seq ID No: 520 & 521 Seq ID No: 522 & 523	413753 425550	U17750 NM 001944	Hs.75517 Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seg ID No: 524 & 525	423573	BE003064	Hs.1695	metrix metalloproteinase 12 (macrophage
	Seq ID No; 526 & 527	418563	AK001100	Hs.41690	desmocolfin 3
25	Seq ID No: 528 & 529	418563	AK001100	Hs.41690	desmocolin 3 LUNX protein; PLUNC (palate lung and nas
35	Seq ID No: 530 & 531 Seq ID No: 532 & 533	429610 406690	AB024937 M29540	Hs.211092 Hs.220529	carcingembryonic antigen-related cell ad
	Sea ID No: 534 & 535	431846	BE019924	Hs.271580	uroniakin 1R
	Sea ID No: 536 & 537	422158	L10343	Hs.112341	protesse inhibitor 3, skin-derived (SKAL
40	Seq ID No: 538 & 539	431958	X63629 AL035864	Hs.2877 He.69517	cadherin 3, type 1, P-cadherin (plecenta differentially expressed in Fanconi's an
40	Seq ID No: 540 & 541 Seq ID No: 542 & 543	437044 428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connex)n 3
	Seg ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
45	Seq ID No: 548 & 549	431009	BE149762 J04129	Hs.48956 Hs.82269	gep junction protein, beta 6 (connexin 3 progestagen-associated endometrial prote
43	Seq ID No: 550 & 551 Seq ID No: 552 & 553	417542 449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloprote nase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disinlegrin and metallioprote nase dome
50	Seq ID No: 558 & 559	424687 418462	J05070 BE001596	Hs.151738 Hs.85266	matrix metaltoproteinase 9 (getafinase B integrin, beta 4
30	Seq ID No: 560 & 561 Seq ID No: 562 & 563	410402	AA381807	Hs.61762	hypoxia-inducible protein 2 -
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seg ID No: 566 & 567	404877			NM_005365; Homo sepiens melenome antigen,
55	Seq ID No: 568 & 569	444781 418543	NM_014400 NM_005329	Hs.11950 Hs.85962	GPI-enchored metastasis-associated prote hyaluronan synthese 3
33	Seq ID No: 570 & 571 Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t protein tyrosine phosphatase, receptor-t
60	Seq ID No: 578 & 579 Seq ID No: 580 & 581	415817 415817	U88967 U88967	Hs.78867 Hs.78867	protein tyrosine phosphatase, receptor-t protein tyrosine phosphatase, receptor-t
00	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphotase, receptor-t
	Sen ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancertestis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589 Seq ID No: 590 & 591	418678 409420	NM_001327 Z15008	Hs.167379 Hs.54451	cancertostis entigen (NY-ESO-1) taminin, gamme 2 (nicein (100kD), katini
05	Sea ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Sea 1D No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860 Hs.250618	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599 Seq ID No: 600 & 601	439223 409757	AW238299 NM_001898	Hs.250618 Hs.123114	UL16 binding protein 2 cystalin SN
70	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Sea ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 608 & 607	428969 428969	AF120274 AF120274	Hs.194689 Hs.194689	ertemin artemin
75	Seq ID No: 608 & 609 Seq ID No: 610 & 611	428909 450701	H39950	Hs.288467	hypothetical protein XP_098151 (leucine-
15	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Sea ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 616 & 617	407944 407944	R34008 R34008	Hs.239727 Hs.239727	desmocollin 2 desmocollin 2
80	Seq ID No: 618 & 619 Seq ID No: 620 & 621	407944 457489	R34008 A1693815	Hs.239727	agsmoodin 2 cryptic gene
00	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTS
	Seq ID No: 624 & 625	407242	M18728		oh:Human nonsnecific crossreacting antiq
	Seq ID No: 626 & 627	407242 407242	M18728 M18728		gb:Human nonspecific crossreacting antig gb:Human nonspecific crossreacting antig
85	Seq ID No: 628 & 629 Seq ID No: 630 & 631	407242	M18728 BE395085	Hs.10086	type I transmembrane protein Fn14
00	Cod to tee cook good	444000	2200000		44

	wo	02/0864	143			PCT/US02/12476
	Seq ID No:		429597 422109	NM_003816 S73265	Hs.2442 Hs.1473	a disinlegrin and metalloproteinasa dome qashin-releasing poptide
	Seq ID No: 6		419235	S73265 AW470411	Hs.1473 Hs.288433	gasonn-reveasing popoue
5	Seq ID No: 6	638 & 6 3 9	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc
Э	Seq ID No: 6 Seq ID No: 6		419216 431462	AU076718 AW583672	Hs.164021 Hs.256311	small inducible cytokine subfamily B (Cy granin-like neurogodocrine peptide procu
	Seq ID No: 1	644 & 645	448243	AW369771	Hs.52620	integrin, beta 8
	Seq ID No:	646 & 647	426427	M86699	Hs.169840	TTK protein kinase EGF-like-domain, multiple 6
10	Seq ID No: 6 Seq ID No: 6		445537 422278	AJ245671 AF072873	Hs.12844 Hs.114218	EGF-tike-domain, multiple 6 frizzled (Drosophila) komolog 6
10	Seq ID No: 1	652 & 653	428450	NM_014791	Hs.184339	KIAAC175 gene product
	Seq ID No:		446619 453392	AU076643 U23752	Hs.313 Hs.32964	scoreted phosphoprotein 1 (osteopontin, SRY (sex determining region Y)-box 11
	Seq ID No: 6 Seq ID No: 6		455592	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic
15	Seq ID No: 1	660 & 661	425776	U25128	Hs. 159499	parathyroid hormone receptor 2
	Seq ID No:		425776	U25128 NM 012152	Hs.159499 Hs.258583	parathyroid hormone receptor 2 endothetal differentiation, lysophospha
	Seq ID No: 6 Seq ID No: 6		431515 419452	NM_U12152	Hs.200063 Hs.90572	PTK7 protein byosine kinase 7
	Seq ID No: 1	668 & 888	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
20	Seq ID No:		432653 432653	N62096 N62096	Hs.293185 Hs.293185	ESTs, Weakly similar to JC7328 amino aci ESTs, Weakly similar to JC7328 amino aci
	Seq ID No: 6 Seq ID No: 6		432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
	Seq ID No: I	676 & 677	410001	ABO41036	Hs.57771	kalifikrein 11
25	Seq ID No:		426501	AW043782	Hs.293616	ESTs
23	Seq ID No: (408369	R38438 AA151342	Hs.182575 Hs.12677	solute carrier family 15 (H??? transport CGI-147 protein
	Seq ID No: 6	684 & 685	422424	AI186431	Hs.296638	prostate differentiation factor
	Seq ID No:	686 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin, distal-less homeo box 5
30	Seq ID No:	689 & 689	420610	AI683183	Hs.99348	gradiness ricined box 5
50	TABLE 15B					
	Pkev:	Helous For	nenhasat i	den/ifier number		
0.5	CAT numbe	r: Gene clusio	er number			
35	Accession:	Genbank a	ocession nu	ımbers		
	Pkey	CAT Numb	er Acce	ssion		
	309931	AW341683				
40	330493 439285	33264_5 47065_1) AW957800 AA633529 H03662 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
70			AA7	75552 N62351 N	59253 AA626243	AI341407 BE175639 AA456968 AI358918 AA457077
	450375	83327_1	AAO	9647 AA131254	AA374293 AW95	4405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
	451320	86576 1	AA1	90993 H03231 H:	59605 H01642 AA T45734 AA22440	.852876 AA113758 AA626915 AA746952 A1161014 AA099554 R69067 15 A1701458 W20198 F26326 AA890670 N90552 AW071907 A1671352 A1375892 T03517 R88265
45	401020	00010_1	Al12	4088 AA224388	A1084316 A13546	86 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
			AA0	17131 AA443303	T33623 Al22255	6 T33511 T33785 AI419606 D59612
50	TABLE 15C					
50	Pkev:	Helaua eur	nhar aarme	ponding to en Eo	e nonheest	
	Ref:	Sequence :	source. Th	e 7 digit numbers	in this column an	Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
		sequence o	f human ch	romosome 22."	Dunham I. et al., I	Nature (1999) 402-489-495.
55	Strand: Nt_position:			rom which exons esitions of prodict		
55	пСровном	INGIORIO II		Jaidone of Modern	ou touto.	
	Pkey	Ref	Strand	Nt_position		2004 404040 404465 404650 405572 100075
	402075 403329	8117407 8518120	Plus	96450-965		921,124019-124161,124455-124610,125672-126076
60	403478	9958258	Plus	116458-11	6564	
	404440	7528051	Plus	80430-815	81	
	404877 405770	1519284 2735037	Plus	1095-2107 61057-620	75	
	405932	7767812	Minus	123525-12		
65						

WO 02/086443 Table 16

Seq ID NO: 1 DNA sequence Nucleic Acid Accession #: NN_001216 Coding sequence: 43..1422

,	Couing sequ	dence: 43	1422				
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		CTGGAGAGGA					360
15	TCCCTGAAGT	TAGAGGATCT	ACCTACTGTT	GAGGCTCCTG	GAGATCCTCA	AGAACCCCAG	420
		ACAGGGACAA					480
		CCCGGGTGTC					540
		TCGCCGCCTT					600
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		GGGCTGCAGG					780
	CCTGCCGAGA	TOCACGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCTTG	840
	@GGCGCCCGG	CAGGCCTGGC	CGTGTTGGCC	GCCTTTCTGG	AGGAGGGCCC	GGAAGAAAAAC	900
~ -	AGTGCCTATG	AGCAGTTGCT	GTCTCGCTTG	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
25	CAGGTCCCAG	GACTGGACAT	ATCTGCACTC	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
	TATGAGCOGT	CTCTGACTAC	ACCCCCCTCT	GCCCAGGCTC	TCATCTGGAC	TGTGTTTAAC	1080
		TGCTCAGTGC					1140
	GGTGACTCTC	GGCTACAGCT	GAACTTCCGA	GCGACGCAGC	CTTTGAATGG	GOGAGTGATT	1200
		TCCCTGCTGG					1260
30		TGGCTGCTGG					1320
	ACCAGCCTCG	CGTTCCTTGT	GCAGATGAGA	AGGCAGCACA	GAAGGGGAAC	CANAGGGGGT	1380
	GTCAGCTACC	GCCCAGCACA	GCTAGCCGAG	ACTOGAGCCT	AGAGGCTQGA	TCTTGGAGAA	1440
		CAGCCAGACG					1500
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Seq ID NO: 2 Protein sequence: Protein Accession #: NP_001207

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	60
MAPLCPSPWL PLLIPAPARG LTVOLLLSLL LLMFVHPQRL PRMQEDSPLG GGSSGEDDPL	
	20
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GLLFAVTSVA FLYGMERGHE RGTKGGVSYE PAEVAETGA	

50		3 DNA seque					
	Nucleic Ac:	Ld Accession	1 #: BC01392	13			
	Coding sequ	uence: 438-	1391				
	1	11	21	31	41	51	
55	1	1	1	1.	ĩ.	ĩ.	
55	* cocooomic	TCTATTAACT	Transport and a second	CTATCAGGAG	TTOTCARGO	AGAGA AGAGA	60
	AGCGGGGT1G	AAGGGGGAAA	CONTRACT	CCCTCTTTAA	CACTACCACT	CACACAAACA	120
	ACACCACACA	GAAAGAAAGG	CACACABACT	TORGETTIAG	COTTABGOOT	TTCCAAAAA	180
	TARTATAL	AATCATOGGC	COCCCCACCA	TOGGCCAGAG	CAGGAGGGAA	CCCCTTTTTTT	240
60		TCCAGTTTCC					300
00	TORTCOTORI	GCCCTGCGCT	COCCACACACC	COCCCCCCCC	COCCIOCIO	TCTCCCCCCG	360
		CCCCAAAGTC					420
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85	TTTAAAAGTT	CTAGTGGTAC	GGTAGGAGCT	TTGCAGGAAG	TTTGCAAAAG	TCTTTACCAA	1800
	TAATATTTAG	AGCTAGTCTC	CAAGCGACGA	AAAAAATGTT	TTAATATTTG	CAAGCAACTT	1860
	TTGTACAGTA	TTTATCGAGA	TAAACATGGC	AATCAAAATG	TOCATTGTTT	ATAAGCTGAG	1920

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	AATTTGCCAA TTAGGACAGT TAAAAATTGT	TATTTTTCAA TGCAAACGTG ACAAAAGGAA GGCAAAAGTT	AAAAGAAGAA AAAATTAGAA	AATTATTCAA TAAGTACTGG	CGAACCATCT	CTGTGGTCTT	1980 2040 2100 2160
5	AAATGGCCAT TTCCATTTTG GTTTGTAATA GTAGTTGTAT	GCAGGTTGAC TTCAGATAAA TTTCTGTAAA TTTAAAAGAT	ACCOTTOGTA AAAAACCATG TTTATTGTGA TCGGCTCTGT	ATTTATAATA AAATTACTGT TATTTTAAGG ATTATTTGAA	GCTTTGTTC GTTTGAAATA TTTTCCCCCC TCAGTCTGCC	GATOCCAACT TTTTCTTATG TTTATTTTCC GAGAATCCAT	2220 2280 2340 2400
10	CCATTATCCA AAAAAAACAA CACAACACAA	GAACTAATAT CAGTTTGAGA AACAAAAAA AACAACAAAA AACAACAACA	TAAATAAATT CAAAAAACAA AAAAAAAAGA	TTTGAAATAT	GGACACTGAA AACAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2460 2520 2580 2640
15	Seq ID NO: Protein Acc	4 Protein s	sequence: NA83435.1				
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25	GPVPGTAING	TLPLSHM 5 DNA seque		ALL CONTRACTOR OF			
30	Nucleic Ac	ld Accession	1 #: U91618				
50	1	11	21	31	41	51	
	COGACTTGGC	TTGTTAGAAG	GCTGAAAGAT	GATGGCAGGA	ATGAAAATCC	AGCTTGTATG	60
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	ACCTUACUA	ACAGGAGAAG GGCTTTAGCT	TTCATGAAGA	GGAGCTTGTT	GCAAGAAGGA	AACTTCCTAC	360
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	AGAGAATAAA	TYPETTATE	ACATOTOATT	GTGATTCATC	ATCCCTTAAT	TAAATATCAA	600
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45	ATTGAATGTG	TTTTTCTGCA AAAAAAAAAA	CTARTAGAAA	TTAGACTAAG	TGTTTTCAAA	TAAATCTAAA	720
-10	Terrende	Autocomon	2001000000	0000111			
50	Seq ID NO: Protein Ac	6 Protein s cession #: J	equence: AB50564				
	1	11	21	31	41	51	
55	VCSLVINILNS	CMLLLAPSSW PAEETGEVHE NDKNGKEEVI	EBLVARRKLP	TALDGESLEA	MLTIYQLHKI	VPSHKMTLLN CHSRAPQHNE	60 120
	Seq ID NO:	7 DNA seque	ence				
60		ld Accession Lence: 109-2		536.2			
	1	11	21	31	41	51 1	
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	GARCTCCCAT	TOOTOGRAGE	TGGAGTACAG	CTTCAAGACA	ATGGGTATAA	TGGATTGCTC	240
	ATTOCASTTA	ATCCTCAGGT	ACCTUAGAAT	CAGAACCTCA	TCTCAAACAT	TAAGGAAATG	300 360
70	ATARAGATTT	CITCATTITA TAATACCTGC	CACATGGAAA	GCTAATAATA	ACAGCAAAAT	AAAACAAGAA	420
	TCATATCAAA	AGGCARATGT	CATACTGACT	GACTOGTATG	GGGCACATGG	AGATGATCCA	480
	TACACCCTAC	AATACAGAGG ATGATAACTT	GTGTGGAAAA	GAGGGAAAAT	ACATTCATTT	CACACCTAAT	540
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75	ATAAATGGGC	AAAATCAAAT	TAAAGTGACA	AGGTGTTCAT	CTGACATCAC	AGGCATTTTT	720 780
	GGATGCACCT	AAGGTCCTTG TTATCTACAA	TAGCACCCAA	ANTICANCTO	CATCAATAAT	GTTCATGCAA	840
	ACTTTATOTT	CHASTAGGALICA	TAATSTITTAAT	GCAAGTACCC	ACAACCAAGA	ACCACCAAAC	900
80	CTACAGAACC	AGATGTGCAG GCTTTCCCAT	CCTCAGAAGT	CATGGGATG	TAATCACAGA	CTCTGCTGAC	960 1020
30	GTACAGGCTG	GTGACAAAGT	GGTCTGTTTA	GTGCTGGATG	TGTCCAGCAA	GATGGCAGAG	1020
	COTTON CROSS	TYPETERS	ACABCARCCC	CCACABTTTT	ATTTCATGCA	CATTOTTCAA	1140
	CACCADAGGA	TOGTGGGCAT ACAGCAATGA	TGCCAGTTTC	GACAGCAAAG	CATATCTCCC	AGCUCAGCTA CACCACTGTA	1200
85	TORGOTABAR	CACACATCAC	CATTEMETTEA	GGGCTTAAGA	AAGGATTTGA	GGTGGTTGAA	1320
	AAACTGAATG	GAAAAGCTTA ATTGCTTACC	TOGCTCTCTC	ATGATATTAG	TGACCAGCGG	AGATGATAAG	1380
	CITCTIGGCA	MITGCITACC	CHCTGTGCTC	No Cho 10011	CONCANTICA	CICATIGCC	1-10

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CHOCOMPONE CHOCOGCOCC AND CHOCOG GRAPHATICAC CECTEACAGG AGGITTABAG 1500 TTCTTTGTTC CAGATATATC AAACTCCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC 1560 TCTGGAACTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAAATGTC 1620 ARACCTCACC ATCAATTGAA ARACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680 5 AUGITICIAG TTACGTGGCA GGCCAGIGGT CCTCCTGAGA TTATATTATT TGATCCTGAT 1740 GGACGARART ACTRICACARA TRATTTTATO ACCARTOTAR CTTTTCGGAC AGCTAGTOTT 1800 GORDINAMI LITTOGOM GONGGONA GOCTOGONA TOGOCTINACA CONTRACAA TACOCATCAR TOGOTOGONA GONGGONA GOCTOGONA TOGOCTINACA CONTRACAA TACOCATCAR TOCTOGONA GOCTOGONA GONGGONA CONTRACA TACOCATCAR TOTOGONA GOCOCATCAR GONGGONA GOCOCATT 1860 1920 1980 10 TATGCCAATG TGAAACAGGG ATTTTATCCC ATTCTTAATG CCACTGTCAC TGCCACAGTT 2040 GAGCCAGAGA CTGGAGATCC TGTTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100 GTTATAAAAA ATGATGGAAT TTACTOGAGG TATTTTTTCT CCTTTGCTGC AAATGGTAGA 3160 TATAGGTTGA AAGTGCATGT CAATGACTCT CCCAGGATAA GCACGCGAAC CCACTCTATT 2220 CONGGRACIC AUGCIATGIA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 15 GCICCARGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340 AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCCACCC TGATGTGTTT CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT 2400 2460 TGGACAGCAC CTGGAGAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG 2520 AGTARAGEC TACAGARTAT CCAAGATGAC TITAACAATG CTATTITAGT AAATACATCA 20 ARGCGARATE CTCAGCAAGC TGGCATCAGG GAGATATITA CGTTCTCACC CCAGATTTCC 2640 ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT 2700 GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTRACAT TGCCCAGGGG CCTCTGTTTA TTCCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2760 2880 GONGTTTTAN CAGCANTOGG TITGATAGGA ATCATTTGGC TTATTATAGT TGTGACACAT CATACTTTAN GCAGGARARA GAGAGCAGAC ANGRARGAGA ATGGARCARA ATTATTATAN 25 2940 CHINCITIAN GONDANAN GRUNGGUIG RODRESSION A GONDACAN ATTATITATA ATRACATIC DARGETICITE CUTTUTINA TATANANCE INSGCTTOS GATACAMAN CATACTANCA NAGICOMATI ARCATERANA CIGIATIRAN ATSCATTANG TITTIGIANA ATRACAGATA GATTITICAS TOTORAGICA CANATCICTI TOSOGGITOS ATTERANC CUTTURGCT TOCCTATGAN CANATANTA NAGITATICI TITANGGIAN GITCATANAG 3000 3060 30 GCMARGGAA GGGTAAGTC GGACCAGTGT CAAGGAAGT TTGTTTTATT GAGGTGGAAA AATAGCCCCA AGCAGAGAAA AGGAGGSTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA 3240 3300 TCATTTAGTT ACTTTGATTA ATTTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG 3360 TTTACATCAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT 3420 CTTOCTATTT TOTTATATAT ATTTCAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480 35 TITCACTOTA AGAGGIAACC TITAACAATA TOGGIATTAC CITTGTCTCT TCATACOGGI 3540 TITATGACAA ACCICIATIG AATITATIIG INTGTAAGIT TCTACICCCA TCAAAGCAGC 3600 TTTCTAAGTT TATTGCCTTG GGTTATTATG GAATGATAGT TATAGCCCCN TATAATGCCT 3660 TACCTAGGAA A

40 seq ID NO: 8 Protein sequence: Protein Accession #: NP 006527.1

45 MTORSIAGPI CNLKFVTLLV ALSSELPFLG AGVOLODNGY NGLLIAINPO VPENONLISN IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANINSK IKQESYEKAN VIVTDWYGAH GDDPYTLOYR GCKEGKYIH FYNFLLMDN LTAGYGSEGR VFVHEWAHLR WGVFDEYMND 120 180 KPFYINOQNQ IKVTROSSDI TGIFYCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240 MEMOSLSSVV EFCMASTENO EAPNLONONC SLRSAWDVIT DSADFHHSFP MNGTELPPPE 50 TFSLVQACDK VVCLVLDVSS KMAEADRILQ LQQAAEFYIM QIVEIHTFVG IASFDSKCEI RAOLMOINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKOF EVVEKLNGKA YGSVMILVTS 360 420 GDDKLLCRCL PTVLSSGSTI HSIALGSSAA PRLEELSRLT GGLKFFVPDI SNSNSMIDAF SRISSGTGDI FOOHIQLEST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 480 540 PDPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWTYTLN NTHHSLQALK VTVTSRASNS 55 POPDORKYT INTETNICER TASUMINETA KNOWNTILM MINISUALAK VYVISAKSKO APRATURAP KURSELHEPH PINITANNIK GIPFILIANT TATURERIOD DVITALIDO AGADVIGNO INSKYFFSPA ANGRYSLKYN VINESSISTP ANSINGSMAN VINITANIA (DNARAKKY GEMERERING PSKYSGOSF SULVAPARH POVEPPCKI UPDITANICA ULTUMYLARGE DPDQQATST SIRMSSLON IQDDFWALL WYSKNYDQ AGIAEIFTS POISTORGEN GUNGETIESS HIVAIRAND RUSKQANUS ILQADPU PROSPURADIO 660 720 780 840 60 LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENGT KLL

Seq ID NO: 9 DNA sequence Nucleic Acid Accession #: Bos sequence

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	1	11	21	31	41	51	
70			GATGCCCAGT				120
70			GCCCTTGACC				180
			TTGAGGCAGG				300
75	GGGTCTGTCT	CTGCCACCTG	GTCTGCCACA	GATCCATGAT	GTGCAGTTCT	CTGGAGCAGG	360
13	AGCTGAGTAA	GGGGGAAATG	ACCTTCCACA	TGCACAAGGA	GCTGCCCAGC	TTTGTGGGGG	480
			CTGAAGAAGC				540 600
80	ACTTCTTCCA	GGGCTGCCCA	GACCGACCCT	GAAGCAGAAC	TCTTGACTTC	CTGCCATGGA	660
80			TGATGCCTTT				720
			GGATCCTGCT				900
0.5	ATTGGAAATC		GCTGACTTTT				960
85	AAATACCA						

Seq ID NO: 10 Protein sequence:

WO 02/086443 Protein Accession #: NP_005969.1

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5	MMCSSLEGAL	MILUTTERINY	gen werkert.	SKGBWKEITH	KEI-DODAGEK	ADEBGI'KKI'N	60
-		VDFQEYAVFL			Table of Foliat		

- 10 Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: Ros sequence
 Coding sequence: 336-626
- 15 CTCCCCTCAC CCCGGTCCAG GATGCCCAGT CCCCACGACA CCTCCCACTT CCCACTGTGG 120 CCTCGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGGAAT GAGTGGGAAT GGCAAGAGGC CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAAAATGCC AAGTTGGGGG 240 CCACTGGGGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCCT 300 20 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 260 OSCINGICITE GOTGGTCACT ACCITICACA AGTACTCCTG CCARGGGGG GACMGGTTCA AGCTGAGTGA GOGGGAANTG ANGAGACTTC TECACHAGGA COTGCCCAGG TITTATGGGGG ATTCCAGGGAA, ACCATGTCGT GTGAGGGCCT TCCGAGTCACA TCTGCTTTAAT CCTGTCATTG 420 ATTICORROR ACCASTORS STUMBERS TAUGMENT TAUGMENT TOTAL TEATURE ACCASEDATE GRANCING ACCASEDATE TAUGMENT TOTAL ACCASEDATE GRANCING ACCASEDATE GRANCING ACCASEDATE GRANCING GRANCING GRANCING GRANCING GRANCING GRANCING GRANCING GRANCING ACCASEDATE AGRACIATOR TRACTICITY CONCINCIANT GRANCING ACCORDING TOTAL TOTAL TRACTICITY CANGOSTOCI CANADORIA AUCTITION GRANCING ACCORDING TOTAL TOTAL CONTINUE ACCORDING TOTAL TOTAL CONTINUE ACCORDING TOTAL CONTINUE TO THE ACCORDING TO THE ACCORDING TOTAL CONTINUE TO THE ACCORDING TO THE 600 25 660 720 780 840 TOTOTTGATA ATATTTTAAT TOCTCAGTGA TOTTCCATAA CCCGGCTGGC TCAGCTGGAG 900 30 TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCCTTCTG GGCTCTGACT CTCCTGGAAA 960 TOTOTOCARG GCCAGAGCTA TGCTTTAGGT CTCAATTTTG GAATTTCAAA CACCAGCAAA AAATTGGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC AAATAAGAT ATTAAAAAAG 1020 GCAAATACCA
- 35 Seq ID NO: 12 Protein sequence: Protein Accession #: Bos sequence
- 1 11 21 31 41 51 1 40 MCGSLEQAL AVLVTTFIKY SCOEGORFIK SKOEMKELLH KELPSFVGHS REPCAVRAFR VHLDPIFVIGD LERGSFEGKS DCFKITCHHR KNOEMERG
- 45 Seq ID NO: 13 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 58-354

31

41

AAATAAAGAT ATTAAAAAAG GCAAATACCA

- - Seq ID NO: 15 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 62-358
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 TTTGGAATTT CARACACOM CAMARATTG GAATCOMGA TAGGTTGCTG ACTTTATTT 600

PCT/US02/12476

WO 02/086443 TGTCAAATAA AGATATTAAA AAAGGCAAAT ACCA

Seq ID NO: 16 Protein sequence: Protein Accession #: NP_005969.1 5

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GSLDENSDQ VDFGEYAVFL ALITYMCNDF FQGCDDRP

Seq ID NO: 17 DNA sequence Nucleic Acid Accession N: Eos sequence Coding sequence: 939-2372 15

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Seq ID NO: 18 Protein sequence:

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				KMNBIQAIAA			960
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40 Seq ID NO: 21 DNA sequence
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PROPERTY TACTICALAGE THRESCIONAL CHICAGOPPICT TECCOPPETS ASSACATATE 2640 TTAAGATAAT AGCATAAAGA CTTTAAAAAT GTTCCTCCCC TCCATCTTCC CACACCCAGT 2700 CACCAGCACT GTATTTTCTG TCACCAAGAC AATGATTTCT TGTTATTGAG GCTGTTGCTT TTGTGGATGT GTGATTTTAA TTTTCAATAA ACTTTTGCAT CTTGGTTTAA AAGAAA 5 Seq ID NO: 22 Protein sequence: Protein Accession #: NP 003713 31 10 MSQSTQTMBF LSPEVFQHIW DFLBQPICSV QPIDLMFVDB PSBDGATNKI BISMDCIRMQ MSQSTQTMSF LSSEWFQHIW DFLSDFICSV QFILLMFVDS PSSEKSTINKI BISDCINGO DSDLSDPMWP QYTNLGLLMS MDQQIQMGSS STSFYNTDHA QMSVTAPSPY AQPSSTFDAL SPSPAIPSMT DYROPHSPDV SPOOSSTAKS ATWTISTELK KLYCOLKKTC PLOIKUMTPP POGAVIRAMP VYKKAEHYTE VVKRCPNHEL SREFNEGOIA PPSHLIRVEG NSHAOYVEDP 240 15 ITGRQSVLVP YEPPQVGTEF TTVLYNFMCN SSCVGSMNRR PILIIVTLET RDGQVLGRRC 300

FEARICACPG RORKADEDSI RKOOVSDSTK NGDGTKRPFR ONTHGIOMTS IKKRRSPDDB

LLYLPVRGRE TYEMLKIKE SLELMQYLPQ HTIETYRQQQ QQQHQHLLQK HLLSACFRNE

Seq ID NO: 23 DNA sequence

LVEPRRETPK OSDVEPRHSK PPNRSVYP

Nucleic Acid Accession #: NM 001944.1 Coding sequence: 84-3083 25 41 61 TTTTCTTAGA CATTAACTGC AGACGGCTGG CAGGATAGAA GCAGCGGCTC ACTTGGACTT TTTCACCAGG GRAATCAGAG ACAATGATGG GGCTCTTCCC CAGAACTACA GGGGCTCTGG CCATCTTCGT GGTGGTCATA TTGGTTCATG GAGAATTGCG AATAGAGACT AAAGGTCAAT 30 ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAAAGAAG GCAAAAACGT GAATGGGTGA 240 AATTIGCCAA ACCCIGCAGA GAAGGAGAAG ATAACICAAA AAGAAACCCA ATIGCCAAGA 300 TTACTTCAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360 TYACHTCAGG TYRCCAGGAR ACCCGAGAGA TCACCAGCG ATCCCGCCC TYTTGGAATC TTTTTTTT ACAAAAACAC TYGAGAGATAT AACATAACAG CTATAGTGGA CCGGGAGGA ACTCCAGGT TCCTGATCAC ATGTCGGGCT CTAAATGCC 420 35 AAGGACTAGA TGTAGAGAAA CCACTTATAC TAACGGTTAA AATTTTGGAT ATTAATGATA 540 ATCCICCAGT ATITICACAA CAAATTITCA TGGGTGAAAT TGAAGAAAAT AGTGCCTCAA 600 ACTURATIGGT GATGATACTA MATGCCACAG ATGCAGATGA ACCAMACCAC TTGAATTCTA
AAATTGCCTT CAAAATTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTC CTCCTAAGCA 660 720 GAAACACTGG GGAAGTCCGT ACTTTGACCA ATTCTCTTGA COGAGAGCAA GCTAGCAGCT 40 ATCOTOTOGT TOTGAGTGGT GCAGACAAAG ATGGAGAAGG ACTATCAACT CAATGTGAAT GTAATATTAA AGTGAAAGAT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 840 900 CAGCACGTAT TGAAGAARAT ATTITAAGTT CTGAATTACT TCGATTCAA GTAACAGATT
TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATT CTTTACCTCT GGGAATGAAG 960 1020 GAAATTGGTT TGAAATACAA ACTGATCCTA GAACTAATGA AGGCATCCTG AAAGTGGTGA 1080 45 AGGCTCTAGA TTATGAACAA CTACAAAGCG TGAAACTTAG TATTGCTGTC AAAAACAAAG 1140 CTGAATTTCA CCAATCAGTT ATCTCTGAT ACCGAGTTCA GTCAACCCCA GTCACAATTC AGGTAACAAA TGTAAGAGAA GGAATTGCAT TCCGTCCTGC TTCCAAGACA TTTACTGTGC 1200 1260 AAAAAGCCAT AAGTAGCAAA AAATTGGTGG ATTATATCCT GGGAACATAT CAAGCCATCG 1320 ATGAGGACAC TAACAAAGCT GCCTCAAATG TCAAATATGT CATGGGACGT AACGATGGTG 1380 50 GATACCTAAT GATIGATICA AAAACTGCIG AAATCAAATT TGTCAAAAAT AIGAACOGAG 1440 ATTCTACTTT CATAGTTAAC AAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA 1500 COGGINARAC TICHACAGG ACGGINTATATG TRAGAGTACC CGATTICANT GACAGTIGTC CAACAGCTG CCICCAAAAA GATCAGGTT TOCAGGGTTCHTC ACCTTGCATG TITTETCTCCG CTATAGAACACT GAATAATAGA TACACTGGGC CCTATACACT TOCACTGGAA GATCAACCTG 1560 1620 1680 55 TARACTICC TOCCOTATEC ACTATCACAA COUTCAATGU TACCTOGGCC CTCCTCAGAG 1740 1000 1860 1920 60 TGGCCCCCCT TCTGCTGTTG ACCTGTGACT GTGGGGCAGG TTCTACTGGG GGAGTGACAG 2040 GTGGTTTTAT CCCAGTTCCT GATGGCTCAG AAGGAACAAT TCATCAGTGG GGAATTGAAG 2100 GAGCCCATCC TGAAGACAAG GAAATCACAA ATATTTGTGT GCCTCCTGTA ACAGCCAATG GAGCCGATTT CATGGAAAGT TCTGAAGTTT GTACAAATAC GTATGCCAGA GGCACAGCGG 2160 2220 TGGARGGCAC TTCAGGAATG GAAATGACCA CTAAGCTTGG AGCAGCCACT GAATCTGGAG 65 GIGCIGCAGG CITTGCAACA GGGACAGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA 2340 CTGGAGTTGG CATCTGTTCC TCAGGGCAGT CTGGAACCAT GAGAACAAGG CATTCCACTG 2400 GAGGAACCAA TAAGGACTAC GCTGATGGGG CCATAAGCAT GAATTTTCTG GACTCCTACT 2460 TTTCTCAGAA AGCATTTGCC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT 2520 TGTTGATCTA TGATAATGAA GGCGCAGATG CCACTGGTTC TCCTGTGGGC TCCGTGGGTT 70 GTTGCAGTTT TATTGCTGAT GACCTGGATG ACAGCTTCTT GGACTCACTT GGACCCAAAT 2640 TTAAAAAACT TGCAGAGATA AGCCTTGGTG TTGATGGTGA AGGCAAAGAA GTTCAGCCAC 2700 CCTCTAAAGA CAGCGGTTAT GGGATTGAAT CCTGTGGCCA TCCCATAGAA GTCCAGCAGA 2760 CAGGATTTGT TAMOTGCCAG ACTITGTCAG GAAGTCAAGG AGCTTCTGCT TTGTCCGCCT 2920 CHOSCICTOR CASCAGET CITTCENTC CHORCECT GONCATGET FIGUREST TRACGERGE TRACTEGET TETEGETCOC CONCERTS CONCENTS ACCULTER TRACGERGE TRACTEGET TETEGETCOC TOUTGEACC TROCACTEG GGCTTGATC 2880 75 2940 CACTTCTCAC ACRAAATGTG ATRGTGACAG ANAGGGTGAT CTGTCCCATT TOCAGTGTTC 3000 CTGGCRACCT AGCTGGCCCA ACGCRGCTAC GAGGGTCACA TACTATGCTC TGTACAGAGG ATCCTTGCTC CCTTCTAATA TGACCAGRAT GAGCTGGAAT ACCACACTGA CCAAATCTGG 3060 3120 ATCTTTGGAC TARAGTATIC ARANTAGCAT AGCARGCIC ACTGTATTGG GCTARTARTI 3180 80 TEGGRETTAT TAGCITETET CATARACTER TERCENTAT ANATTANATE TITEGGITCA TACCECARRA GERATETT GTERCTECTA ATTETERAT ACTATECRA TIGTAGIARA 3240 3300 TOTTAAAGTT TITCAAAACC CTAAAATCAT ATTOGO

Sed ID NO: 24 Protein segmence: Protein Accession #: NP 001935.1

85

WO 02/086443 MMGLEPRITG ALAIFVVVIL VHGELRIETK GOYDESEMIM QOAKROKRE WVKFAKPCRE 60 GEDNSKRNPI AKITSDYGAT OKITYRISGV GIDOPPFGIF VVDKNTGDIN ITAIVDREET 120 PSFLITCRAL MAGGLDVEKP LILTVKILDI NONPPVPSQQ IFMGEIEENS ASNSLVMILN 180 ATDADEPNIL NSKIAFKIVS QEPAGTPMFL LSRNTGEVRT LINSLDREQA SSYRLVVSGA 240 DEDGEGLSTQ CECNIKVEDV NONFFMFRDS QYSARIEENI LSSELLRPQV TOLDEEYTON 300 MILAVYFFTSG NEGNWFSIQT DPRINEGILK VVKALDYEQL QSVKLSIAVK KRAEFEQSVI SRYRVOSTPY TIQVINVRSG LAFREASKTF TVQKGISSKK LVDYILGIYQ ALDEDTNKAA 360 SNVKYVNGRM DGGYLMIDSK TABIKFVKNM NRDSTFIVNK TITARVLAID BYTGKTSTGT 480 10 VYVRVPDFND NCPTAVLEKD AVCSSSPSVV VSARTLANRY TGPYTFALED QPVKLPAVWS 540 ITTLNATSAL LRAQEQIPPG VYHISLVLTD SQNNRCEMPR SLTLEVCQCD NRGICGTSYP 600 TTSPGTRYGR PHSGRIGPAA IGLLLIGLIL LILAPLLLIT CDCGAGSTGG VTGGFIPVPD GSBGTINGWG IEGANPEDKE ITNICVPPVT ANGADFMESS EVCTNTYARG TAVEGTSGME 660 720 MITKLGAATE SGGAAGFATG TVSGAASGFG AATGVGICSS GQSGTMRTRH STGGTMKDYA 780 15 DGAISMNFLD SYFSQKAFAC AREDDOQEAN DCLLIYDNEG ADATGSFVGS VGCCSFIADD 840 LODSPLDSIC PEFEKLARIS LCVDGEGKEV OPPSEDSGYG IESCHEPIEV QCTGFVECOT 900 LSGSQGASAL SASGSVQPAV SIPDPLQHGN YLVTETYSAS GSLVQPSTAG PDPLLTQNVI 960 VTERVICEIS SVEGNLAGET OLEGSHTMLC TEDECSRLI 20 Seq ID NO: 25 DNA sequence leic Acid Accession #: Bos sequence Coding sequence: 56-1642 21 25 AGTATCCCAG GAGGAGCAAG TOGCACGTCT TOGGACCTAG GCTGCCCCTG CCGTCATGTC GCAAGGGATC CTTTCTCCGC CAGCGGGCTT GCTGTCCGAT GACGATGTCG TAGTTTCTCC 120 CATGITIGAG TCCACAGGIG CAGATITGGG GICTGTGGTA CGCAAGAACC TGCTATCAGA 180 CTGCTCTGTC GTCTCTACCT CCCTAGAGGA CAAGCAGCAG GTTCCATCTG AGGACAGTAT 240 30 GGAGAAGGTG AAAGTATACT TGAGGGTTAG GCCCTTGTTA CCTTCAGAGT TGGAACGACA 300 GGAAGATCAG GGTTGTGTCC GTATTGAGAA TGTGGAGACC CTTGTTCTAC AAGGACCCAA GGACTCTTTT GCCCTGAAGA GCAATGAACG GGGAATTGGC CAAGCCACAC ACAGGTTCAC 360 420 CTITTCCCAG ATCTTTGGGC CAGAGTGGG ACAGGCATCC TTCTTCAACC TAACTGTGAA 480 GGAGATGGTA AAGGATGTAC TCAAAGGGCA GAACTGGCTC ATCTATACAT ATGGAGTCAC 35 TAACTCAGGG AAAACCCACA CGATTCAAGG TACCATCAAG GATGGAGGGA TICTCCCCCG 600 GTCCCTGGCG CTGATCTTCA ATAGCCTCCA AGGCCAACTT CATCCAACAC CTGATCTGAA 660 GCCCTTGCTC TCCAATGAGG TAATCTGGCT AGACAGCAAG CAGATCCGAC AGGAGGAAAT GAAGAAGCTG TCCCTGCTAA ATGGAGGCCT CCAAGAGGAG GAGCTGTCCA CTTCCTTGAA 720 780 GAGGAGTGTC TACATCGAAA GTCGGATAGG TACCAGCACC AGCTTCGACA GTGGCATTGC 840 UMANANISTE TALITUMAN UTGSATING TALUNGKOLO NGCTTORICA GROCATING TOGOCICICT TCATACHTC AGRITACOGO GAPTACCAG GROTAGANA CARCATO NTOGOCICA CEMANACTO COCOCTACO TSCCOGOSA ANANTOGOT TCTCOLUCTO GATCICATTC TTTGGATCT ACANCGAACT GCTTTATRIAC CTATTAGAAC COCCHAGCA ACACCCCAG AGCCAGACT TGCGGCTATG CARGATCA ANTOGCATC CCTATGGA 40 900 960 1020 1080 AGATOTORAC TOGATTCATG TGCAAGATGC TGAGGAGGCC TGGAAGCTCC TAAAAGTGGG 45 TOSTANGANO CAGAGOTITG CONGCACCON COTCANOCAG ANCTOCAGOO GONGTONCAG 1200 CATCTTCTCA ATCAGGATCC TACACCTTCA GGGGGAAGGA GATATAGTCC CCAAGATCAG 1260 CGAGCTOTCA CTCTGTGATC TGGCTGGCTC AGAGCGCTGC AAAGATCAGA AGAGTGGTGA 1320 ACGGTTGAAG GAAGCAGGAA ACATTAACAC CTCTCTACAC ACCCTGGGCC GCTGTATTGC 1380 TOCCCTTCOT CANANCCAGO AGAACOGGTO ANAGONGANO CTGGTTCCCT TCCGTGACAG 50 CAAGTTGACT COAGTGTTCC AAGGTTTCTT CACAGGCCGA GGCCGTTCCT GCATGATTGT 1500 CANTOTGAAT COCTGTGCAT CTACCTATGA TGAAACTCTT CATGTGGCCA AGTTCTCAGC 1560 CATTGCTAGC CAGGTGACTT GTGCATGCCC CACCTATGCA ACTGGGATTC CCATCCCTGC 1620 ACTOGITCAT CAAGGAACAT AGTOTTCAGG TATCCCCCAG CTTAGAGAAA GGGGCTAAGG 1680 CAGACACAGG CCTTGATGAT GATATTGAAA ATGAAGCTGA CATCTCCATG TATGGCAAAG 1740 55 AGGAGCTCCT ACAAGTTGTG GAAGCCATGA AGACACIGCT TTTGAAGGAA CGACAGGAAA 1800 AGCTACAGCT GGAGATGCAT CTCCGAGATG AAATTIGCAA TGAGATGGTA GAACAGATGC 1860 AACAGCOGGA ACAGTGGTGC AGTGAACATT TGGACACCCA AAAGGAACTA TTGGAGGAAA 1920 TGTATGRAGA AAAACTAAAT ATCCTCAAGG AGTCACTGAC AAGTTTTTAC CAAGAAGAGA
TTCAGGAGGG GGATGAAAAG ATTGAAGAGC TAGAAGCTCT CTTGCAGGAA GCCAGACAAC 1980 60 AGTCAGTGGC CCATCAGCAA TCAGGGTCTG AATTGGCCCT ACGGCGGTCA CAAAGGTTGG 2100 CAGCTTCTGC CTCCACCCAG CAGCTTCAGG AGGTTAAAGC TAAATTACAG CAGTGCAAAG 2160 CAGAGCTAAA CTCTACCACT GAAGAGTTGC ATAAGTATCA GAAAATGTTA GAACCACCAC 2220 CONCROCAL COCCUTOROS ATTRACTOROS ACARGAMENTA MARAGAMENTO CAGRAGAMENTA 2280 TRACCIOTOTT GOGGACAGAG CTTCAGAAAC TIGGTGAGTC TCTCCAATCA GCAGAGAGAG TRANSPIRITY GUSSACRASS CITCHANARC TISSTEMPT TUTCHATCH CONGRESSION CITCHTOTOCO ACCRACHOS GROGADARC TICTCRACC CITGRACACT TIGRATSKA TUTCHATCHA ACAGACAGA ACTCTOGCTU AACTGCAGAA CAACATGGTG CTAGTASAC TIGRACTTC GRAGAGAGGT TUTCHACTIGT TIGRAACTCC AAGGCCAGT TUTCHACTGT TIGRAACTCC AAGGCCAGAC TIGRAACTCC GAAAATCAACC 65 2400 2460 2520 2580 AACAACCACC AGGGAAGAAA CCATCCTTC GAAATTTACT TCCCCGAACA CCAACCTGCC 2600 AAAGCTCAAC AGACTGCAGC CCTTATGCCC GGATCCTACG CTCACGGGGT TCCCCTTTAC 2700 70 TCAAATCTGG GCCTTTTGGC AAAAAGTACT AAGGCTGTGG GGAAAGAGAA GAGCAGTCAT 2760 OGCCCTGAGG TGGGTCAGGT ACTCTCCTGA AGAAATAGGT CTCTTTTATG CTTTACCATA
TATCAGGAT TATCCAGG ATGCAATACT CAGACACTAG CTTTTTCCC ACTCTTTGTAT 2820 2880 TATAACCACC TATGTAATCT CATGTTGTTG TTTTTTTTTA TTTACTTATA TGATTTCTAT 75 GCACACAAAA ACAGTTATAT TAAAGATATT ATTGTTCACA TITTTTATTG AATTCCAAAT 3000 GTAGCAAAAT CATTAAAACA AATTATAAAA GOGACAGAAA AA Sed ID NO: 26 Protein sequence: Protein Accession #: Bos Sequence 80 MSQGILSPPA GLLSDDDVVV SPMFESTAAD LGSVVRENLL SDCSVVSTSL EDKOOVPSED SMEKVKVYLR VRPLLPSELE RQEDQGCVRI ENVETLVLQA PKDSPALKSN ERGIGQATER 120 85 FTFSQIFGPE VGQASFFNLT VKEMVKDVLK GQNWLIYTYG VTNSGKTHTI QGTIKDGGIL 180 PRSLALIFNS LOGGLHPTPD LKPLLSNEVI WLDSKQIRGE EMKKLSLLNG GLGESELSTS 240 LKRSVYIESR IGTSTSFDSG IAGLSSISQC TSSSQLDBTS HRWAQPDTAP LEVPANIEFS 200

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5	IWISFFEIYN WGRKNQSFAS GERLKEAGNI	ELLYDLLEPP THINQUISERS	HSIFSIRILE IAALROMOON	LQGEGDIVPK RSKQNLVPFR	ISELSLCDLA DSKLTRVFQG	DAREAWKLLK GSERCKDQKS FFTGRGRSCM	360 420 480
_	Nucleic Ac	27 DNA sequid Accession ence: 13-1	ı ∦: Eos se	Juence			
10	1	11	21	31	41	51	
	CTTCCCCTGA	CAATGAAGTT ACAGCTCTAC TTTATGGCCT	AAGCCTGGAA	AAAAATAATG	TGCTATTTGG	TGAAAGATAC	60 120 180
15	GGAAACTTAA GGGCAACTGG GTCCATCATT AGAATCAATA	TGAAGGAAAA ACACATCTAC TCAGGGAAAT ATTACACACC TATGGAGTAA	AATCCAAGAA CCTGGAGATG GCCAGGGGGG TGACATGAAC	ATGCAGGACT ATGCACGGAC CCCGTATGGA CGTGAGGATG	TCTTGGGTCT CTCGATGTGG GGAAACATTA TTGACTACGC	GAAAGTGACC AGTCCCCGAT TATCACCTAC AATCCGGAAA	240 300 360 420 480
20	GCTGACATTT AAAGGTGGAA TTCGATGAGG GTTCACGAGA	TGGTGGTTTT TCCTAGCCCA ACGAATTCTG TTGGCCATTC	TGCCCGTGGA TGCTTTTGGA GACTACACAT CTTAGGTCTT	GCTCATGGAG CCTGGATCTG TCAGGAGGCA GGCCATTCTA	ACTTCCATGC GCATTGGAGG CAAACTTGTT GTGATCCAAA	TTTTGATGGC GGATGCACAT CCTCACTGCT GGCCGTAATG	540 600 660 720
25	GCATTCAGT TCAGAACCAG	ACAAATATGT CCCTGTATGG CTCTCTGTGA TCITCAAAGA TAATTTCTTC CCAGAAATCA	AGACCCAAAA CCCCAATTTG	GAGAACCAAC AGTTTTGATG	GCTTGCCAAA CTGTCACTAC	TOCTGACAAT CGTGGGAAAT	780 840 900 960 1020
30	AATTTAAGAC GTGAAAAAAA GATAACCAGT	CCAGAAATCA CAGAGCCAAA TTGATGCAGC ATTGGAGGTA AGAACTTCCA	TTATCCCAAG TGTTTTTAAC TGATGAAAGG	AGCATACATT CCACGTTTTT AGACAGATGA	ATAGGACCTA TGGACCCTGG	CTTCTTTGTA TTATCCCAAA	1080 1140 1200 1260 1320
35	AACAAATACT CGTATCACCA TGGTTTTTGT	ACTATTTCTT AAACACTGAA TAGTTCACTT ACTTAGAGAT TACATAATAT	CCAAGGATCT AAGCAATÁGC CAGCTTAATA	AACCAATTTG TGGTTTGGTT AGTATTTATT	AATATGACTT GTTGAAAATG GCATATTTGC	CCTACTCCAA GTGTAATTAA TATGTCCTCA	1380 1440 1500 1560 1620
40	CTCTACTATT CTCTGTAAGT TAAAATTAAG	AAGTTTGAAA TGCTTCCTAA TATATATATT	ATAGTTACCT CATCCTTGGA TTGGCTCAAA				1680 1740
45	Protein Ac	28 Protein cession #: 1	sos sequence		41	51	
	1	11	21	31	41	21	
					1	1	
50	KEKIQEMQHF YTPDMNREDV LAHAFGPGSG KYVDINTFRL FKDRFFWLKV	ATASGALPIN LGLKVTGQID DYAIRKAPQV IGGDAHFDED SADDIRGIQS SERPKTSVNL	TSTLEMMHAP WSNVTPLKFS EFWTTHSGGT LYGDPKENQR ISSLWPTLPS	ROGVPDVHHF KINTGMADIL NLFLTAVHEI LPNPDNSEPA GIEAAYEIEA	REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDPNLSFDA RNQVFLFKDD	KHYITYRINN FHAFDGKOGI DPKAVMFPTY VTTVGNKIFF KYWLISNLRP	60 120 180 240 300 360
50 55	KEKIQEMQHF YTPDMNREDV LAHAFGPGSG KYVDIHTFRL FKDRFFWLKV EPNYPKSIHS NFQGIGPKID	LGLKVTGQLD DYAIRKAFQV IGGDAHFDED SADDIRGIQS SERPKTSVNL FGFPNFVKKI AVFYSKNKYY	TSTLEMMHAP WSNVTPLKFS EFWTTHSGGT LYGDPKENQR LYSCLWPTLPS DAAVFNPRPY YFFQGSNQFE	ROGVPDVHHF KINTGMADIL NLFLTAVHEI LPNPDNSEPA GIEAAYEIEA RTYFFVDNOY	REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDPNLSFDA RNQVFLFKDD WRYDERRONM	KHYITYRINN FHAFDGKOGI DPKAVMFPTY VTTVGNKIFF KYWLISNLRP	120 180 240 300
55	KEKIQEMQHF YTPDMNREDV LAHAFGPGSG KYVDINTFRL FKDRFFWLKV EPNYPKSIHS NFQGIGPKID Seq ID NO: Nucleic Ac:	LGLKVTGQLD DYAIRKAFQV IGGDAHFDED SADDIRGIQS SERPKTSVNL FGFPNFVKKI	TSTLEMMHAP WSNVTPLKFS EFWTTHSGOT LYGDPKENQR ISSLWPTLPS DAAVFNPRFY YFFQGSNQFE LENCE 1#: NM_0061	ROSVPDVHHF KINTGMADIL HLFLTAVHBI LPNPDNSEPA GIEAAYBIEA RTYFFVDNQY YDPLLQRITK	REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDPNLSFDA RNQVFLFKDD WRYDERRONM	KHYITYRINN FHAFDGKOGI DPKAVMFPTY VTTVGNKIFF KYWLISNLRP	120 180 240 300 360
	KEKIQEMQHF YTPDMNREDV LAHAFGPGSG KYVDINTFRL FKDRFFWLKV EPNYPKSIHS NFQGIGPKID Seq ID NO: Nucleic Ac:	LGLKVTGQLD DYAHRKAFQV IGGDAHFDED SADDIRGIQS SERPKTSVNL FGFPNFVKKI AVFYSKNKYY 29 DNA sequid Accession	TSTLEMMHAP WSNVTPLKFS EFWTTHSGOT LYGDPKENQR ISSLWPTLPS DAAVFNPRFY YFFQGSNQFE LENCE 1#: NM_0061	ROSVPDVHHF KINTGMADIL HLFLTAVHBI LPNPDNSEPA GIEAAYBIEA RTYFFVDNQY YDPLLQRITK	REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDPNLSFDA RNQVFLFKDD WRYDERRONM	KHYITYRINN FHAFDGKOGI DPKAVMFPTY VTTVGNKIFF KYWLISNLRP	120 180 240 300 360
55	KEKIGEMOMP TYPPONNREDV LAHAFGPGSG KYVDINTFRL EPNYPKSIHS NFGGIGPKID Seq ID NO: Nucleic Ac. Coding seq 1 GCTTCAGGGT GGGSACACCC ACTCTCTGAG GAGACCTTGAG ACGAAAGGGAT ACGAAAGGGAT	LGLKYTGQLD DYATKARPOV IGDAHFDED SADDIRGIGS SERPKTSVNL FGFPNFVKKI AVFYSKNKYY 29 DNA seq id Accession Lence: 236. 11 ACMGCTCCCC CMCCGGTTC GRARARCCAT AATCCAACGG	TSTLEMMHAP WENNTPLES EFWITHSGOT LYGDPKENGR LYGDPKENGR ISSLWPTLPS DAAVENPRPY YPFQGSNQFE 1810Ce 1#: NM_0061 1765 21 CGCAGCCGAG CCAGAGCTGA TTTGATTATT TTGGAGGTGAG CCATTGAGAG	ROGYDOWHIP KINTGMONIC NLPITAVHEI LPNPONSEPA RTYFFVDNQY YDFLLQRITK 115.1 31 AGCCUGGCCT CCTGTCAACA TCAGGAC TGAGGCCAGC TGAGGCCAGC TGAGGCCAGC	REMEGGPUNG VERARGAUG GHSLGLGHSS LCDRNLSFDA RNQVFLEKED WRYDERROMM TLKSRSWFGC 41 GCAGCCCCTC GCAACTTGGC GTGGGTGGCA GTGGGTGGCA GTGGGTGGCA	SITITYRING FHAPEGKGGI DPKAVMFPTY VITVONKIFF DPGYPKLITK 51 AGCACCGCTC GGTGTGGTGGA ACAAGTGACT TCAAAATGGA ACTGCACACA	120 180 240 300 360 420 60 120 180 240 300
55	KEKCJOHOHE TYPDMNREDV LAHAFGPG9S KYVDINTFRL KVDRFFHIKK KYVDINTFRL FKDRFFHIKK SEQ ID NO: Nucleic Ac Coding seq GCTTCAGGT GGGACACC ACTCTTGAG GAGACTACA ACGAAGCCT CCACCGGAA TCCACGGACA TCCACGGACA TCCACGGACA TCCACGGACA TCCACGGACA	LGLAYTOGLD DYATRARPO DYATRARPO IOGDAHPBE SADDIRGIOS SERPKTSVM. PGPPHYKM. AVPSNMKYY 29 DNA seq did Accession Lence: 236. 11 ACAGTTOCCC CACCOGTTOG GARAACCAT AATOCAAGCA TYGTOGGOTT CTTOTGGAGA CACTOTTOTGGAGA CACTOTTOTGGA	TSTLEWHAP SENTPLASS ENTHAGOT LYOPERIOR LISSIMPLES ENTHAGOT LISSIMPLES ENTHAGOT LISSIMPLES LAMPRIPER YPPQGSINGE LOCAL LITTOR CCAGOCCTIA TTTORAGIACT CCATTORAGIACT TTTORAGIACT CCATTORAGIACT TTORAGIACT	ROSUPDUHHF KINTOMADIL NEFIZAWHEI LEPPINNESP GIEAAYEIRA RTIFPUNNOY YOPILORITK 31 AGCCUSSOCT CCTOTCAGCA ACTCTCAGAC TURNOGCCAGC COSATCACTC CTTCCGSCCA COTTCAGCC CTTCCGSCCA CTTCCCGCCA CTTCCCCTCGACA CTCCCCTGGAC TCACCTTGGAC TCACCTTGCAC TCACCTTCAC	REMPOGOVER WYPARGAHOU GISLIGLIGHS LUCPRILEPEA RROYFE/FRO RROYFE/FRO LUCPRILEPEA GCAGCCCCCC GCACATTCCC GTGCGTGGCA CTARATTCGC ACCATCAGC ACCATCAGC CCTARATTCCC ACCATCAGC ACCATCACC	SITUTYRING FHAFDGROGI DPKAVMEPTY VITYONKIFF KYMLISHLEP DPGYPKLITK 51 AGCACCGCTC GGTGTGGGACAG TCAAAATGGA TGTGGACAG CCCTGCCAC CACCCTTCCC CCTGTCCCCC CCTGTCCCCCC CCTGTCCCCC CCTGTCCCC CCCCC CCCCC CCCCC CCCC CCCC CCCC CCCC	120 180 240 300 360 420 60 120 180 240 300 420 480 540 600
55 60 65	REMICISHORM TYPONNSEDUL LAHAROPOSO LAHAROPOSO KYVDINTFRI FKDRYPHLKY ENTYPHILIN SEQ ID NO: NCLOCK COCING COCTICAGGG COCTICAGG COCTI	LOLAYTOGLE DYARKARDY LOGARITHEE SADDIRGING SERVICE SER	TSTLEWSHAP KNNTPLKES EPNTHSGOT LYOPESHOR LSKINPLES EPNTHSGOT LYOPESHOR LSKINPLES EPNTHSGOT LSKINPLES EPNTHSGOT LSKINPLES EPNTHSGOT LSKINPLES LSKI	ROJUPOUHHF KINTOMADIL NEFIZAWHEI LENPENSERS GIEANYSIER GITANYSIER ACCOUSCICT COCTOTOMACA ACTOTOMACA CONTOMOCOC	REMOGOPWR VYPARGAMO GISLICIAISS LOPRISPES ROYUELERD RETURN TEXES GCASCCCCCC GCAACTTCCC GCAACTTCCCA AAGGATCACC AATGGAAAC ACAAGAAC AATGGAAAC ATTGGAAAC ATTGGAAAC	SITETY FRIM FRAPERIOR ID PRANNEPTY VITTORIETY FRAPERIOR ID PRANNEPTY VITTORIETY FAMILIAN FRANCISCO GOTTOTOTO A COMMITTAN TO A COMMITTAN A	120 180 240 300 360 420 180 240 360 480 540 660 660 780 840 900
55 60 65 70	REMICISHQUE YEPONNESS DE VERTOR DE L'ALENDRO	LOLAYTOOLD DYARKARDY IODAHADA DYARKARDY IODAHADA DA SADDIROIDS SERVETSVAL POPEN FYRAI ANY SYSIKKY I SERVETSVAL POPEN FYRAI ANY SYSIKKY I SERVETSVAL POPEN FYRAI ANY SYSIKKY I SERVETSVAL PACKARDY IN SERVETSVA	TSTLEWSHAP MENUTPLESS EMPTTHSOOT LETOPERSON EMPTTHSOOT LETOPERSON EMPTTHSOOT LETOPERSON EMPTTHSOOT LETOPERSON EMPTTHSOOT LETOPERSON EMPTTHSOOT	ROSUPDIVIBLE RESIDENCE PROPERTIES OF THE PROPERTY OF THE PROPE	REMPROPOVIEW VIVENDAMA GISSIZIATISS LEOPITISETS LEOPITISETS GRACCICTIC GCAGCICCTIC GAGGITCTIC GAAGGITCTIC GAAGGITC	SILITATIVALIMA PRAPERIORIO PRAPERIORIO SILITATIVALIMA SILITATIVAL SIL	120 180 240 300 360 420 180 240 300 420 480 600 600 720 780

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	TGTTGAAAAT	AAAGAGAAGC	AATGTGAAGC	ARARARARA	AAAAAAAA		

Seq ID NO: 30 Protein sequence:

	Dealinin Box	ession #: N	D 006106 1				
15	FIOCEIN ACC	Gapton *	_000100.1				
13		11	21	31	41	51	
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	GCTTCAGGGT	ACAGCTCCCC	CGCAGCCAGA	AGCCGGGCCT	GCAGCGCCTC	AGCACCGCTC	60
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		GATGAGTGTG					1440
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Seq ID NO: 31 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 64-2754

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		CAGCACAGAA					600
		TAAATTTGTT					660
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	GGATATTCAG						780
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	TCATTGATAA						1080
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AGTAGACTGT GGAGCCTCAC CAAAGTTAAT GATACAGCTG COOSTCTTTC ATATCAGAAA 1920 ANTOCTOGAT TICAAGAATA TACCATTCCT ATTACTGTAA AAGACAGGC CGGCCAAGCT GCAACAAAAT TATTGAGAGT TAATCTGTGT GAATGTACTC ATCCAACTCA GTGTCGTGCG 2040 2100 10 ACTICAAGGA GTACAGGAGT AATACITGGA AAATGGGCAA TCCITGCAAT ATTACTGGGT 2160 ATAGCACTGC TOTTTTCTGT ATTGCTAACT TTAGTATGTG GAGTTTTTGG TGCAACTAAA 2220 GGGARACGTT TTCCTGAAGA TTTAGCACAG CAAAACTTAA TTATATCAAA CACAGAAGCA 2280 CCTOGAGACO ATAGAGTGTG CTCTGCCAAT GGATTTATGA CCCAAACTAC CAACAACTCT AGCCAAGGTT TTTGTGGTAC TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAAACCATT 2400 15 GAAATGATGA AAGGAGGAAA CCAGACCITG GAATCCTGCC GGGGGGCTGG GCATCATCAT 2460 ACCUTGGACT CUTGCAGGGG AGGACACACG GAGGTGGACA ACTOCAGATA CACTTACTCG 2520 GAGTGGCACA GTTTTACTCA ACCCCGTCTC GGTGAAAAAT TGCATCGATG TAATCAGAAT 2580 GAAGACCGCA TGCCATCCCA AGATTATGTC CTCACTTATA ACTATGAGGG AAGAGGATCT 2640 CCAGCTGGTT CTGTGGGCTG CTGCAGTGAA AAGCAGGAAG AAGATGGCCT TGACTTTTTA 2700 20 AATAATTTGG AACCCAAATT TATTACATTA GCAGAAGCAT GCACAAAGAG ATAATGTCAC 2760 AGTGCTACAA TTAGGTCTTT GTCAGACATT CTGGAGGTTT CCAAAAATAA TATTGTAAAG 2820 TICANTITA ACAIGNATGE ATAGANGAT TITTTTCCA ATTITAAT ACGICACTA
CCAATTITA TITTAAAG CAGTGITGC TIATCITTC CAAAAAGGA AAAATGTA 2880 2940 AACAGACAAC TOGTAAATCT CAAACTCCAG CACTGGAATT AAGGTCTCTA AAGCATCTGC 3000 25 TCTTTTTTT TTTTACGGAT ATTTTAGTAA TAAATATGCT GGATAAATAT TAGTCCAACA ATAGCTAAGT TATGCTAATA TCACATTATT ATGTATTCAC TTTAAGTGAT AGTTTAAAAA 3060 3120 ATAMACANGA RATATTGAGT ATCACTATOT GAAGAAAGTT TITGGAAAGG AACAATGAAG ACTGAATTAA ATTAAAAATG TTGCAGCTCA TAAAGAATTG GGACTCACCC CTACTGCACT 3180 3240 ACCARATTCA TITGACTITG GAGGGAAAAT GIGITGAAGI GCCCTATGAA GIAGCAATIT 30 TCTATAGGAA TATAGTTGGA AATAAATGTG TGTGTGTATA TTATTATTAA TCAATGCAAT 3360 ATTERARATS RAKTGAGRAC ARAGAGGRAR ATGGTRARRA CTTGRARTGA GGCTGGGGTA TAGTTTGTCC TACARTAGRA RAKAGAGRAG GCTTCCTAGG CCTGGGCTCT TARATGCTGC 3420 3480 ATTATARCTS ASTOTATIONS GARACTASTIC CIGTOCART TOTSTARTIT STITARARTT 3540 GTARATARAT TARACTITIC TGGTTTCTGT GGGAAGGAAA TAGGGAATCC AATGGAACAG 35 TAGCTTTGCT TTGCAGTCTG TTTCAAGATT TCTGCATCCA CAAGTTAGTA GCAAACTGGG 3720 GRATACTOSC TSCAGOTGGG GTTCCCTGCT TTTTGGTAGC AAGGGTCCAG AGATGAGGTG TITITITOS GENECIATA ACADAMONI TITAMACET ACTITACTO RAGITAMIC CICCATITOC ETITOTACTO COCTUTATAS TORCORACIO TITITITATA TORCOSACIO TARRESCANDA CITACTORA RAGIORAGIO ACCIONAGAT CITACTORAN 3780 3900 GENERATEGE GREATTEATT CRETTARAC CTRAGGCCCA CARACTTGAC ACCTGATCAG GTCTGGGAGC TACARATT CATTTTCTC CTCACTGCC TTCTTCTGA TGGCATTGGC 40 3960 4020 CTGRATCARG GRAAGCCAGG CCTTGTGGGC CCCCTTCTTT CGGCTTTCTG CTARAGCAAC 4080 ACCTCCAGCA GAGATTCCCT TAAGTGACTC CAGGTTTTCC ACCATCCTTC AGCGTGAATT 4140 AATTTTAAT CAGTTIGCTT TCTCCAGAGA AATTTTAAAA TAATAGAAGA AATAGAAATT 4200 45 TTGAATGTAT AAAAGAAAAA GATCAAGTTG TCATTTTAGA ACAGAGGGAA CTTTGGGAGA 4260 AAGCAGCCCA AGTAGGTTAT TIGTACAGTC AGAGGGCAAC AGGAAGATGC AGGCCTICAA 4320 CONCREGOR ACCOUNTING CARTATIONS REGISTERAL SCREENING CONCRETE CONC 4380 CONTINUE ASCENDAR GARTAIGG TO THE THE THE CONTINUE CONTINUE CANTIGORAL TECCHITTER GEOGRAPHS GARTAGERA ACCITITICE TATOSCIPAC CITATIOS GISAGANATO 4500 50 GYCCGGTCNG GGAYCNGCCA ACCTCTTCTC TATGGTCNC CTRATTINGA GYMANGANT. AMGGRAGACHG AGCTNACTGC TATGATGGTCT TAGAGGGATTG AGCGGATGA GCCTGACTG GYTGTGCAGA ACLANCAAGG CATTCAYGGG AATTGTTGTA TACCTTCTGC AGCCCTCCTT CTGGGCACTA AGAAGGTCTA TGAATTAAAT GCCTATCTAA AATTCTGATT TATTCCTACA TTTTCTGTTT TCTAATTTGA CCCTAAAATC TATGGTTTT AGACTTAGAC TYTTTATTGC 4560 4620 4600 4740 CCCCCCCCC TTTTTTTTT AGACGGAGTC TCGCTCTGAC GCACAGGCTG GAGTGCAGTG 55 GCTCCGATCT CTGCTCACTG AAAGCTCCGC CTCCCGGGTT CATGCCATTC TCCTGCCTCA 4860 GCCTCCTAG TAGCTGGGAC TACAGCGCC CACCACCAC CCCGCTAAT TTTTTGTATT
TTTAATAGAG AGGGGTTC ACTGTGTTAG CACGACTGG CTCGACTCC TGACCCTGA
ATCGGCGTGC CTGGGCCTC CAAAGTGTG GGATTACAGG CATGACCAC CGCTCCCGGC 4920 4980 5040 CITGITITICC GITTANAGIC GICTICITIT ANTGIANTCA TITTGANCAT GIGIGANAGI 60 TGATCATACG AATTGGATCA ATCTTGAAAT ACTCAACCAA AAGACAGTCG AGAAGCCAGG 5160 GGGAGAAAGA ACTCAGGGCA CAAAATATTG GTCTGAGAAT GGAATTCTCT GTAAGCCTAG 5220 5280 TIGGIGAAAT TIGGIGGT AACCAGAAGC CAGITITATC TAACGGCTAC TGAAACACCC ACTOTOTTTT OCTCACTCCC TCACTCACCG ATCAAAACCT GCTACCTCCC CAAGACTTTA 5340 CTAGTGCCGA TAAACTTTCT CAAAGAGCAA CCAGTATCAC TTCCCTGTTT ATAAAACCTC 5400 65 TAACCATCTC TTTGTTCTTT GAACATGCTG AAAACCACCT GGTCTGCATG TATGCCCGAA 5460 TITGTAATIC TITTCTCTCA AATGAAAATT TAATTITAGG GATTCATTTC TATATTTTCA 5520 CATATGTAGT ATTATTATTT CCTTATATGT GTAAGGTGAA ATTTATGGTA TTTGAGTGTG 5500 CARGAAAATA TATTTTTAAA GCTTTCATTT TTCCCCCAGT GAATGATTTA GAATTTTTTA TOTABATATA CAGARGITT TITCTTACTI TEATARGRA GEAGGTGTCT ABARTGEAG GGGGTTGTT TIGCRATGIT TITABACAGAG TITTAGTATT GCTATTABAR GAAGTTACTI 70 5760 TGCTTTTAAA GAACTTGGC TGCTTAAAAT AAGCAAAAAT TGGATGCATA AAGTAATATT TACMGATGTG GGGGGATGTA ATAAAACAAT ATTAACTTGG TTTCTTGTT TTGCTGTATT 5820 5880 TAGAGATTAA ATAATTCTAA GATGATCACT TIGCAAAATT ATGCTTATGG CIGGCATGGA 5940 AATAGAAATA CTCAATTATG TCTTTGTTGT ATTAATGGGG AATATTTTGG ACAATGTTTC 6000 75 ATTATCAAAT TOTOGACATO ATTAATATAT ATTGTAATGT TOOGAAGAGA TCACTATTTT 6060 GAACCACAGC TITACAGATG AGRATCHATG ATACATATGH ATAATAAATT TIGATCGGGT ATTAAAAGTA TIAGAAGGTG GITATAATTG CAGAGTATTC CATGAATAGT ACACTGACAC 6120 6180 AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA 6240 GGCAATATTG CAGTCTTGAT TUTGCCAUTT ACAGGATAGA TAATGCCTGA ACTTTAATGA 6300 80 CAAGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG 6360 ACTOTOCICO OCIACARACO TERMINACIÓN TONTITOMA RATCIATRAS CTATATORAS ACCOTRACAT TITRATATAS GITAMACCA ANTITOCATI CONTRACTO TOTATOCIC TONTACOT TOTATOCIC TONTACOT TOTATOCIC TONTACOT TOTATOCIC TONTACAT. 6420 6480 6540 ACCEGATACA TITCACETET CETTCAGTAT TGATTTGGTT GAATATTGGG TCATAATGGT 6600 85 TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC 6660 TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTTCTCAT TAAAATCAAT 6720 GAACAATGCC AGCCTCATGG GGTTGTTGAA TGATTAAATT AGTTAATATA CCTAAAGTAC 6780

PCT/US02/12476

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5 Seq ID NO: 32 Protein sequence: Protein Accession #: NP_001932.1

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	TELLEVALCE	CTHPTCCRAT	SRSTGVILGK	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720
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Seq ID NO: 33 DNA sequence

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	Chanage Coac	ATTTCAAAAT	Caccacacac	ANAGRADOTE	ATCAMCCTOT	TOTTTOTOTT	1320
55	CENTRACOCKC	TGAATTATGA	AGRADACOGE	CARCINGTON	MOCA SATTOO	ACTABACAAT	1380
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	ATTEMPORE	TCATAAAGAA	TTGGGACTCA	CCCCTACTGC	ACTACCAAAT	TCATTTGACT	3300
	ATOL TOCKOC	*CUTUMONO	TIOUGHCICH	occurrence.			-500

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	GGAAATAAAT	GTGTGTGTGT	ATATTATTAT	TAATCAATGC	AATATTTAAA	ATGAAATGAG	3420
	BACBBBBBBB	AAAATGGTAA	ASSCRICTEDAS	TGAGGCTGGG	GTATAGITTIG	TCCTACAATA	3480
	CANADARACAC	ACACCTTCOS	ACCOUNTCOOR	TOTTABATOO	TOCATEATAA	CTGAGTCTAT	3540
5	andananana	MGMGCIICCI	MOGCCIOGGC	TOTTANATOC	TOCATINIA		3600
,	GAGGAAATAG	TTCCTGTCCA	ATTIGTGTAA	TITGTTTAAA	ATTGTAAATA	AATTAAACTT	
	TTCTGGTTTC	TGTGGGAAGG	AAATAGGGAA	TCCAATGGAA	CAGTAGCTTT	GCTTTGCAGT	3660
	CTGTTTCAAG	ATTTCTGCAT	CCACAAGTTA	GTAGCAAACT	GGGGAATACT	CGCTGCAGCT	3720
	GGGGTTCCCT	acrerrage.	AGCAAGGGTC	CAGAGATGAG	GTGTTTTTTT	CGGGGAGCTA	3780
	2020770007	Commerce	CHARLCCAMORY	CHICA ACTION A	AUCCOCCUANT	GCTGTTTCTA	3840
10	ATAACAAAAA	CATTITAOUN	CTTACCTTTA	CIGAAGITAA	ATCCICIATT	GCIGITICIA	
10	TTCTCTCTTA	TAGTGACCAA	CATCTTTTTA	ATTTAGATCC	AAATAACCAT	GTCCTCCTAG	3900
	AGTITAGAGG	CTAGAGGGAG	CTGAGGGGAG	GATCTTACTG	AAAGCACCCT	CCCCAGATTC	3960
	ACTOTOCOTTA	AACCTBAGCC	CCACAAACTT	CACACCICAT	CAGGTCTGGG	AGCTACAAAA	4020
	MI TOTCCTIA	OTTO OTTO	occommon on	CACHOOLONS	OCCCOCC AMC	AAGGAAAGCC	4080
	TITCATITIT	CICCICACIG	CCCTTCTTCT	GRGIGGCRII	OGCCIGANIC	MIGGRADIGCC	4140
1.5	AGGCCTTGTG	GGCCCCCTTC	TTTCGGCTTT	CIGCIAAAGC	ANCACCICCA	GCAGAGATTC	
15	CCTTAAGTGA	CTCCAGGTTT	TCCACCATCC	TTCAGCGTGA	ATTAATTTT	AATCAGTTTG	4200
	CTTTCTCCAG	AGAAATTTTA	AAATAATAGA	AGAAATAGAA	ATTTTGAATG	TATAAAAGAA	4260
	A B B C B TC B B C	THEOREM THEFT	BOX NOR CROSS	CHACTTWICK	AGRANGENCE	CCAAGTAGGT	4320
	MUNICHNO	TIGICATITI	AGRACIONOC	-act 0000	CARCOCCANO.	CACAGOOGAC	4380
	TATTIGTACA	GTCMGMGGGC	ANCHIGANIGA	TGCNGGCCTT	CAMOGGCAMG	GAGAGGCCAC	
	AAGGAATATG	GGTGGGAGTA	AAAGCAACAT	CGTCTGCTTC	ATACTTTTTC		4440
20	CACTGCCTTT	TCCTTTCTCA	GGCCAATGGC	AACTGCCATT	TGAGTCCCGT	GAGGGATCAG	4500
	OCA ACCORCOS	COCTATGGCT	CACCUTATUT	CCACTCACAA	ATCAMGGAGA	CAGAGCTGAC	4560
						AGAACAAACA	4620
	AGGCATTCAT	GGGAATTGTT	GTATTCCTTC	TOCAGCCCTC	CTTCTGGGCA		4680
	CTATGAATTA	AATGCCTATC	TARABITCTG	ATTTATTCCT	ACATTTTCTG	TTTTCTAATT	4740
25	TOROCCURAR	ATCTATOTOT	TTTAGACTTA	GACTTTTTAT	TRICCCCCCCCCC	CCCTTTTTTT	4800
	mmas as coas	ATOTACOTO:	Character Character	COCCACOCCA	OTCOCTOCO	TCTCTGCTCA	4860
	TIGHUNCOGA	0.01000.01	GACCICACOG	CIGGNOIGCN	GIGGCICCON	aram some	
						GAGTAGCTGG	4920
	GACTACAGGC	GCCCACCACC	ACGCCCGGCT	AATTTTTTGT	ATTTTTAATA	GAGACGGGGT	4980
	TTCACTGTGT	TAGCCAGGAT	GGTCTCGATC	TCCTGACCTC	GTGATCCGCC	TGCCTCGGCC	5040
30	magazzzana	ORGODONETO C	MOCCATORCO	Chococococ	COCCTTOTTT	TCCGTTTAAA	5100
50	1000001010	CIGGGHIANC	Madentance	CACCOCICCO		10001111111	5160
	GTCGTCTTCT	TTTAATGTAA	TCATTTIGAA	CATGTGTGAA	AGTIGATOAT	ACGAATTGGA	
	TCAATCTTGA	AATACTCAAC	CAAAAGACAG	TCGAGAAGCC	AGGGGGAGAA	AGAACTCAGG	5220
	GCACAAAATA	TTGGTCTGAG	AATOGAATTC	TCTGTAAGCC	TAGTTGCTGA	AATTTCCTGC	5280
	TOTALOCAGA	AGCCAGTTTT	ATCTALOGGC	TACTGARACA	CCCACTGTGT	TTTGCTCACT	5340
35	OCCUPATION OF	0200222200	TOOTS COTOC	CONNENTE	ACTACHOOCG	ATAAACTTTC	5400
33	CCCMCTCMCC	CMICHOOLCC	TOCINCCICC	CCANONCITI	ACTAGIGCCO	ATACOCCI I TO	
	TCAAAGAGCA	ACCAGTATCA	CTTCCCTGTT	TATAAAACCT	CTAACCATCT	CTTTGTTCTT	5460
	TGAACATOCT	GAAAAOCACC	TGGTCTGCAT	GTATGCCCGA	ATTTGTAATT	CTTTTCTCTC	5520
	AAATGAAAAT	TTAATTTTAG	GGATTCATTT	CTATATTTTC	ACATATGTAG	TATTATTATT	5580
	macrona mana	more accords	AATTTATOOT	ATTTCACTOR	CCDAGAAAAT	ATATTTTTAA	5640
40	ICCIININIO	101NAGG1GA	7411141001	ALL LONG TOT	* COLDINATION	ACAGAATGTT	5700
40	AGCTTTCATT	TTTCCCCCAG	TGMATGATTT	AGAATITIT	VIGINWALVI	ACAGARIGII	
	TTTTCTTACT	TTTATAAGGA	AGCAGCTGTC	TAAAATGCAG	TGGGGTTTGT	TTTGCAATGT	5760
	TTTAAACAGA	GTTTTAGTAT	TGCTATTAAA	AGAAGTTACT	TTGCTTTTAA	AGAAACTTGG	5820
	CTGCTTABAA	TANGCARARA	TTGGATGCAT	AAAGTAATAT	TTACAGATGT	GGGGAGATGT	5880
	110000000000	ma mma a commo	COTTOCTORADA	ATTROCCADE	ATTYGGATGCA	TAAAGTAATA	5940
45	WINDOOKON	TATIMACTIC	GCIGCIIAAA	AIAAGCAAAA	ATTOORTOON	mmama anama	
43	TTTACAGATG	TGGGGAGATG	TAATAAAACA	ATATTAMCTT	GGTTTCTTGT	TTTTGCTGTA	6000
	TTTAGAGATT	AAATAATTCT	AAGATGATCA	CTTTGCAAAA	TTATGCTTAT	GGCTGGCATG	6060
	GAAATAGAAA	TACTCAATTA	TGTCTTTGTT	GTATTAATGG	GGAATATTTT	GGACAATGTT	6120
	CONTRACTOR A	APPOTOTACE	TOATOARTAT	A TATTOTA AT	GTTGGGAAGA	GATCACTATT	6180
	- CAL TALCON	AT TOTOGRAM		#4111017011	COLUMNIA	TTTTGATCOG	6240
50	TTGAAGCACA	GCTTTACAGA	TGMGTATCTA	TOATACATAT	GINIMAIAAA	TITIONICOG	
30	GTATTAAAAG	TATTAGAAGG	TGGTTATAAT				6300
					TOCATGAATA	GINCHCIGAC	
		TACTTTGAGG	ACCAGTGTAG	TCAAGGGAAA	ACATGAGTTA	AAAAGAAAAG	6360
	CAGGCAATAT	TACTTTGAGG	ACCAGTGTAG	TCAAGGGAAA	ACATGAGTTA	AAAAGAAAAG	6360 6420
	CAGGCAATAT	TGCAGTCTTG	ACCAGTGTAG ATTCTGCCAC	TCAAGGGAAA TTACAGGATA	ACATGAGTTA GATAATGCCT	GAACTTTAAT	6420
	CAGGCAATAT GACAAGATGA	TGCAGTCTTG	ACCAGTGTAG ATTCTGCCAC AAGGTGCTCT	TCAAGGAAA TTACAGGATA GTGCTTCACA	ACATGAGTTA GATAATGCCT GTGAATCTTT	AAAAGAAAAG GAACTTTAAT TCCCCATGCA	6420 6480
	CAGGCAATAT GACAAGATGA GGAGTGTGCT	TGCAGTCTTG TCCAACCATA CCCCTACAAA	ACCAGTGTAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT	TCAAGGAAA TTACAGGATA GTGCTTCACA GATCATTTCA	ACATGAGTTA GATAATGCCT GTGAATCTTT AAAATCTATT	AAAGAAAAG GAACTTTAAT TCCCCATGCA AGCTATATCA	6420 6480 6540
55	CAGGCAATAT GACAAGATGA GGAGTGTGCT AAAGCCTTAC	TGCAGCCATA CCCCTACAAA ATTTTAATAT	ACCAGTGTAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT AGGTTGAACC	TCAAGGGAAA TTACAGGATA GTGCTTCACA GATCATTTCA AAAATTTCAA	ACATGAGTTA GATAATGCCT GTGAATCTTT AAAATCTATT TTCCAGTAAC	AAAGAAAG GAACTTTAAT TCCCCATGCA AGCTATATCA TTCTATTGTA	6420 6480 6540 6600
55	CAGGCAATAT GACAAGATGA GGAGTGTGCT AAAGCCTTAC	TGCAGCCATA CCCCTACAAA ATTTTAATAT	ACCAGTGTAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT AGGTTGAACC	TCAAGGGAAA TTACAGGATA GTGCTTCACA GATCATTTCA AAAATTTCAA	ACATGAGTTA GATAATGCCT GTGAATCTTT AAAATCTATT TTCCAGTAAC	AAAGAAAG GAACTTTAAT TCCCCATGCA AGCTATATCA TTCTATTGTA	6420 6480 6540 6600
55	CAGGCAATAT GACAAGATGA GGAGTGTGCT AAAGCCTTAC ACCATTATTT	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTTTAATAT TTGTGTATGT	ACCAGTGTAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAAT	TCAAGGAAA TTACAGGATA GTGCTTCACA GATCATTTCA AAAATTTCAA GTTCATTGGA	ACATGAGTTA GATAATGCCT GTGAATCTTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG	AAAGAAAG GAACTTTAAT TCCCCATGCA AGCTATATCA TTCTATTGTA TAATAGTAAA	6420 6480 6540 6600 6660
55	CAGGCAATAT GACAAGATGA GGAGTGTGCT AAAGCCTTAC ACCATTATTT ATACCGGATA	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTTTAATAT TTGTGTATGT CATTTCACGT	ACCAGTGTAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAAT GTCCTTCAGT	TCAAGGAAA TTACAGGATA GTGCTTCACA GATCATTTCA AAAATTTCAA GTTCATTGGA ATTGATTTGG	ACATGAGTTA GATAATGCCT GTGAATCTTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG	AAAAGAAAAG GAACTTTAAT TCCCCATGCA AGCTATATCA TTCTATTGTA TAATAGTAAA GGTCATAATG	6420 6480 6540 6600 6660 6720
55	CAGGCAATAT GACAAGATGA GGAGTGTGCT AAAGCCTTAC ACCATTATTT ATACCGGATA GTTGAGAAGC	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTTTAATAT TTGTGTATGT CATTTCACGT ATGGACACTA	ACCAGTGTAG ATTCTGCAC AAGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT	TCAAGGAAA TTACAGGATA GTGCTTCACA GATCATTTCA AAAATTTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT	ACATGAGTTA GATAATGCT GTGAATCTTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA	AAAAGAAAAG GAACITTAAT TCCOCATGCA AGCTATATCA TTCTATTGTA TAATAAGTAAA GGTCATAATG TCTGTCACIT	6420 6480 6540 6600 6660 6720 6780
	CAGGCAATAT GACAAGATGA GGAGTOTGCT AAAGCCTTAC ACCATTATTT ATACOGGATA GTTGAGAAGC ACTTCTGTGT	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTTTAATAT TTGTGTATGT CATTTCACGT ATGGGCACTA GACCTTTGAA	ACCAGTGTAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT AGGTTGAAGC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT AGGCTACTTA	TCAAGGAAA TTACAGGATA GTGCTTCACA GATCATTCA AAAATTTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT	ACATGAGTTA GATAATGCCT GTGAATCTTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCTC	AAAAGAAAAG GAACITTAAT TCCCCATGCA AGCTATATCA TTCTATTGTA TAATAGTAAA GGTCATAATG TCTGTCACIT ATTAAAATCA	6420 6480 6540 6600 6660 6720 6780 6840
	CAGGCAATAT GACAAGATGA GGAGTOTGCT AAAGCCTTAC ACCATTATTT ATACOGGATA GTTGAGAAGC ACTTCTGTGT	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTTTAATAT TTGTGTATGT CATTTCACGT ATGGGCACTA GACCTTTGAA	ACCAGTGTAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT AGGTTGAAGC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT AGGCTACTTA	TCAAGGAAA TTACAGGATA GTGCTTCACA GATCATTCA AAAATTTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT	ACATGAGTTA GATAATGCCT GTGAATCTTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCTC	AAAAGAAAAG GAACITTAAT TCCCCATGCA AGCTATATCA TTCTATTGTA TAATAGTAAA GGTCATAATG TCTGTCACIT ATTAAAATCA	6420 6480 6540 6600 6660 6720 6780
55 60	CRGCAATRT GACAAGATGA GGACTGTCCT AAAGCCTTAC ACCATTATTT ATACOGGATA GTTGAGAAGC ACTTCTGTGT ATGACAATG	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTTTAATAT TTGTGTATGT CATTTCACGT ATOGACACTA GACCTTTGAA CCAGCCTCAT	ACCAGTGTAG ATTCTGCAC AAGGTGCTCT COTTAAGACT AGGTTGAACC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT AGGCTACTTA GGGGTTGTTG	TCAAGGAAA TTACAGATA GTGCTTCACA GATCATTCA AAAATTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT AATGATTAAA	ACATGAGTTA GATAATGCCT GTGAATCTTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGG AAGCTTCTC TAGGTTAATA	ANAGANAG GAACTTAAT TCCCCATGCA AGCTATATCA TCTATTOTA TAATAGTAAA GGTCATAATG TCTGTCACTT ACTAAAATCA TACCAAAAGT	6420 6480 6540 6600 6660 6720 6780 6840 6900
	CRGGCAATRT GACARGATGA GGAGTGTGCT AAAGCCTTAC ACCATTATTT ATACOGGATA GTTGAGAAGC ACTTCTGTGT ATGAACAATG ACATAGAACA	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTITAATAT TTGTGTATGT CATTICACGT ATGGACACTA GACCTTTGAA CCAGCCTCGAT CCAGCCTCGAT	ACCAGTGTAG ATTCTGCCAC AAGGTGCTCT COTTAAGACT AGGTTGAACC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT AGGCTACTTA AGGGGTGTTG ATAGTAAAAG	TCAAGGAAA TTACAGGATA GTGCTTCAC GATCATTCA AAAATTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT AATGATTAAA AATTATAAGT	ACATGAGTTA GATANTGCT GTGAATCTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCT TTAGTTAATA GTGAGGTAGT	ANAGANAG GAACTITAAT TCCCCATGCA AGCTATATCA TCTATTGTA TAATAGTAAA GGTCATAATG TCTGTCACTT ATTAANATCA TACCTAAAGT TOGTAAAATT	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960
	CRGGCAATRT GACARGATGA GGAGTGTGCT AAAGCCTTAC ACCATTATTT ATACOGGATA GTTGAGAAGAC ACTTCTGTGT ACGACAAC ACTAGAACAA ACTAGAACA ATGTAGATGA ATGTAGATGA	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTTTAATAT TTGTGTATGT CATTTCACGT ATGGACACTA GACCTTGAA CCAGCCTCAT CTGCCTGCAC ATATACTACC	ACCAGTGTAG ATTCTGCAC ARGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT AGGCTACTTA GGGGTTGTTG GAGCTAAAAG GAACAATATC	TCAAGGAAA TTACAGGATA GTGCTTCAC GATCATTCA AAAATTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT AATGATTAAA AATTATAAGT	ACATGAGTTA GATANTGCT GTGAATCTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCT TTAGTTAATA GTGAGGTAGT	ANAGANAG GAACTTAAT TCCCCATGCA AGCTATATCA TCTATTOTA TAATAGTAAA GGTCATAATG TCTGTCACTT ACTAAAATCA TACCAAAAGT	6420 6480 6540 6600 6660 6720 6780 6840 6900
	CRGGCAATRT GACARGATGA GGAGTGTGCT AAAGCCTTAC ACCATTATTT ATACOGGATA GTTGAGAAGAC ACTTCTGTGT ACGACAAC ACTAGAACAA ACTAGAACA ATGTAGATGA ATGTAGATGA	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTITAATAT TTGTGTATGT CATTICACGT ATGGACACTA GACCTTTGAA CCAGCCTCGAT CCAGCCTCGAT	ACCAGTGTAG ATTCTGCAC ARGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT AGGCTACTTA GGGGTTGTTG GAGCTAAAAG GAACAATATC	TCAAGGAAA TTACAGGATA GTGCTTCAC GATCATTCA AAAATTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT AATGATTAAA AATTATAAGT	ACATGAGTTA GATANTGCT GTGAATCTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCT TTAGTTAATA GTGAGGTAGT	ANAGANAG GAACTITAAT TCCCCATGCA AGCTATATCA TCTATTGTA TAATAGTAAA GGTCATAATG TCTGTCACTT ATTAANATCA TACCTAAAGT TOGTAAAATT	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960
60	CRGGCAATRT GACARGATGA GGAGTGTGCT AAAGCCTTAC ACCATTATTT ATACOGGATA GTTGAGAAGAC ACTTCTGTGT ACGACAAC ACTAGAACAA ACTAGAACA ATGTAGATGA ATGTAGATGA	TGCAGTCTTG TCCAACCATA CCCCTACAAA ATTTTAATAT TTGTGTATGT CATTTCACGT ATGGACACTA GACCTTGAA CCAGCCTCAT CTGCCTGCAC ATATACTACC	ACCAGTGTAG ATTCTGCAC ARGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT AGGCTACTTA GGGGTTGTTG GAGCTAAAAG GAACAATATC	TCAAGGAAA TTACAGGATA GTGCTTCAC GATCATTCA AAAATTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT AATGATTAAA AATTATAAGT	ACATGAGTTA GATANTGCT GTGAATCTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCT TTAGTTAATA GTGAGGTAGT	ANAGANAG GAACTITAAT TCCCCATGCA AGCTATATCA TCTATTGTA TAATAGTAAA GGTCATAATG TCTGTCACTT ATTAANATCA TACCTAAAGT TOGTAAAATT	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960
60	CAGGCAATAT GACAAGATGA GGAGTGTGCT AAAGCCTTACT ATACTATTAT GTTGAGAAGC ACTTCTGTGT ATGAACAATG ACATAGAACA ATGTAGATGA CATAGAACA ATGTAGATGA CATAGAACA	TGCASTCTTG TCCAACCATA CCCTACAAA ATTTAATAT TTGTGTATGT TATGGACTA ATGGACACTA GACCTTTGAA CCAGCCTCAT CTGCCTGCAC ATACATACCAAAAC	ACCACTOTAG ATTCTGCCAC AGGTGCTCT COTTANGACT MOTTGAACC CTTCAAGRAT GAGCCAGAAT AGGCTACTTCA AGGCTACTTCA ATGCTACTTCATCA ATGCTAATAAAC GAGCTATTTCATCATCATCATCATCATCATCATCATCATCATC	TCAAGGAAA TTACAGGATA GTGCTTCAC GATCATTCA AAAATTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT AATGATTAAA AATTATAAGT	ACATGAGTTA GATANTGCT GTGAATCTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCT TTAGTTAATA GTGAGGTAGT	ANAGANAG GAACTITAAT TCCCCATGCA AGCTATATCA TCTATTGTA TAATAGTAAA GGTCATAATG TCTGTCACTT ATTAANATCA TACCTAAAGT TOGTAAAATT	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960
	CREGCATAT GACARGATGA GGAGTOTOCT AAAGCCTTAC ACACTTATT ATACCOGATA GTTGAGAAGA ACTTCTGTGT ATGAACAATA ACATGAACA ATGTAGTTGG CATATATATA Seq ID NO:	TGCAGCATTG TCCAGCATA ATTTTATAT TTGTGTATG CATTCAGGT GACCITTGA GCCTTTGA CCAGCTCAT GCGCTGCAC ATATACTACC ATCCCGAAAC 34 Protein	ACCAGTATAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAT GCCCAGAAT AGGCTACTTA GGGCTACTTA GGGCTACTTA GAACAATATC ATG Sequence:	TCAAGGAAA TTACAGGATA GTGCTTCAC GATCATTCA AAAATTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT AATGATTAAA AATTATAAGT	ACATGAGTTA GATANTGCT GTGAATCTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCT TTAGTTAATA GTGAGGTAGT	ANAGANAG GAACTITAAT TCCCCATGCA AGCTATATCA TCTATTGTA TAATAGTAAA GGTCATAATG TCTGTCACTT ATTAANATCA TACCTAAAGT TOGTAAAATT	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960
60	CREGCATAT GACARGATGA GGAGTOTOCT AAAGCCTTAC ACACTTATT ATACCOGATA GTTGAGAAGA ACTTCTGTGT ATGAACAATA ACATGAACA ATGTAGTTGG CATATATATA Seq ID NO:	TGCASTCTTG TCCAACCATA CCCTACAAA ATTTAATAT TTGTGTATGT TATGGACTA ATGGACACTA GACCTTTGAA CCAGCCTCAT CTGCCTGCAC ATACATACCAAAAC	ACCAGTATAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAT GCCCAGAAT AGGCTACTTA GGGCTACTTA GGGCTACTTA GAACAATATC ATG Sequence:	TCAAGGAAA TTACAGGATA GTGCTTCAC GATCATTCA AAAATTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT AATGATTAAA AATTATAAGT	ACATGAGTTA GATANTGCT GTGAATCTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCT TTAGTTAATA GTGAGGTAGT	ANAGANAG GAACTITAAT TCCCCATGCA AGCTATATCA TCTATTGTA TAATAGTAAA GGTCATAATG TCTGTCACTT ATTAANATCA TACCTAAAGT TOGTAAAATT	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960
60	CAGGCAATA GACAGATGA GGAGTGTOCT AAAGCCTTAC ACCATTATTT ATACCCCATA ATTGAGAAGA CATTGTGT ATGAACAATA ACCATGAGACA ACGATGAGACA ACGTGTGG CATATATATA Seq ID NO: Protein Acc	TGCAGTOTTE TGCAGCATA CCCTACAAA ATTITAATAT TTGGGTATG ATGGAGATG ACGTGAG GACCTTGAA CCAGCTCAT CTGCCTGCAC ATCCCGAAAC ATCCCGAAAC ATCCCGAAAC 34 Protein cession #:]	ACCAGTATAG ATTCTGCAC AAGGTGCTCT COTTAAGAC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT AGGCTACTTA GGGCTACTTA GGGCTACTTA GGGCTACTTA GGACCAGAAT ATAGTAAAAG GAACAATATC ATG SEQUENCE: NP_077741.1	TCAAGGAAA TTACAGGATA GTGCTCACA GATCATTCAA AAAATTCACA GTTCATTGGA ATTGATTGGA GTTCATTGGA TTTCCTCTCT AATGATTAG AATTGATTAG AATTGATTAG TTCCTCTCT AATGATTAAGT TAATCTCTTT	ACATGAGTTA GCTGATGATTA GTGATATGCTT ANANTCTATT TTCCAGTAAC TTTTGTTGC TTGATATCTGT TGAATATTGC TAGGTTACT TAGGTTATATA GTGAGGTAGT TTAGGGAAAT TTAGGGAAAT TTAGGGAAAT	ANAMGARAGE GAACITHAT TCOCATGCA AGCTATATCA TCOTATOTA TAATAGTAAA GGTCATAATC TCTGTCACTT ACTAAATCA ACTAAAATCA TACCTAAAGT TOGTAAAATT AAAGTTTOTO	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960
60	CREGCATAT GACARGATGA GGAGTOTOCT AAAGCCTTAC ACACTTATT ATACCOGATA GTTGAGAAGA ACTTCTGTGT ATGAACAATA ACATGAACA ATGTAGTTGG CATATATATA Seq ID NO:	TGCAGCATTG TCCAGCATA ATTTTATAT TTGTGTATG CATTCAGGT GACCITTGA GCCTTTGA CCAGCTCAT GCGCTGCAC ATATACTACC ATCCCGAAAC 34 Protein	ACCAGTATAG ATTCTGCCAC AAGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAT GCCCAGAAT AGGCTACTTA GGGCTACTTA GGGCTACTTA GAACAATATC ATG Sequence:	TCAAGGAAA TTACAGGATA GTGCTTCAC GATCATTCA AAAATTCAA GTTCATTGGA ATTGATTTGG GCTTGGATAT TTTCCTCTCT AATGATTAAA AATTATAAGT	ACATGAGTTA GATANTGCT GTGAATCTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG TTGAATATTG GAATCCTGGA TAGCTTTCT TTAGTTAATA GTGAGGTAGT	ANAGANAG GAACTITAAT TCCCCATGCA AGCTATATCA TCTATTGTA TAATAGTAAA GGTCATAATG TCTGTCACTT ATTAANATCA TACCTAAAGT TOGTAAAATT	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960
60 65	CAGGCAATA GACAGATGA GGAGTGTOCT AAAGCCTTAC ACCATTATTT ATACCCCATA ATTGAGAAGA CATTGTGT ATGAACAATA ACCATGAGACA ACGATGAGACA ACGTGTGG CATATATATA Seq ID NO: Protein Acc	TGCAGTOTTE TGCAGCATA CCCTACAAA ATTITAATAT TTGGGTATG ATGGAGATG ACGTGAG GACCTTGAA CCAGCTCAT CTGCCTGCAC ATCCCGAAAC ATCCCGAAAC ATCCCGAAAC 34 Protein cession #:]	ACCAGTATAG ATTCTGCAC AAGGTGCTCT COTTAAGAC CTTCAAGAAT GTCCTTCAGT GAGCCAGAAT AGGCTACTTA GGGCTACTTA GGGCTACTTA GGGCTACTTA GGACCAGAAT ATAGTAAAAG GAACAATATC ATG SEQUENCE: NP_077741.1	TCAAGGAAA TTACAGGATA GTGCTCACA GATCATTCAA AAAATTCACA GTTCATTGGA ATTGATTGGA GTTCATTGGA TTTCCTCTCT AATGATTAG AATTGATTAG AATTGATTAG TTCCTCTCT AATGATTAAGT TAATCTCTTT	ACATGAGTTA GCTGATGATTA GTGATATGCTT ANANTCTATT TTCCAGTAAC TTTTGTTGC TTGATATCTGT TGAATATTGC TAGGTTACT TAGGTTATATA GTGAGGTAGT TTAGGGAAAT TTAGGGAAAT TTAGGGAAAT	ANAMGARAGE GAACITHAT TCOCATGCA AGCTATATCA TCOTATOTA TAATAGTAAA GGTCATAATC TCTGTCACTT ACTAAATCA ACTAAAATCA TACCTAAAGT TOGTAAAATT AAAGTTTOTO	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960
60 65	CAGGCAATATA GACAAGATATA GGAGTGTOCT AAAGCCTTAC ACCATTATTT ATACOGGATA GTGAGAAGA ACTTCTGTGT ATGAACAATA ACATTAGTTAGAACAA ACATTAGTTAGAACAATA ACATTAGTTGG CATATATATA Seq ID NO: Protein Acc	TGCAGTOTTE TGCAACCATA CCCCTACAAA ATTITAATAT TTGGGTATOT CATTCACOT ATOGACACTA ATOGACACTA CCAGCOTCAT CTGCCTGCAC ATATACTACC ATATACTACC ATCCCGAAAC ATATACTACC ATCCCGAAAC ATCCCGAAAC ATCCCGAAAC ATCCCGAAAC ATCCCGAAAC	ACCAGTATIAG ATTOTGCCA AAGGTGCTCT CGTTAAGACT AGGTTGAACC CTTCAAGAAT GTCCTTCAAG GAGCAGAAT AGGCTACTTA AGGCTACTTA ATAGTAAAAG GAACAATATC ATG Sequence: P_077741.1	TCAAGGAAA TTACAGATA TTACAGATA TTACAGATA GATCATTCA GATCATTCA GTTCATTGA ATTGATTCA ATTGATTCA ATTGATTCA AATTATAAGT TAATCATTTAA	ACATGAGTTA GATAATOCT GTGAATCTTT AAAATCTATT TTCCAGTAAC TTTTGTTTG GATCCTGGA TAGCTTCC TTAGTTAATA GTGAGGTAGT TTAGTTAATA GTGAGGTAGT TTAGGTAGT	ANAMGARAGE GAACHTHAN TCCCCATGCA ACCCATGCA ACCCATGCA TCCTATTGTA TAATAGTARA GGTCATAATG TCTGATCACTT ACTGAACTT ACTGAACTT ACCTAAAGT TGGTAAATT TGGTAAATT AAAGTTTGTG	6420 6480 6540 6600 6600 6720 6780 6840 6900 6900 7020
60	CAGGCARTAT GACARGATGA GGAGTGTGCT AAAGCCTTAC ACCATTATT ATACCGGATA ATGTGAGAMG ACTTAGTGT ATGACAACA ATGTAGTTAGTTAG CATATATTATTAGTAGTAGT ACTATAGTTAGTTGG CATATATATA Seq ID NO: Protein Acc	TGCAGCTTTE TGCAACCATA CCCTACAAA ATTITATAT TTGTGTATGT CATTICAGTT ATGGACACTA GACCTTTGAA CCAGCCTCTGA CTGCCTGCAC ATCACCTACC ATCCCTACCTA	ACCAGTATIAG ATTCTGCCAC AAGGTGCTCT CGTTTAAGACT CTCTAAGAAT GTCCTTCAAGAAT AGGCTACTTA AGGCTACTTA AGGCTACTTA AGGACTACTTA ATAGTAAAAA GAACAATATC ATG Sequence: NP_077741.1 21 TUNIFSRDGE	TCAAGGGAAA TTACAGGATA GTGCTTCACA GATCATTCCA AAAATTTCAA GTTCATTGGA ATTGATTGG CCTTGGATAT TTTCCTCTCT TTTCCTCTCT TATGATTAAAA AATTATAAGT TAATCTCTTT	ACATGAGTTA GATAATGCT GTGAATCTATT ARAATCTATT TTCCAGTAAC TTTTGTTTG GAATCCTGGA TAGGTTAATA GTGAGGTTAATA GTGAGGTAGT TTAGGTAATA GTGAGGTAGT	ANAGRARGE GAACTITANT TCCCCATGCA AGCHATACTA TCTATTGTA TATATAGTAAA TCTATAGTA ATTATAATCA ATTATAATCA ATTATAATCA TCTATCCACTT TCGTATAGT TCGTCCACTT TCGTAAAGT TCGTAAAAGT TCGTAAAAAGT TCGTAAAAAGT TCGTAAAAAAAAAA	6420 6480 6540 6600 6660 6720 6780 6840 6900 6960 7020
60 65	CMGGCATHT GACAAGATGA GGACTGTCT AAAGCCTTATT ATACCGGATA CTTGAGATA ACCATTATT ATACCGGATA ACTAGAACA ATGTAGTGG CATATATA Seq ID NO: Protein Acc 1 MAAAGGPRRSV ADLIRSSDPD	TGCAGCTATE TCCAACCATA CCCCTACAAA ATTITAATAT TTGTGTATOT CATTICACGT ATGGGATCAT GACCTTTGAA CCAGCTCAT CTGCCTGCAC ATATACTAC ATCCCGAAAC ATATACTAC ATCCCGAAAC 14 Protein	ACCAGTATIAG ATTOTGCCA AAGGTGCTCT COTTALAGACT AGGTTGAACA CTTCAAGAAT GAGCCAGAAT AGGCTACTTA GGGTTGTTG ATAGTAAAAA GGAACAATATC ATG SEQUENCE: SP_077741.1 21 LUIFSRDGE TARAVALSDK	TCAAGGAAA TTACAGGATA TTACAGATTCACA GATCATTTCA GATCATTTCA GTTCATTGGA ATTGATTGGA TTTTCCTCTTGGATAT TTTCCTCTCT AATGATTAAA AATTATAAGT TAATCTCTTT 31 ACKKVILNVP KRSFTINLSD	ACATGAGTTA GATAATOCT GTGAATCTTT AAAATCTATT TTCCAGTAAC TTTTTGTTTG GAATCCTGGA TAGCTTGCT TAGCTTAATA GTGAGGTAGT TTAGGTGAT TAGGTGGA TTAGGTGAT TAGGTGGAAT TAGGTGGA TAGGTGGA TAGGTGGA TAGGTGGA TAGGTGGA TAGGTGGA TAGGTGGA TAGGTGGA	ANAMGARAGG GAACITIANT TCCOCATGCA AGCIATATCA TCCTATCCTA TCTATTCTA TCTATTCTA ACTATACTA ACTATACAT ACTATACAT TCCTATACAT TCCTATACAT TCCTATACAT TCCTAAAGT VALGECFRE VVLLEBCKEVS	6420 6480 6540 6600 6660 6720 6720 6720 6720 6720 672
60 65	CMGCCATTAT GACARGATGA GGACTGTOCT AARGCCTTAC ACCATTATT ATACCOGATA ATGACAATG ACGATAGTAGATG ACGATAGTAGATG ACGATAGATG ACGATAG	TGCAGCTTTE TGCAGCCATA CCCTACANA ATTITATAT TTOTGTATOT CATTICACT TATOGCACTA GACCTITGAA CCAGCCTCAC ATATACTACC ATCCCAANAC 34 Protein Dession #: 1	ACCAGTATIAG ATTOTOCCA AAGOTGCTCT COTTANAGAT AGGTTGAACC CTTCAAGGAT GAGCCAGAAT AGGCTACTTA GGGTTGTATA GAGCTACTTA GGGTTGTATA GAGCAACATATA ATG PP_077741.1 21 TLVIFSRDGE TARAVALSDK PCSMOESSLG PCSMOESSLG PCSMOESSLG PCSTATTACCAAGAT TCATTACAAGAT TATATATAAAAAAAAAA	TCAAGGAAA TTACAGGATA GTGCTTCACA GATCATTCAA GATCATTCAA GTTCATTCGA GTTCATTCGA GTTCATTCGA TTTTCCTCTTCAATGATTAAA AATTTTAAA AATTTTAAA AATTTTAAA AATTTTAAA AATTTTTCATTTT 31 ACKKVILNVP KRSFTINLSD	ACATGAGTTA GATAATGCT GTGAATCTT TAAAATCTATT TTCCAGTAAC TTTTGATTATC GAATCCTGGA TAGGTTTCTC TTAGTTAATG GTGAGGTGAT TTAGGGAAAT TTAGGGAAAT TTAGGGAAAT GTGAGGTGAT TTAGGGAAAT	ANAGRARGE GAACTITANT TCCOCATGCA GACGATTATCA TCCTATTGTA TAATAGTAAA TCATATGTA TAATAGTAAA TCTGTCACTT TCGTCAAATT TCGTAAAATT TAAAGTTTGTG 51 RVNLBECFRS VLLEBCKVS VLSEGKVDK VSISGROVDK	6420 6480 6540 6600 6660 6720 6840 6900 6900 7020
60 65	CMGCCATTAT GACARGATGA GGACTGTOCT AARGCCTTAC ACCATTATT ATACCOGATA ATGACAATG ACGATAGTAGATG ACGATAGTAGATG ACGATAGATG ACGATAG	TGCAGCTTTE TGCAGCCATA CCCTACANA ATTITATAT TTOTGTATOT CATTICACT TATOGCACTA GACCTITGAA CCAGCCTCAC ATATACTACC ATCCCAANAC 34 Protein Dession #: 1	ACCAGTATIAG ATTOTOCCA AAGOTGCTCT COTTANAGAT AGGTTGAACC CTTCAAGGAT GAGCCAGAAT AGGCTACTTA GGGTTGTATA GAGCTACTTA GGGTTGTATA GAGCAACATATA ATG PP_077741.1 21 TLVIFSRDGE TARAVALSDK PCSMOESSLG PCSMOESSLG PCSMOESSLG PCSTATTACCAAGAT TCATTACAAGAT TATATATAAAAAAAAAA	TCAAGGAAA TTACAGGATA GTGCTTCACA GATCATTCAA GATCATTCAA GTTCATTCGA GTTCATTCGA GTTCATTCGA TTTTCCTCTTCAATGATTAAA AATTTTAAA AATTTTAAA AATTTTAAA AATTTTAAA AATTTTTCATTTT 31 ACKKVILNVP KRSFTINLSD	ACATGAGTTA GATAATGCT GTGAATCTT TAAAATCTATT TTCCAGTAAC TTTTGATTATC GAATCCTGGA TAGGTTTCTC TTAGTTAATG GTGAGGTGAT TTAGGGAAAT TTAGGGAAAT TTAGGGAAAT GTGAGGTGAT TTAGGGAAAT	ANAGRARGE GAACTITANT TCCOCATGCA GACGATTATCA TCCTATTGTA TAATAGTAAA TCATATGTA TAATAGTAAA TCTGTCACTT TCGTCAAATT TCGTAAAATT TAAAGTTTGTG 51 RVNLBECFRS VLLEBCKVS VLSEGKVDK VSISGROVDK	6420 6480 6540 6600 6660 6720 6720 6720 6720 6720 672
60 65	CMGCCATTAT GACAGAGAGA GACAGAGAGA GACATTATT ATACOGGAGA CATTATTT ATACOGGAGA CATTATTATA ATGAACAATA ACGATGAGACA ATGTAGTGG CATATATATA Seq ID NO: Protein Acc 1 MAAAGGPRSV MAAAGGPRSV ADLIRSSDPD KTRHTRETVIE	TGCAGTOTTE TCCAACCATA CCCOTACAAA ATTITAACAT TTGIGTATOT CATTICACGT TATGIGTATOT CAGCTICAA CCAGCCTCAA CCAGCCTCAC ATCCCGAAAC ATCCCGAAAC ATCCCGAAAC ATCCCGAAAC TGCGTACA TCCCGAAAC TGCGTACA TCCCGAAAC TCCCGAACCACAC TCCCGAACCACACACACACACACACACACACACACACACA	ACCAGTATMA ATTCTGCCAC AMGGTGCTCT AMGGTGCTCT AMGGTTGAACC CTTCAAGAT GTCCTCAGT GACCCAGAT AGGCTACTA AGGCTACTA AGGCTACTA AGGCTACTA AGGCTACTA AGGCTACTA CACCAGAT ATG Sequence: IP_077741.1 21 ILVIFSRDGE TARAVALSDK PCSMGENSIG PCMGENSIG	TCAAGGGAAA TTACAGGAAA GTGCTTCACA GATCATTCAA GATCATTCAA GTTCATTGA GCTTCGATTGA CCTTCGATTTGA AATATTACAT TTTCCTCTCT AATGATTGA AATGATTGA AATGATTAAGT TAATCTCTTT 31	ACATGAGTTA GATAATOCT GTGAATCTT TAAAATCTATT TTCCAGTAAC GAATCCTGT TTTTGTTATC TTGAATATTG GAATCTGT TTAGTTAAT GTGAGGTAGT TTAGGGAAAT GTGAGGTAGT TTAGGGAAAT	ANAGRARGE GAGCITTANT TCCCCATGCA AGCIATATCA TCCTATCAT TCTATCAT TANTACTAT ACTATACT ACTATACT ACTATACAT TCCTAAAGT TCGTAAAGT VALGECFRS VLLEEGKEVS YSISGROVDE KIVEDERDEN	6420 6480 6540 6600 6660 6720 6780 6840 6900 7020
60 65	CMGGCARTAT GACARGATGA GGAGTATGAT AAGGCGTTAC ACCATTATT ATACCGGAT ATTACACGAT ACTAGACAAT ACTAGACAAT ACTAGAACAAT ACTAGAACAAT ACTAGAACAAT Seq ID NO:	TGCAGTOTTE TCCAACCATA CCCOTACAAA ATTITAACAT TTGIGTATOT CATTICACGT TATGIGTATOT CAGCTICAA CCAGCCTCAA CCAGCCTCAC ATCCCGAAAC ATCCCGAAAC ATCCCGAAAC ATCCCGAAAC TGCGTACA TCCCGAAAC TGCGTACA TCCCGAAAC TCCCGAACCACAC TCCCGAACCACACACACACACACACACACACACACACACA	ACCAGTGTAG ACCAGTGTAG ATTCTGCCAC ANGUTGCTCC COTTLANGCT AGGTTGTAGACC CTTCAAGAAT GASCAGAAT ANGUTGTTTAG GASCAGAAT ATG SEQUENCE: SEQUENCE: LUIFSRDGE TARAVALSKK PCSMQERIPYP TUCVYCATBG TUCVYCATBG TUCVYCATBG	TCANGGANA TTACAGGANA GTGCTTCACA GATCATTCAA GATCATTCAA GTTCATTGAA ATTGATTGAA GTTCATTGAA ATTGATTGAA ATTGATTGAA ATTGATTGAA ATTGATTTAA ATTGATTTAA 31 ACKVILNUP KRSFTINLED PFPLETLOOV LIAVASTAXA DEPDTMETRIL	ACATGAGTTA GATAMICOCI GROANICTT AAAAACTATT TOCAGTAAC TITTIGTTO TIGAGTATO TIG	AAAAGAAAG GAACITTAAT TCCOCATGCA AGCIATATCA TCCTATOCTA TCTATOCTA TCTATATCA TCTATACAT ACTATACAT ACTATACAT TCTATCACT ACTATACAT TCATACAT TACCTAAAGT TOGTAAAATT AAAGTTTOTO 51 RVNILBECFRS VLLEBOKEVS LIVEDERDEN LIV	6420 6480 6540 6600 6660 6720 6840 6900 6900 7020

	1	11	21	31	41	51	
		1	1	1	1	1	
70	MAJAGPRRSV	RGAVCLHLLL	TLVIFSRDGE	ACKKVILNVP	SKLEADKIIC	RVNLBECFRS	60
		FRVLNDGSVY					120
		RRAKRRWAPI					180
	EPLNLFYIER	DIGNLECTRP	VDREEYDVFD	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
	PVFTEAIYNF	EVLESSRPGT	TVCVVCATDR	DEPOTMETRL	KYSILOQTPR	SPGLPSVHPS	300
75	TGVITTVSHY	LDREVVDKYS	LIMKVQDMDG	QPPGLIGTST	CIITVTDSND	NAPTPRONAY	360
		VEILRIPIED					420
	KPLNYEENRO	VNLEIGVNNE	APPARDIPRV	TALNRALVTV	HVRDLDEGPE	CTPAAQYVRI	480
	KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSIITS	KILDREVETP	540
		AIDKODRSCT					600
80		SLPNTSPEIS					660
	TKLLRVNLCE	CTHPTOCRAT	SRSTGVILGK	WAILAILLGI	ALLPSVLLTL	VCGVPGATKG	720
	KRFPEDLAGO	NLIISNTEAP	GDDRVCSANG	FMTQTTNNSS	QGFCGTMGSG	MKNGGQBTIB	780
	MIKGGNOTLE	SCRGAGHHHT	LDSCRGGHTE	VDNCRYTYSE	WHSPTOPRLG	EESIRGHTG	

Seq ID NO: 35 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 146-1273

PCT/US02/12476

	1	11	21	31	41	51	
		1	1		1	1	
-	GGGAGTGGGC	GTGGCGGTGC	TGCCCAGGTG	AGCCACCGCT	GCTTCTGCCC	AGACACGGTC	60
5	GCCTCCACAT	CCAGGTCTTT	GTGCTCCTCG	CTTGCCTGTT	CCTTTTCCAC	GCATTTTCCA	120
		GACTCCAGGC					180
	CGTTGATCTG	TTCAAACAAC	TATGTGAAAA	GGAGCCACTG	OGCAATOTOC	TCTTCTCTCC	240
	AATCTGTCTC	TCCACCTCTC	TGTCACTTGC	TCAAGTGGGT	GCTAAAGGTG	ACACTGCAAA	300
		CAGGTTCTTC					360
10	AGTAACATOG	GATGTAAACA	AACTTAGTTC	CTTTTACTCA	CTGARACTAR	TCAAGCGGCT	420
		AAATCTCTGA					480
		TTGGAAACTG					540
		ATTANGGATC					600
	CONCLUSION OF CO.	CAGACCAAAA	TOTTOTOTO	TA ATTACTION	TACTPROTEC	CCARCTCCAT	660
15		CCTGAATCAG					720
13		CAGATGATGA					780
		ATCATAGAGC					840
		GTGGAGGATG					900
		TCACAGTGGA					960
20							1020
20		TTTAAGGTGG					1020
	GCTGAAACAT	ATCTTCAGTG	AAGACACATC	TGATTTCTCT	GGAATGTCAG	AGACCAAGGG	
		TCAAATGTTA					1140
		GTGCCAGGAG					1200
0.5		TACATCATCA					1260
25	CTGTTCTCCT	TAAGTGGCAT	AGCCCATGTT	AAGTCCTCCC	TGACTTTTCT	GTGGATGCCG	1320
	ATTTCTGTAA	ACTOTOCATO	CAGAGATTCA	TTTTCTAGAT	ACAATAAATT	GCTAATGTTG	1380
	CTGGATCAGG	AAGCCGCCAG	TACTTGTCAT	ATGTAGCCTT	CACACAGATA	GACCTTTTTT	1440
	TTTTTCCAAT	TCTATCTTTT	GTTTCCTTTT	TTCCCATAAG	ACAATGACAT	ACGCTTTTAA	1500
	TGAAAAGGAA	TCACGTTAGA	GGAAAAATAT	TTATTCATTA	TTTGTCAAAT	TGTCCGGGGT	1560
30	AGTTGGCAGA	AATACAGTCT	TCCACAAAGA	AAATTCCTAT	AAGGAAGATT	TGGAAGCTCT	1620
	TOTTCOCAGO	ACTATGCTTT	CCTTCTTTGG	GATAGAGAAT	GTTCCAGACA	TTCTCGCTTC	1680
	CCTTGAAAGAC	TGAAGAAAGT	GTAGTGCATG	GGACCCACGA	AACTGCCCTG	GCTCCAGTGA	1740
	AACTTYGGCA	CATGCTCAGG	CTACTATAGG	TOCAGAAGTO	CTTATGTTAA	GCCCTGGCAG	1800
		ATTAAAATTC					1860
35	CTCTATCTTA	TAGAACTTCA	TOGATCAGAT	CTGGGGGGGGG	AACCTATAAA	TCAACACCTT	1920
55	ATTO MODERA	AACAAAATGT	ACT A TRANSPORT	CLCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ATACATAAAG	ACTRACTACC	1980
	COMMANDOCIOC	TCAAAATTTG	ADDACTALICA CONTRACTOR	COMPANDED	CONCERNO	AAACACTTCG	2040
	CCATANGGGG	TTTTCAGATT	CIGCCAMATO	COLUMN	CHACTINGON	CENCENCTICS	2100
	TICGCAGAGC	CCCCAAGAGG	GIGGALAIGIT	GGATANGGAN	TIMINGACCI	CIMOINGCIG	2160
40							2220
40		CTGGTCATGT					2220
		TCTCACAATA					
	TCTAATATGA	TAGOGGGAAA	AGGAGAGGAA	ACTACTGCCT	TTAGAAAATA	TANGTANAGT	2340
	GATTAAAGTG	CTCACGTTAC	CTTGACACAT	AGTTTTTCAG	TCTATGGGTT	TAGTTACTTT	2400
	AGATGGCAAG	CATGTAACTT	ATATTAATAG	TAATTTGTAA	AGTTGGGTGG	ATAAGCTATC	2460
45		GTTCATGGAT					2520
		TCTCCCATCT					2580
	AGATTCAATA	TTGAATTTCT	CCTATGCTAT	TGACAATAAA	ATATTATTGA	ACTACC	
	Sec ID NO:	36 Protein	sequence:				
50		cession #: 1					
	1	11	21	31	41	51	
	rî .	i.	ĩ	1	i	i-	
	MOREOTANCA	FAVDLFKQLC	PUPPI (MILL)	ODTOLOTOLO	LAGUGARGOT	AMETGOVERE	60
55	PERSONAL PROPERTY	QTVTSDVNKL	CODVOT VI TV	DI PUDVOI NI	OTDDTOOTED	DVAVDI DTVD	120
55	PHANTILLER.	QINNSIKDLT	DOLLORS IN	VOTANICODELLI	TUDIS TABLES	UMUVEDEDET	180
	PADADEETKG	DTKPVQMMNM	DOUGHTENTEN	MOANTALKID	DOMINIT OND	T.I. DANNIALDER	240
							300
		nseslsontn					
60		KGVALSNVIH	KVCLEITEDG	GUSIEVPGAR	TPOHKDEIWY	DHFFITIRH	360
60	NKTRNIIFFG	KPCSP					

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_0168583
Coding sequence: 72-842

	1	11	21	31	41	51 	
70	TAAGAGCAAA	AGAGAGAGGA GATGTTTCAA GTTTGGAGGC	ACTGGGGGCC	TCATTGTCTT	CTACGGGCTG	TTAGCCCAGA	120 180
	ATCCAGCCCT	GCCCTTGAGT GTCTGGGGGC	CCCACAGGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
75	TGAAGCCTGG	AGGAGGTACT TGGCCTGAAC	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGA	AAAGTGACGT	360 420
, ,	AACTTGGCCT	TGTGCAGAGC AGTGAATACG	CCTGATGGCC	ACCGTCTCTA	TGTCACCATC	CCTCTCGGCA	480 540
	TGGACATCAC	TGCAGAAATC CACCCATTCC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGGTCC	600 660
80	CCCTCCCCAT	TCAAGGTCTT	CTGGACAGCC	TCACAGGGAT	CTTGAATAAA	GTCCTGCCTG	720 780
	CCCTGGTGCA	TGACATTGTT	AACATGCTGA	TCCACGGACT	ACAGTTTGTC	ATCAAGGTCT	840 900
85	GCCCATGTGC	TGGAAGATGA CGTGTGTAAC	CACAGTTGCC	TTCTCTCCGA	GGAACCTGCC	CCCTCTCCTT	960 1020
	AAAAAAAAA	АЛЛАЛЛАЛА	АЛЛЛАЛАЛ				

WO 02/086443

Seg ID NO: 38 Protein seguence: Protein Accession #: NP 057667

5 NPQTGGLIVF YGLLAQINAQ FGGLFVPLDQ TLPLNVNFAL PLSFTGLAGS LTNALSHGLL SGGLAGILEN LPLIDILERG GGTSGGLLGG LLGKVTSVIP GLMNIIDIKV TDPQLLELGL 120 VOSPEGHRLY VTIPLGIKLQ VNTPLVGASL LRLAVKLDIT ABILAVRDKQ BRIHLVLGDC 180 THEFGSLQIS LLDGLGFLFI QGLLDSLTGI LMKVLFELVQ GNVCPLVNEV LRGLDITLVH 240 10

Seq ID NO: 39 DNA sequence Nucleic Acid Accession \$: NM_004363.1

15 Coding sequence: 115-2223 21 31 41 CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT TCCTGGAACT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACATGGAG 20 120 TOTOCCTOGG COCCTOCCCA CAGATGGTGC ATCCCCTGGC AGAGGCTCCT GCTCACACCC 180 TCACTTCTAR CCTTCTGGAR CCCGCCCRCC ACTGCCARGC TCACTATTGR ATCCRCGCCG TTCAATGTCG CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCITCAAT TATAGGATAT GTAATAGGAA CTCAACAAGC TACCCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC CCCAATGCAT CCCTCGTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCCTA 360 25 420 480 COSTICATA ASTERBATCH TOTATATOLA GARCEAGTE GEORGTTCOS GOTATACECO GASCIGOCCA ASCOCITOCATA COTOGOLACO CONTRACCO GARCECOTOCAT CONTRACCO GOTOGOLACO ACOCOTOCA CONTRACA COTOGOLACO CONTRACO GARCACOTA GARCECOTA GARCECOTA COTOGOLACO CONTRACA CONTR 540 600 ... 30 CAGAGCCTCC COGTCAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720 TTCRATGICA CARGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA COCAGTGAGT 780 GCCAGGCGCA GTGATTCAGT CATCCTGAAT GTCCTCTATG GCCCGGATGC CCCCACCATT 840 TOCCCTCTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCCTG CCACGCAGCC TOTARCCCAC CIGCACAGTA CICTIGGITI GICAATGGGA CITTCCAGCA ATCCACCCAA 960 35 GAGCTCTTTA TCCCCRACAT CACTOTGAT AATAGTGGAT CCTATACGTG CCAAGCCCAT AACTCAGACA CTGCCCCCAA TOGACCACA GTCAGGACGA TCACGGTCA TGCAGGCTA TGCAGGCCA CCCAAACCCT TCATCACCAG GAGCAACTCC AACCCCTTGA GGATGAGGA TGCTGTAGGC 1020 1080 1140 TTARCCTOTO ARCCTGAGAT TOMGARCACA ACCTACCTOT GGTGGGTANA TARTCAGAGC CTCCCGGGTGA GTCCCAGGCT GCAGCTGTCC ARTGACACA GGACCCTCAC TCTACTCAGT 1260 GTCACARGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTTGAC 40 1320 CACAGOGACC CAGTCATCCT GAATGTCCTC TATGGCCCAG ACGACCCCAC CATTTCCCCC 1380 TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGGCTCTAAC 1440 CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAACATCC AGCAACACAC ACAAGAGCTC TITATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCCAAG 1560 45 1620 COCTOCATOT CCAGCARCAR CTCCAARCCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680 CECTICATET COMBERGAR CICCAMUREE GIGGRORGE ROARISTOT GOECTICACE TOTOGRORGE RARTESTE GRECTECCA GEOTECCA GEOTECAGA CACARCETAC CTOTOGROGG TARATESTE GRECTECCA GEOTECAGA CACARCET GIGGRORGE GRACATOR GRECTECAT CARTOTCACA 1740 ACALATGACG CARGAGOCTA TOTATOTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1060 GACCCAGTCA COCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTC CCCCCCAGAC 50 1920 TOSTOTTACO TITOGGGAGO GAACOTCAAO CIOTOCOGOC ACTOGGOCTO TAACOCATOO 1980 CCGCAGTATT CTTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040 GCCARATA COCCARATA TARCEGRAC TATGCTOFT TOTCTCTA CTTGCTACT GGCGCARAT ATTCCATAG CARAGEATC ACASTCTCT CATCTGGACT TOTCCTORA GGCGCARTA ATTCCATAG CARAGEATC ACASTCTCT CATCTGGACT TOTCCTGGAT 2160 55 2220 TAGCAGCCCT GGTGTAGTTT CTTCATTTCA GGAAGACTGA CAGTTGTTTT GCTTCTTCCT 2280 TARRECATTI GCARCAGCIA CAGTCIARAA TIGCITCITI ACCAAGGATA TITACAGANA AGACTCIGAC CAGGATACGA GACCATCCIA GCCAACATG TGAAACCCA TCTCTACTAA 2340 2400 ANATACAAAA ATGAGCTGGG CTTGGTGGCG CGCACCTGTA CTCCCAGTTA CTCGGGAGGC 2460 60 TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520 ACTGCACTCC MOTCTGGCAR CAGAGCARGA CTCCATCTCA ARAAGAAAAG AAAAGAAGAC TCTGACCTGT ACTCTTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2580 2640 ARCTITARIG ARCTARCIGA CAGCITCAIG ARACTOTCCA CCAAGATCAA GCAGAGAAAA 2700 TARTTARTT CATGOGACTA ARTGARCTAR TGAGGATTGC TGATTCTTTA ARTGTCTTGT 2760 65 TTCCCAGATT TCAGGAAACT TTTTTCTTT TARGCTATCC ACTCTTACAG CAATTTGATA 2820

70 Sec ID NO: 40 Protein sequence: Protein Accession #: NP 004354.1

21 31 41 75 MESPSAPPHE SCIPWORLLL TASLLTPHINP PITAKLTIES TPPHVAEGKE VLLLVHULPQ HLFGYSWYKG ERVDGHRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120 TLHVIKSDLV NEBATGQFRV YPELPRPSIS SNNSKPVEDK DAVAFTCERE TODATYLWWV NNQSLPVSPR LQLSMCHREL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP 180 TISPLATSYR SCENLINGSCH AASHPPAQYS WFVNGTFQQS TQELFIPNIT VMNSGSYTCQ 200 ARMSDTGLMR TTVTTITVYA EPPKPFITSN NSMPVEDEDA VALTCEPEIQ MTTYLWWVNN 80 360 QSLPVSPRLQ LSNDNRTLTL LSVTRNDVGP YECGIQMELS VORSDPVILM VLYGEDDETI SPSYTYYRPG VNLSLSCHAA SNPPAQYSWL IDGNIQQHTQ ELFISNITEK NSGLYTCQAN 420 480 NSASGHERTT VKTITVEAEL PKPSISSNNS KPVEDKDAVA FTCEPEAGNT TYLWWVNGQS 540 LPVSFRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDTPIISP 85 PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQQHTQVL FIAKITPNNN GTYACFVSNL 660 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC

AGACTITOGGA AACTATICAT GAXTATITAT ATTOTATOGT AATATAGTTA TIGCACAAGT TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 41 DNA sequence Nucleic Acid Accession #: NM_006952.1

WO 02/086443

Coding sequence: 11-793 31, ANTICODIACA ATGGORNAGA ACAACTAAC TOTTCOTTOC TT.CO.000000 TUCTUALTITT.
TUGAANUTU ATTATTUTUT TOTTCOOTOC TOTCOTTOC TT.CO.000000 TUCTUALTITT.
TUGAANUTU ATTATTUTUT TOTTCOOTOCA TOTCOTTOC TUCTUAL TOTCOTTOC TECTOC TOTCOTTOC
TUCTUAL TOTCOTTOC TUCTUAL TOTCOTTOC TUCTUAL TOTCOTTOC TUCTUAL TOTCOTTOC TUCTUAL TOTCOTTOC TUCTUAL TUCT 120 10 180 240 300 ACCCAACCTC TTCCTGAAGC ACATGCTAGA GAGGTACCAA AACAACAGCC CTCCAAACAA 420 15 TOATGACCAG TOGAAAAACA ATGGASTGAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA CAATIGCTGT GGCGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGA TOAGAATAAT GATGCTGACT ATCCCTGGC CTGTCAAAGC TGTTTATGA ACAATCTTAA 480 540 600 AGAACCICTC AACCIGGAGG CITGIAAACT AGGCGTGCCT GGTTTTTATC ACAATCAGGG CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720 20 ATTIGOCATE CECTGCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG 780 AATTGAATAT TAAGAA

Seq ID NO: 42 Protein sequence: Protein Accession #: NP_008883.1

35 Seq ID NO: 43 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 83-2605

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	GCCCGGACAGA	TCTGCGCGTA	TCCTGGAGCC	GCCCAGTTG	TGAACTAGGA	GAGCTTTGGG	60
	ACCTCTGTCC	CAAGCAAGAG	AGATGAATGG	AGAGTATAGA	OGCAGAGGAT	TTGGACGAGG	120
	AAGATTTCAA	AGCTGGAAAA	GGGGANGAGG	TOGTGGGAAC	TTCTCAGGAA	AATGGAGAGA	180
	AAGAGAACAC	AGACCTGATC	TGAGTAAAAC	CACAGGAAAA	CGTACTTCTG	AACAAACCCC	240
45	ACAGETTETTG	CTTTCAACAA	AGROCCACA	GTCANTGCAG	TCAACATTGG	ATCGATTCAT	300
	ACCATATAAA	GGCTGGAAGC	TTTATTTCTC	TGAAGTTTAC	AGCGATAGCT	CTCCTTTGAT	360
	TORGARGATT	CARGCATTTG	PRABATTTT	CACAAGGCAT	ATTGATTTGT	ATGACAAGGA	420
	TGAAATAGAA	AGAAAGGGAA	GTATTTTGGT	AGATTTTAAA	GAACTGACAG	AAGGTGGTGA	480
	AGTARCTARC	TTGATACCAG	ATATAGCAAC	TGAACTAAGA	GATGCACCTG	AGAAAACCTT	540
50	GGCTTGCATG	GGTTTGGCAA	TACATCAGGT	GTTAACTAAG	GACCTTGARA	GGCATGCAGC	600
	TGAGTTACAA	GCCCAGGAAG	GATTGTCTAA	TGATGGAGAA	ACAATGGTAA	ATGTGCCACA	660
	TATTCATGCA	AGGGTGTACA	ACTATGAGCC	TTTGACACAG	CTCAAGAATG	TCAGAGCAAA	720
	TTACTATGGA	AAATACATTG	CTCTAAGAGG	GACAGTGGTT	CGTGTCAGTA	ATATAAAGCC	780
	TCTTTGCACC	AAGATGGCTT	TTCTTTGTGC	TGCATGTGGA	GAAATTCAGA	CCTTTCCTCT	840
55	TOCAGATGGA	AAATACAGTC	TTCCCACAAA	GTGTCCTGTG	CCTGTGTGTC	GAGGCAGGTC	900
	ATTTACTGCT	CTCCGCAGCT	CTCCTCTCAC	ACTTACGATG	GACTGGCAGT	CAATCAAAAT	960
	CCAGGAATTG	ATGTCTGATG	ATCAGAGAGA	AGCAGGTCGG	ATTCCACGAA	CAATAGAATG	1020
	TGAGCTTGTT	CATGATCTTG	TGGATAGCTG	TGTCCCGGGA	GACACAGTGA	CTATTACTGG	1080
	AATTGTCAAA	GTCTCAAATG	CGGAAGAAGG	TTCTCGAAAT	AAGAATGACA	AGTGTATGTT	1140
60	CCTTTTGTAT	ATTGAAGCAA	ATTCTATTAG	TAATAGCAAA	GGACAGAAAA	CAAAGAGTTC	1200
	TGAGGATGGG	TGTAAGCATG	GAATGTTGAT	GGAGTTCTCA	CTTARAGACC	TTTATGCCAT	1260
	CCRAGAGATT	CAAGCTGAAG	ABBACCTGTT	TARACTCATT	CTCAACTCGC	TTTGCCCTGT	1320
	CATTTTTTGGT	CATGAACTTG	TTAAAGCAGG	TTTGGCATTA	GCACTCTTTG	GAGGAAGCCA	1380
	GARATACGCA	GATGACAAAA	ACAGAATTCC	AATTCGGGGA	GACCCCCACA	TCCTTGTTGT	1440
65	TOGRGATOCA	GGCCTAGGAA	AAAGTCAAAT	GCTACAGGCA	GCGTGCAATG	TTGCCCCACG	1500
	TOCCUTGTAT	GTTTGTGGTA	ACACCACGAC	CACCTCTGGT	CTGACGGTAA	CTCTTTCAAA	1560
	AGATAGTTCC	TCTGGAGATT	TTGCTTTGGA	AGCTGGTGCC	CTGGTACTTG	GTGATCAAGG	1620
	TATTTGTGGA	ATCGATGAAT	TTGATAAGAT	GGGGAATCAA	CATCAAGCCT	TGTTGGAAGC	1680
	CATGGAGCAG	CAAAGTATTA	GTCTTGCTAA	GGCTGGTGTG	GTTTGTAGCC	TTCCTGCAAG	1740
70	AACTTCCATT	ATTGCTGCTG	CARATCCAGT	TGGAGGACAT	TACAATAAAG	CCANANCAGT	1800
	TICTGAGAAT	TTARARATGG	GGAGTGCACT	ACTATOCAGA	TTTGATTTGG	TCTTTATCCT	1860
	GTTAGATACT	CCAAATGAGC	ATCATGATCA	CTTACTCTCT	GAACATGTGA	TTGCAATAAG	1920
	ACCTGGAAAG	CAGAGAACCA	TTACCAGTCC	CACAGTAGCT	CGTATGAATA	GTCAAGATTC	1980
	ARATACTTCC	GTACTTGAAG	TAGTTTCTGA	GAAGCCATTA	TCAGAAAGAC	TARAGGTGGT	2040
75	TCCTGGAGAA	ACANTAGATO	CCATTCCCCA	CCAGCTATTG	AGAAAGTACA	TTGGCTATGC	2100
	TOGGCAGTAT	GTGTACCCAA	GGCTATCCAC	AGAAGCTGCT	CGAGTTCTTC	AAGATTTTTA	2160
	CCTTGAGCTC	COGARACAGA	GCCAGAGGTT	AAATAGCTCA	CCAATCACTA	CCAGGCAGCT	2220
	GGAATCTTTG	ATTOGTCTGA	CAGAGGCACG	AGCAAGGTTG	GAATTGAGAG	AGGAAGCAAC	2280
	CARAGAAGAC	GCTGAGGATA	TAGTGGAAAT	TATGAAATAT	AGCATGCTAG	GAACTTACTC	2340
80	TGATGAATTT	GGGAACCTAG	ATTTTGAGCG	ATCCCAGCAT	GGTTCTGGAA	TGAGCAACAG	2400
	GTCAACAGCG	AAAAGATTTA	TTTCTGCTCT	CAACAACGTT	GCTGAAAGAA	CTTATAATAA	2460
	TATATTTCAA	TTTCATCAAC	TTCGGCAGAT	TGCCAAAGAA	CTAAACATTC	AGGTTGCTGA	2520
	TTTTGAAAAT	TTTATTGGAT	CACTAAATGA	CCAGGGTTAC	CTCTTGAAAA	AACCCCCAAA	2580
	AGTITACCAG	CTTCAAACTA	TGTAAAAGGA	CTTCACCAAG	TTAGGGCCTC	CTGGGTTTAT	2640
85	TGCAGATTAA	AGCCATCTCA	GTGAAGATAT	GCGTGCACGC	ACAGACAGAC	AGACACACAC	2700
	ACACACACAC	ACACACACAC	ACACACACAC	ACACACAGTC	ARATACTGTT	CTCTGAAAAA	2760
	TGATGTCCCA	AAAGTATTAT	AATAGGAAAA	AAGCATTAAA	TATAATAAAC	TAATTTAAGA	2820

Seq ID NO: 47 DNA sequence Nucleic Acid Accession #: Bos sequence

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	AGTGATANAG	TCTCCAGATG	CAGTAGCTCA	CACIGTAATC	ACAGTGACTC	AGGAGGCTGA	2880
	GGTGAGAGGA	TTCCTTGAGG	CCAGGGTTCG	AGACCAACCT	TGGGCAACAT	AGCAAGACCC	3000
	CATTTCTTAA	AAAAAAAAA	AAAAAATTTA	CACCAMMOTO	TOTATOGIGG	CACATGCCTA AGTTTGAGGT	3060
5	TAGTCTCAGC	CACAATCACA	CCAATCACTG	CACTOCAGOC	TORGCCCANA	AGTAACTCTT	3120
,	CACTUADADA	AATDABAAAA	ATTGTAGTGG	TAGCCATGTG	TTAATTGTTA	AATAAATTCT	3180
	CCALAGGGCT	AAAAGTAAAT	TACTTATAAA	TTTTTTATAG	TIGTATETE	GACCTGCCTT	3240
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	A DACCORPAGA	ATATATTACA	TATTOTYTYTY	тогратарра	CTTTATTTAT	GGACACTAAA	3360
10	ATTTGAATTT	CATAAAATTT	TCCCATGTCA	AGAATACAAA	ATACTTGAGT	TTTGTTTTTA TGCTTGAAAC	3420
	GCTATTTAAT	AATAGGTCTC	ATTTATTCCA	CAGGCTGTAG	TTTGTAGTCT	TGCTTGAAAC	3480
	AATAGAAACA	GACTGATTAA	GCAGGAGAAG	TTTTTTGAAA	GAATTTTGTT	TGGCTCACGG	3540
	AATTATTAGA	AGGCAGGTGA	ACCAGGAGGG	TAAGCTTCCA	GCAGCAATTT	GTAAAACCAT	3600
15	GCCTTAGAAT	TGGACTAAGG	AAGAAGCTGC	TGACACTCCA	CTGCCACACA	GGGCACTGGA ATAGGTAGAA	3660
13	AGAAAGTGCT	Gergeereee	TGCCCCACCT	TIGCCACITC	TGCAGCAGGA	ATMOSTAURA GOOGGOOGEA	3780
	GAATGCCCCC	ACCCGCACCG	GAACAGCAAC	AAAAAGGATTC	CATGAGAT	GCCTCCCTAA	3840
	ATTGCTGAAT	TCAMANANGA	CTACCCACAC	PROCEGUE	TACTTTCAGG	GOGTATGTTA TGGTGGGATC	3900
	TATGCCCCTT	CALMOGUIG	CINGGGNOTI	ChCCAGGIC	ATCTTACAGG	GTTGCCAGCC	3960
20	ANDCTATCAL	TOATGTATAA	ATCCARCAGA	CACTTTGTAA	CATACAAGAA	CTCAGGAAAT	4020
20	CHICAROCATT	GTTGGAGAAT	CTACTABAAT	ACGGCTTCCC	GCAAACGAAG	ATGAATGGAA	4080
	AATGTAAATA	AAAAGAACTG	GCAGTGTATA	TCAGATGTTT	AACTATAGGA	CCAGAACTAA	4140
	CAMPOROGRADA.	CENTROCCAT	ACACCA CAAT	OTABATTTTT	A DOTTO AGGINA	CCARARATCA	4200
	GGAATCAAAA	GGGGCCAGGT	GCAGTGGCTC	ACATCTATAA	TOCCAGAGCT	TTGGGAGTTC	4260
25	GAGGCAGGAG	GATCACTTGA	AGCCAGTTTT	GAGACCAGCC	TATGCAACAC	ATTGAGACCC	4320
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	GTGGAGGCTG	AAGTAGGAAA	TCACTTGAGC	CCGAGAGTTT	GAGGTTACAG	TGAGCTATGA	4440
	TTATACCACT	GCACTCCAGC	CTGGGCAAGA	GAGCAAGACC	TIGTCTCTT		
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30		44 Protein cession #: 0					
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35	MOSSEYRORGE	GRGREOSWKR	GROGGNFSGK	WREREHRPDL	SKTTGKRTSE	OTPOFLLSTK	60
	TPOSMOSTLD	RFIPYKGWKL	YFSEVYSDSS	PLIEKIQAFE	KFFTRHIDLY	DKDEIERKGS	120
	ILVDFKELTE	GGEVINLIPD	IATELRDAPE	KTLACMGLAI	HQVLTKDLER	HAAELQAQEG	180
	LSNDGETMVN	VPHIEARVYN	YEPLTQLKNV	RANYYGKYIA	LRGTVVRVSN	IKPLCTKMAF	240
40	LCAACGEIQS	FPLPDGKYSL	PIKCPVPVCR	GRSFTALRSS	PLTVTMDWQS	IKIQELMSDD	300
40	QREAGRIPRT	IECELVHDLV	DSCVPGDTVT	ITGIVKVSNA	EBGSRNKNDK	CMFLLYIEAN	360
	SISNSKOOKT	KSSEDGCKHG	MIMEPSIKDL	AVIÖRIÖVEE	NLFKLIVNSL	CPVI FGHELV	420
	KAGLALALFG	GSQKYADDKN	RIPIRGDPHI	LVVGDPGLGK	SQMLQAACNV	APRGVYVCON LEAMEQQSIS	480 540
	TTTTSGLTVT	LSKDSSSGDF	ALEAGALVLG	DOGICGIDER	DKMGNQHQAL	PRAMEGÓSIS	600
45	LAKAGVVCSL	PARTSIIAAA	SSATVARMOS	KTVSENLKNG	SALLSKYDLV	FILLDTPNEH	660
43	HUHLLSEHVI	ATRIGRORED	SSATVARINS LOWESTRATE	DEALES APPLE	ODIMOODITT	RQLESLIRLT	720
	TANADADARATI	GIMMUTVIPA	TO I PULL AND THE	TYPERFERENCE	DEB CONGCOM	SNRSTAKRFI	780
	CATANNIZAURT	VANIT POPUOL	RQIAKELNIQ	VARPENPIGS	INDOGYLLKK	GPKVYOLOTM	
	DALLIN VALUE	1111121 61 1160	regarmentana g				
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		45 DNA sequ					
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	POGP GP GOOD	a caccerosa	CACCOTOCACC	THETETRACEC	ACCACATOAT	CCCTGAGCAG	60
	CTGAAGACCA	CASSOCIONA	TANGACTITC	TGCTTAATTC	AGGAGCTTAG	AGGATTCTTC	120
	AAAGAGTGTG	TCCACGATCC	TTTGAAGCAT	GAGTTCTTAC	CAGCAGAAGC	AGACCTTTAC	180
60	OCCUPACION COM	CACCTTCAAC	AGCAGCAGGT	GARACARCOC	AGCCAGCCTC	CACCTCAGGA	240
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65	CAAGGTCCCT	GAGCCAGGTT	GTACCAAGGT	CCCTGAGCCA	GGCTACACCA	AGGTCCCTGA	480
05	ACCAGGCAGC	ATCAAGGTCC	CTGACCAAGG	CTTCATCAAG	TTTCCTGAGC	CAGGTGCCAT	540 600
	CARAGTTCCT	GAGCAAGGAT	ACACCAAAGT	TOCTOTOCCA	GGCTACACAA	AGCTACCAGA	660
	DOCUMENT	*CANCOCCEM	CICCAGGCCC	AGCT CAGCAG	CTCGACACACC	AGAAGTAATT TCTTCCCATC	720
	TOTTOTOTOTO	TOTTABTTOT	CTOTAGACOT	TOTALTORGE	ACATTGTCAC	CCCAAGCCAT	780
70	PULLICION	TEATTTGTAT	CTABABATA	CCTACTATAA	AGCTTTTGTT	CACACACACT TCTGGTCTTC	840
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	GGCTGCTCAG	GGTTCATCTG	AAGATTCGAA	TGAAAAGAAA	TGCATGTTTC	CTGCTCTTCC	960
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75							
		46 Protein					
	Protein Ac	cession #: 1	XP_005407.1				
	1	11	21	31	41	51	
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. •	MSSYQQKOTF	TREPROTOCOO	TRODGODDDO	RIPUPTTKEP	CHSKVPQPGN	TKIPEPGCTK	60
	VPEPGCTKVP	EPGCTKVPEP	GCTKVPEPGC	TKVPEPGCTK	VPEPGYTKVP	EPGSIKVPDQ	120
	GFIKFPEPGA	IKVPBQGYTK	VPVPGYTKLP	EPCPSTVTPG	PAQQKTKQK		

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	1	11	21	31	41	51	
	OCCUPATION TO	CAGGGGTCCC	connectores	ATRATTACAC	VCCanacatacc	CTCATTGCCC	60
-	AAGGCTCGTT	AGAATTOGCC	CTAGAGCTGT	ATCATGTATT	TTCTTTCAAA	TTAACTTTGC	120
5	TTGCAATTAA	GCTTAGGGAA TAGAGAAACT	CCAGCAACAA	AAGCAAACTT	GGCCCGAGGT	CGTTCACCGC	180 240
	TTTGGGGAAA	GTGCCCCGAC	CGCAGAGGCG	ACGACAGGGG	AGCAGGAAGC	TGCTCACGGT	300
	AGTCGGCGTT	GGCGGCAGCG ATCCTGGAAA	GTGGCCTTCC	TCATCTGGGC	GATGTGGGCT	CCTAGAAGAG	360 420
10	TTGGAGCTGC	CCTGTGGAGT	TACAGTTTAC	CAAACACATT	CATGAACATA	ATCTCATTTA	480
	CTAAAAACTT	TGTGAGAATT	TTCTTTTACT	AAAATTTTTT	CTTATTACAA	A	
	Sec ID NO:	48 DNA seq	ience:				
15	Nucleic Ac	id Accession	1 #: CAT clu	ster			
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	1	11	21	31	41	51	
	TTCCAAATTT	TTTTTTTTTTT	AATAAGAAAA	AATTTTAGTA	AAAGAAAATT	CTCACAAAGT	60
20	TTTTAGTAAA	TGAGATTATG	TTCATGAATG	TGTTTOGTAA	ACTOTAACTO	CACAGGGCAG	120 180
	TOCTTACTO	TGAGTGTGCA TCTCGGAGCC	CACATCGCCC	AGATGAGGAA	GGCCACCGCT	GCCGCCAACG	240
	CCGACTACCG	TGAGCAGCTT	CCTGCTCCCC	TGTCGTCGCC	TCTGCGGTCG	GGGCACTTTC	300
25	ATTTTCGCGG	TGGCCGCAGG TGAACGACCT	CGGGCCAAGT	TEGCETTTEGT	TGCTGGTTCC	CTAAGCTTAA	360 420
	TTGCAAGCAA	AGTTAATTTG	AAAGAAAATA	CATGATACAG	CTCTAGGGGG	AATTCTAACG	480
	AGCCTTGGGC	AATGAGGGAA	GAACGTGTCT	AGTTATCCAC	AGCCCGGGGA	CGCCTGCACA	540
30							
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35	TCTTTCTTCT	GCTGCTCGTT TCTGTTGTCT	TGTCTCTCCT	GTGCTCTTCT	TCTTTCTTTC	CCTCGCCGCT	60 120
	ACCGTAGACC	CGAAACCATT	GGGTGTCACA	AGCCGGTCGC	CGGCTTTTTT	GGGAGAACCC	180
	GACACATGCA	GACCAGTTTT GTGTTTAAAA	CCTGGAA CNG	CATGACCATG	TTATTACTAT	GGGCCGCCTC	240 300
40	TTCATTTAAA	AAACTCTAAT TCTGTGTCTT	ATTTATATTA	AATACAAAGA	TACCCAAACC	CTTTATGCTT	360
	CTTTCTCTGA	TCTGTGTCTT	TTTTCTTTGA	CAGCATCTCC	ATTTTTTTC	TGCTGCTTCA	420 480
	TAAAGAAACT	CATGGGAATC GACACAGGAG	AATCACTTGA	ACTTGGGAGG	CAGAGTTTGC	AGTGAGCCGA	540
45	GATTGAACCA	GTGCACTCCA	OCCTTGGCAG	COGAGCAAGA	TTCTGTCACA	GTTCCTGAAG	600 660
43	GACGTGGGGA	GTCCTGCAGC GAGCTGGTCT	ATATATCCCG	GTTCCATTGC	GCTGTGGCAG	ACCTTGGATG	720
	CCGGGTCTCT	CCTGGCCCCG	GGGACCTAGT	ATTTTTTGCCA	CGAGTGTACA	CCAAACAAAG	780 840
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50	000 TD WO.	50 DNA sequ					
	Nucleic Ac	id Accession	1 #: L05187				
	Coding seq	ience: 1991	2260				
55	1	11	21	31	41	51	
	CTGCAGGGAG	GCAGGTAGAA	AAGGCTTTTG	GGTTTTCAGG	TGGGGGGGCAG	TCTAGCCTGA	60
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60	TGBAGGBAAG	ATTAGCCCCT	CAGATTAGCA	ACCAGTCAGG	CCCCACCAACC	TGAGAGTGGG	180 240
	AGAGTCATAA	GTAAATTATT	CTGAATGTGT	GTAGTTTAAT	GGAATTGGGA	AAAAGATGGG	300
	GGAAATGGAT	GGAAGGTCTT	GGACTCTGAG	ACAAGGGGTC	CCACCTCAGC	CCATTTCATT	360 420
60	CCCCTCCCTT	TOOCACCTAT	TCATGTGTGC	AAGAGTGCCC	TGTCCCACAG	AACACGGGGA	480
65		CAATGACAAG CTCATGAAAC					540 600
	COCTGCACCT	GGGTCTGAGG	ATGAGGGTGG	CAGTGAAAAT	TAGGCCAGTG	ACATCATTTT	660
	CAGCCAGCTA	GTGCCAAAAA GTAGTGTGAG	ATATCAGGTG TCATGTGTON	CAGGTGAGGA	ATTARGCCGA	AGTGCCCGAG	720 780
70	AGCTTCTATT	TOCTTGAGGC	AGGGCTCATT	CATCTTATAA	AAGCCAGCTG	GCCATTGCCT	840
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	ATATGTGTAA	GCAGGTTAAT	CCAGGGTTTC	AATGGGAGAT	AGAGAATAGT	GGAATATCTT	1020
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	AGTTCATAGC	AGAACTAGAA	CTCAGGCCAG	AGCACTCTCA	GTAACACTGC	AATTTCCCCC	1200
	TGACAAGATA	TTTATAGAAA GTATGCTAGG	CACTUTGGAG	TTAGATGGAT	CTCTACTGAG	CATTTATTCC	1260
00	AACATAAAAC	CTAGCAGGAA	GGTAATACAT	ATATATAAAT	AAATGAAATG	CAAAGTAGAT	1380
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	AGATGGGAAG	AAAAGCATTT	GGAAGGGACT	GTGTAAGCAC	AGACCAGAAG	CAAAACCATA	1560
	GAGGCTTAGA	TGAATATAAA GTCTGATGCC	GCCATCCTAT	AAGTCACAGG	CTTTCTACAT	GGTACTAGGA	1620 1680
85	GAAGCCAGCT	TTAGTAGGGC	ATTTTTCCAG	AACAGATATA	AGGTGCCTTG	GGTAGGAAGG	1740
	GAGCCAAGAA	GAGAACTCCA CTGAAAATTA	ATAAAATGGA	GCNGAAGAAA	TTGCCTTTTA	GCTCCTCCTC	1860
	LICHARDOGC	CTGGGGATTA	ICCAMBCITA	IIICAIIIII	MAIGINAIG	GGGMGCTAA	1000

5	OGGAGATGAA TIGTATCCAT TATTGAAGC GCMGCMCAG CAAGGAGCAC CACCCAAGC TIGAGGAGCT GCCTATIGAC CTAAAAAGAT GTCTCACTGA AGGTCAAGTG AGGTCAAGTG	//086443 AGGCTTTCTC CTTTCTTTTAA ATGAATTCTC GTGAAACAAC TTGCCAACCCA ATTCCAGAGC CCAGCCCAGC	TTGAATCACT AGCAGCAGCA AGCTGCCAGCC AGAAGACCAA ATACTGAACAC GCATGCTGTC CTCATTCTGG G	GTGTCAGCTT GCAGCCTGC TCCACCCAG GCCTGCCAC CAAGGTGCCT GCAGAAGTAC CCTACTCCAT ACCCTGAATCA AGGCTCCTGA	TCTGTCTCTA ACCCCACCCC GAACCATGCA CCCAAAGTGC GAGCCCTGCC TGTGGTCCAC TCTGCTTATG ATAATCGCTC GCCTCTGCGT	GARARARCA CTCAGCCTCA TCCCCAMAC CTGAGCCCG CTTCARCOGG AGCCATGCCC AATCCCATTT CTTTGCACCT AAGGCTGAAC	1920 1980 2040 2100 2150 2220 2220 2340 2400 2460 2520
15	Seq ID NO: Protein Ac	51 Protein cession #:AJ	sequence:				
20	1 MNSQQQKQPC PEPCQPKVP	11 TPPPQPQQQQ EPCPSTVTPA	21 VKQPCQPPPQ PAQQKTKQK	31 EPCIPKTERP	41 CQPKVPEPCH	51 PKVPEPCQPK	60
25	Nucleic Ac:	52 DNA sequid Accession dence: 120-	#: NM 002	538.1			
30	GCTGGACTGC TGAGGGCCAG AGGCAGCTGT	11 AAGGAATTAT ATAAAGATTG CAGGTTCTTG CACGGGAGTT AGATCCCGTT	GTATGGCCTT ATCGTGGTGG CCTGTTAAAG	AGCTCTTAGC TGTTCCTCAT GTCAAGACAC	CAAACACCTT CGCTGGGACG TGTCAAAGGC	CCTGACACCA CTGGTTCTAG CGTGTTCCAT	60 120 180 240 300
35	CGCAAGAGCC TCCGGTGCGC TCAAGAAGTG CGGTCCTTGC	AGTCAAAGGT CATGTTGAAT CTGTGAAGGC TGCACCTGTG	CCAGTCTCCA CCCCCTAACC TCTTGCGGGA CCGTCCCCAG	CTAAGCCTGG GCTGCTTGAA TGGCCTGTTT AGCTACAGGC	AGATACTGAC CGTTCCCCAG CCCATCTGGT	ATTATCTTGA TGCCCAGGAA TGAAGGGAGC CCTAAGTCCC	360 420 480 540
40	GAGCTGCCTC Seq ID NO:	CCCCTTCCCA TCTCATCCAC 53 Protein cession #: 1	TTTCCAATAA sequence:	A A	ATTCAGGATG	COCACGGCTG	600
45	1 MRASSFLIVV AQEPVKGPVS	11 VFLIAGTLVL TKPGSCPIIL	21 EAAVTGVPVK IRCANLEPPN	31 GQDTVKGRVP RCLKDTDCPG	41 FNGQDPVKGQ IKKCCBGSCG	51 VSVKGQDKVK MACFVPQ	60
50	Nucleic Ac	54 DNA sequid Accession	1 #: NM 0196	518			
55	GAGACAACCA ATCAATCAAT	11 ACGATTCAGT CACTATGAGA GTGTAAACCT	GGCACTCCAG ATTACTGGGA	GAGACGCTGA CTATTAATGA	TGGTGGAGGA	AGGGCCGTCT CAAGTGTGGA	60 120 180
60	TTGCTGTTAT ATTTGGGAAT CATTGCAGCT CCTTCCTTTT	TCAGAACCTT CACATGCAAG CCAGAATCCA AAAAGAGCAG CTACCGTGCC CATTGCCTCC	TATCCAGAGG GAAATGTGTT AAGATCATGG AAGACTGGTA	CTCTTGAGCA TGTATTGTGA ATCTGTATGG GGACCTCCAC	AGGCAGAGGG GAAGGTTGGA CCAACCCGAG CCTTGAGTCT	GATCCCATTT GAACAGCCCA CCCGTGAAAC GTGGCCTTCC	240 300 360 420 480 540
65	GGAGGTGATA GCAGCTTGGT AGTGTCATTT TAATGAAGAA	CAACACTGCC CTTTGTCTTA TCACGCTGGT GAAGCAATTA	TTTGAATTAA AAGTTTCTGG GCTGAGACAG CTTCATAGCA	ATATAAATGA TTCCCAATGT GGGCAAGGCT ACTGAAGAAC	GTTTTCGTCT GCTGTTATCA AGGATGTGGC	ACATTTTCTT TCTCATTTTA CTCAGAAGCA	600 660 720 780
70	GGAGAGCTGG CTGCATGAGT TGAAGATGCT CTCTGTTTCT CCAATATACC TAATTCTTGT	GTOGTATAAG GACTTTAAGA TCAGAGCTCA GTTTTGCTTT TCATTGTGTG GTTAAGTTAA	GCTGTCCTCT CTCAAAGACC TGCGCGTTAC ATTCCCTCTT TAATAGAACC ATCATTTTTG	CARGCTGGTG AARCACTGAG CCACGATGGC GGGATGATAT TTCTTAGCAT TCCTAATTGT	CTGTGTAGGC CTTTCTTCTA ATGACTAGCA CATCCAGTCT TAAGACCTTG AATGTGTAAT	CACAAGGCAT GGGGTGGGTA CACAGCTGAT TTATATGTTG TAAACAAAAA	900 960 1020 1080 1140
75	Seq ID NO:	GTGTATTTAT 55 Protein cession #: 1	ATAATAAAAA sequence:	AAAAAAAA	AAA		
					41	51	
80	CKYPEALEQG	11 GGRAVYQSMC RGDPIYLGIQ ESVAFPDWFI	NPEMCLYCEK	VGBQPTLQLK	NLVAVPRSDS BQKIMDLYGQ	VTPVTVAVIT	60 120

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5 10 15	CAGCATGAGT GCAGGTGAAA GCCCTGCCAC CAAGCTTCCA AGCACCAGCC AGCOGGCCAC CAATTAGCAT TCTGAGTCTC	AGGGACCATA TCCCAGCAGC CAGCCTTGCC CCCAAGGTGC GAGCCATGCC CAGCAGAAGA CAGATGCTGA TCTGTCTCCC TGAATGAAGC AGAGAGACTT	AGAAGCAGCC AGCCTCCACC CTGAGCCCTG ACCCCAAGCT CCAAGCAGAA ATCCCCTATC CCAAACAAAAA TGAAGGTCTT	CTGCATCCCA TCAGGAACCA CCACCCCAAA GCCTGAGCCC GTAATGTGGT CCATTCTGTG ATGTGCTATG AGTACCAGAG	CCCCTCAGC TGCATCCCA GTGCCTGAGC TGCCTTCAA CCACAGCCAT TATGAGTCCC AAGCTTTCTT CTAGTTTTCA	TTCAGCAGCA AAACCAAGGA CCTGCCAGGCC TAGTCACTCC GCCCTTGAGG ATTTGCCTTG TCCTACACAC GCTGCTCAGA	60 120 180 240 300 360 420 480 540
20		57 Protein cession #: N		31	41	51	
	1	11	ī ·	ī ·	1	ĺ.	
	MSSQQQKQPC	IPPPQLQQQQ	VKQPCQPPPQ	EPCIPKTKEP	CHPKVPEPCH	PKVPEPCQPK	60
25	LPEPCHPKVP	EPCPSIVTPA	PAQQKTKQK				
23	Sec ID NO:	58 DNA sequ	ence				
	Nucleic Ac:	ld Accession	#: NM 001	793.2			
	Coding sequ	ence: 71-25	60				
30	1	11	21	31	41	51	
	Ĩ	1	1	Ĭ.	1	1	
	AAAGGGGCAA	GAGCTGAGCG ATGGGGCTCC	GAACACCGGC	CCGCCGTCGC	GGCAGCTGCT	TCACCCCTCT	60 120
	CTCTGCAGCC	TGCGCGGCCT	CCGAGCCGTG	COGGGGGGGTC	TTCAGGGAGG	CTGAAGTGAC	180
35							240
	CIGCCCTOGG	CARGAGCCAG GTCCAGGAAA	CTCTGTTTAG	CACTGATAAT	GATGACTTCA	CTGTGCGGAA	300
	TOGOGAGACA	ATCTTACGAA	GAAGGTCACT	AGATTGGGTG	GTTGCTCCAA	TATCIGTCCC	360 420
	TGAAAATGGC	AAGGGTCCCT	TCCCCCAGAG	ACTGAATCAG	CTCAAGTCTA	ATAAAGATAG	480
40	AGACACCAAG	ATTTTCTACA	GCATCACGGG	GCCGGGGGCA	GACAGCCCCC	CTGAGGGTGT	540 600
		GAGAAGGAGA TATGAGCTCT					660
	CCCCATGAAC	ATCTCCATCA	TCCTGACCGA	CCAGAATGAC	CACAAGCCCA	AGTTTACCCA	720
45							780 840
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50	COCTORGAT	GCCAATGACA GCAGTGGGCC	ATGGTCCCAT	GAGGCTGACG	GTCACTGATC	TGGACGCCCC	1140
50	CONTROL COL	COMPOCOMEC	CONCORNOCT	TATCATCCC	GGTGA CGACG	GGGACCATTT	1200
	TACCATCACC	ACCCACCCTG	AGAGCAACCA	GGGCATCCTG	ACAACCAGGA	AGGGTTTGGA	1260 1320
	COMOUNT OCTO	AAAAACCAGC CCAACCTCCA	Character	ACTOCIOCAC	CTYGGAGGATYG	TGAATGAGGC	1380
55	ACCTGTGTTT	GTCCCACCCT	CCAAAGTCGT	TGAGGTCCAG	CAGGGCATCC	CCACTGGGGA	1440
	CCTGTGTGT	GACCCAGCAG	CAGAAGACCC	TGACAAGGAG	AATCAAAAGA	TCAGCTACCG	1500 1560
	CATCCTGAGA	CTCGACCGTG	AGGATGAGCA	GTTTGTGAGG	ARCARCATCT	ATGAAGTCAT	1620
	GGTCTTGGCC	ATGGACAATG GTCAATGACC	GAAGCCCTCC	CACCACTGGC	ACGGGAACCC	TTCTGCTAAC	1680
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	GGAAGGTGAC	ACAGTGGTCT CTGTCTGACC	TGTCCCTGAA	GAAGTTCCTG	AAGCAĞGATA	CATATGACGT	1920
65	GCACCTTTCT	CTGTCTGACC	ATGGCAACAA	AGAGCAGCTG	ACCOTGATCA	GGGCCACTGT	1980
03	COCTOTOCTO	CATGGCCATG	TGGAAACCTG	GTTCCTCCTG	CIGGIGCIGC	TTTTGTTGGT	2100
	GAGAAAGAAG	GGGGCTGTCC	AGGAGCCCCT	CCTACTCCCA	GAAGATGACA	CCCGTGACAA	2160
	COTCTTCTAC	TATGGCGAAG GGTCTGGAGG	AGGGGGGTGG	CGAAGAGGAC	CAGGACTATG	ACATCACCCA	2220
70	CATCATCCCC	ACACCCATGE	ACCOTOCTO	GCCAGCCAAC	CCAGATGAAA	TCGGCAACTT	2340
							2400
	CTTGGTGTTC	GACTATGAGG GACCAAGACC	GCAGCGGCTC	CGACGCCGCG	TCCCTGAGCT	CCCTCACCTC	2460 2520
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75	GGGACCAAAC	GACATGTACG GTCAGGCCAC	AGAGCATCTC	CAAGGGGTCT	CAGTTCCCCC	TTCAGCTGAG	2640
		CTTGTCAGGA GGTTGCTTCC					2700 2760
	AGCACTGAAA	ACCTCTCCAC	CTGGGCCAGG	GTTGCCTCAG	AGGCCAAGTT	TCCAGAAGCC	2820
00	TCTTACCTGC	CGTARARTGC	TCAACCCTGT	GTOCTGGGCC	TEGECCTECT	GTGACTGACC	2880
80	TACAGTGGAC	TTTCTCTCTG	GAATGGAACC	TTCTTAGGCC	TOCTGGTGCA	ACTTAATTTT	2940 3000
	GCTGGGGCCCA	GCTATCTTCA CTGGCCGTCC	TGCATTTCTG	GTTTCCAGAC	COCAATGCCT	CCCATTCGGA	3060
	TEGRATETETE	COTTTTTATA	CTGAGTGTGC	CTAGGTTGCC	CCTTATTTTT	TATTTTCCCT	3120
85	GTTGCGTTGC	TATAGATGAA TTTCCCAGAA	GGGTGAGGAC	AATOUTGTAT	ATGTACTAGA	ACTITITAT	3180
33							
		EO Drotein					

Seq ID NO: 59 Protein sequence:

WO 02/086443 Protein Accession #: NP_001784.2

	1	11	21	31	41	51	
		1	1	1	1		
5		LLLLQVCWLQ					60
		DDFTVRNGET					120
		LKSNKDRDTK					180
		NGASVEDPMN					240
		GVVAYSIHSQ					300
10	TDMDGDGSTT	TAVAVVEILD	ANDNAPMFDP	QKYEAHVPEN	AVGHEVORLT	VTDLDAPNSP	360
		GDDGDHFTIT					420
	PTSTATIVVH	VEDVNEAPVF	VPPSXVVEVQ	EGIPTGEPVC	VYTAEDPDKE	MOKISYRILR	480
	DPAGWLAMDP	DSGQVTAVGT	LDREDEQFVR	BHIYEVMVLA	MONGSPPTTG	TGTLLLTLID	540
		RQITICNQSP					600
15		KODTYDVHLS					660
	GAVLALLPLL	LVLLLLVRKK	RKIKEPLLLP	EDDTRONVFY	YGEEGGGEED	QDYDITQLHR	720
	GLEARPEVVL	RNDVAPTIIP	TPMYRPRPAN	PDEIGNFILE	NLKAANTDPT	APPYDTLLVF	780
	DYEGSGSDAA	SLSSLTSSAS	DODODYDYLN	EWGSRFKKLA	DMYGGGEDD		

20 Seq ID NO: 60 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 162-428

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	GCGTTCCGTT	GGCGGCGGAT	TOGAACGITC	GGACTGAGGT	TTTTCTGCCT	GAAGAAGCGT	60
		GGATTGTTTT					120
		AAGCTGAGGC					180
•		GAAGCAGATA					240
30		GCCTCAACTT					300
		TGTTCATCGA					360
		TAACAAGGAG					420
		GTCAAAGAAC					480
35	AGATCATAAA	GACATTTTTT	ACACATCAGT	TAATATGGGA	TTATTAAATA	TTOG	

Seq ID NO: 61 Protein sequence: Protein Accession #: Bos sequence

	1	11	21	31	41	51	
40	1	1	1	1	1		
	MALSTIVSOR	KQIKRKAPRG	FLKRVFKRKK	POLRLEKSGD	LTAHTMCTTL	VHRLAEESRT	60
	NACASKCRVI	NKEHVLAAAK	VILKKSRG				

	NACASKCRVI	nkehvlaaak	VILKKSRG				
45	Nucleic Ac:	62 DNA sequid Accession dence: 99-8:	a #: NM_000	094.2			
	1	11	21	31	41	51	
50		1	1		1		
20	GGGCTGGAGG	GGCGCTGGGC TCCTAGCTGA	TOGGACCTGC	CAAGGCCACC	GCAGGGGGA	GCAAGGGACA	60 120
		CGCCGGGATC					180
		CACGCGCCTT					240
		CAGCAATTTC					300
55		AGCCAGTGCA					360
00	Caccogacaga	GTTCGGCCTG	CATGCACTTC	actronaga	TOTATOTALTO	CGCCCATCC	420
		CTACAAGGGG					480
		CCTGCCCCAG					540
		GTCCCAGGAC					600
60	TCAAGCTATT	TGCTGTGGGG	ATCAAGAATG	CTGACCCTGA	GGAGCTGAAG	CGAGTTGCCT	660
	CACAGCCAAC	CTCCGACTTC	TTCTTCTTCG	TCAATGACTT	CAGCATCTTG	AGGACACTAC	720
	TGCCCCTCGT	TTCCCGGAGA	GTGTGCACGA	CTGCTGGTGG	CGTGCCTGTG	ACCOGACCTC	780
	CGGATGACTC	GACCTCTGCT	CCACGAGACC	TGGTGCTGTC	TGAGCCAAGC	AGCCAATCCT	840
	TGAGAGTACA	GTGGACAGCG	GCCAGTGGCC	CTGTGACTGG	CTACAAGGTC	CAGTACACTC	900
65	CTCTGACGGG	GCTGGGACAG	CCACTGCCGA	GTGAGCGGCA	GGAGGTGAAC	GTCCCAGCTG	960
		TGTGCGGCTG					1020
	TTGCCCTCTA	CGCCAACAGC	ATCGGGGAGG	CTGTGAGCGG	GACAGCTCGG	ACCACTGCCC	1080
	TAGAAGGGCC	GGAACTGACC	ATCCAGAATA	CCACAGUUCA	CAGCCTCCTG	Grogeerage	1140
70	GGAGTGTGCC	AGGTGCCACT	GGCTACCGTG	TGACATGGCG	GGTCCTCAGT	GGTGGGCCCA	1200
70	CACAGCAGCA	GGAGCTGGGC TGAGGTGACC	CCTGGGCAGG	GTTCAGTGTT	GCTGCGTGAC	COCCOCCIO	1320
	GCACGGACTA	TCGCACTGACC	GTGAGCACCC	TATTTGGCCG	CAGTOTOGGG	*mooncooc	1380
	CCCTGATGGC	CCTCCTTTCC	CONTROL OF THE	TOCOTORGO	CCCTTGCCTAC	CCCCCCCCCC	1440
		GACTGGCTTG					1500
75	COUNCERCEN	GGATGGGCTG	CAGCCCCCCCC	CTCACTACCC	CCTCACACTC	TACACTCTGC	1560
,,,	TOGAGGGCCA	CGAGGTGGCC	acccccccca	COGREGATICE	CACTEGACCA	GAGCTGCCTG	1620
	TGAGCCCTGT	AACAGACCTG	CARGOCACOS	AGCTGCCCGG	GCAGCGGGTG	CGAGTGTCCT	1680
	GGAGCCCAGT	CCCTGGTGCC	ACCCAGTAGG	GCATCATTGT	GCGCAGCACC	CAGGGGGTTG	1740
	AGCGGACCCT	OCTGCTTCCT	GGGAGTCAGA	CAGCATTOGA	CTTGGATGAC	GTTCAGGCTG	1800
80	GGCTTAGCTA	CACTGTGCGG	GTGTCTGCTC	GACTOGGTCC	CCGTGAGGGC	AGTGCCAGTG	1860
	TCCTCACTGT	CCCCCGGGAG	CCGGAAACTC	CACTTGCTGT	TCCAGGGCTG	CGGGTTGTGG	1920
		AACGCGAGTG					1980
		GAGCACAGGC					2040
		CATCACAGGG					2100
85		AGAGGAGGGC					2160
	CAGTGAGGAC	GGTCCATGTG	ACTCAGGCCA	GCAGCTCATC	TGTCACCATT	ACCTGGACCA	2220
	GGGTTCCTGG	CGCCACAGGA	TACAGGGTTT	CCTGGCACTC	AGCCCACGGC	CCAGAGAAAT	2280

	CCCAGTTGGT	TTCTGGGGAG	GCCACGGTGG	CTGAGCTGGA	TGGACTGGAG	CCAGATACTG	2340
	AGTATACGGT	GCATGTGAGG	GCCCATGTGG	CTGGCGTGGA	TGGGCCCCCT	GCCTCTCTGG	2400
	TTGTGAGGAC	TGCCCCTGAG	CCTGTGGGGTC	GTGTGTCGAG	GCTGCAGATC	CTCAATGCTT	2460
	CCAGCGACGT	TOTACGGATC	ACCTOGGTAG	GGGTCACTGG	AGCCACAGCT	TACAGACTGG	2520
5	0000000001	Ch Charles a CCC	000000000000000000000000000000000000000	GGC CGTGC C	NOTICO CONTRACTOR	ANCROACACE	2500
5	CCTGGGGCCG	GAGIGAAGGC	GGCCCCATGA	GGCACCAGAI	ACTOCCACOA	AMONOMOTO	2500
	CIGCAGAGAT	COGGGGTCTC	GAAGGTGGAG	TOMOCTACIC	MGIGGGRGIG	ACIGCACTIO	2640
	TCGGGGACCG	CGAGGGCACA	CCTGTCTCCA	TTGTTGTCAC	TACCCCCCCT	GAGGCTCCGC	2700
	CAGCCCTGGG	GACGCTTCAC	GTGGTGCAGC	GCGGGGAGCA	CTCCCTCACC	CTGCGCTGGG	2760
	AGCCGCTGCC	CAGAGCGCAG	GGCTTCCTTC	TGCACTGGCA	ACCTGAGGGT	GGCCAGGAAC	2820
10	AGRECCOORGE	cergggggggg	GAGCIYCAGCA	CCTATCACCT	GGACGGGCTG	GAGCCAGCGA	2880
	CO CO CON COC	COTTONOCOCO	ACTOTOCTAC	COCCOCCTOC	AGAAGGGGCCC	TCTGCAGAGG	2940
	CHCHGIACCG	CGIGNOGCIO	AGIGICCIAC	0000000100	A CONTROCCOC	CONCORDING COM	2000
	TGACTGCGCG	CACTGAGTCA	Cercurerre	CARGCATTGA	ACTACGIGIG	GIGGACACCI	3000
	CGATCGACTC	GGTGACTTTG	GCCTGGACTC	CAGTGTCCAG	GGCATCCAGC	TACATCCTAT	3060
	CCTGGCGGCC	ACTCAGAGGC	CCTGGCCAGG	AAGTGCCTGG	GTCCCCGCAG	ACACTTCCAG	3120
15	GGATCTCAAG	CTCCCAGCGG	GTGACAGGGC	TAGAGCCTGG	CGTCTCTTAC	ATCTTCTCCC	3180
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	gececcarge	CCTGGCGGAT	GEGGEGETECC	TACCACATGC	CACTCAAGAC	AATGCTCACC	3300
	aracanaac	TACCAGGAGG	GEOCEGGAGO	GTCTGGTGTT	GGCACTTGGG	CCTCTTGGGC	3360
	Ch Ch Cocch Cff	mencemecee	OTTO CTYCETT	A CACTCATCO	acceptorces.	CTGTTCCCAC	3420
20	CHCMGGCMGI	TCAGGITGGC	CIGCIGICAL	macata a acas	acceptance	00000100000	3400
20	TGANTGGCTC	CCATGACCTT	GGCATTATCT	TOCHOOMS OF THE	CCGTGMCNTG	COC: NCA:00	3540
	ACCCAAGTGG	GAACAACCIG	OGCACAGCG	TOSTUNDAGO	TCACAGATAC	AIGITOSCAC	3540
	CAGATGCTCC	TGGGCGCCGC	CAGCACGTAC	CAGGGGTGAT	GGTTCTGCTA	GTGGATGAAC	3600
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	OTOTOCOCCAC	AGCCCCTGTGT	CAGGCATCCT	TOACTACTOA	GCCCCGGCCA	GMGCCCTGCC	3840
	Cacacan	MOCOLIGICO.	CACAAGGGGG	A D C CTTTTTTTT	CATOGGCCTG	AGAGGACAAG	3900
	CAGIGIATIO	100000000	CHIGHNOGOGG	ANCOTOGNOA	macroccocc	CCCCPGGGGG	2060
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	0000000000	ACCCOMMOCIA	CONTROL COCCO	mena accorda	CARAGOCGAT	COTTOGGGAGC	4320
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40	TGCCAGGGGT	TGCTGGACGT	CCTGGAGCCA	AGGGTCCTGA	AGGGCCACCA	GGACCCACTG	4680
	GCCGCCAAGG	AGAGAAGGGG	GAGCCTGGTC	GCCCTGGGGA	CCCTGCAGTG	GTGGGACCTG	4740
	OTO TO TOO	ACCOUNTAGES	Changeone	ATOTOGOGGG	egerggggeee	AGAGGAGGTA	4800
	000001000	10000011001	00000000000	COMMOGRACIE	MOCTOCAGAC	CCTCCCCCCC	4060
	CCGGAGTCCA	AGGGGAACGG	GGCCCACCCG	GCTTGGTTCT	OLGAGORGAC	000000000	4000
45	AGGGAGACCC	TGGAGACCGG	GGTCCCCATIG	GCCTTACTGG	CAGAGCAGGA	CCCCCAGGTG	4720
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	GCCCCCGAGG	TODTADACOA	GAAGTTGGAG	AGAAAGGTGA	CCAGGGTCCT	CCGCCTGACC	5040
	CGGGTTTGCC	TGGAAAAGCA	GGCGAGCGTG	GCCTTCGGGG	GGCACCTGGA	GTTCGGGGGC	5100
	CTGTGGGTGA	AAAGGGAGAC	CAGGGAGATC	CTGGAGAGGA	TGGACGAAAT	GGCAGCCCTG	5160
	GATCATCTGG	ACCCAAGGGT	GACCCTGGGG	AGCCGGGTCC	CCCAGGACCC	COGGGAOGGC	5220
50	TOGTAGACAC	AGGACCTGGA	GCCAGAGAGA	AGGGAGAGCC	TOGGGGACCCC	GGACAAGAGG	5280
20	amacmoasaa	COCCARCOCK	CAMPOONCOO.	macamacana	CCCTCCCCAA	AGGGGGCATTG	E240
	GICCICGNGG	00000000	***********	aggs gggs ag	mamacasaaa	CONCONCINC	6400
	AAGGGTTTCG	GGGACCCCCA	GGCCCACAGG	GGGACCCAGG	TOTOGRAGE	CONSCINOSAS	5400
	AAAAGGGTGA	CORGGGTCCC	CCTGGGCTGG	ATGGCCGGAG	COGACTOGAT	GGGAAACCAG	5460
	GAGCCGCTGG	GCCCTCTGGG	CCGAATGGTG	CIGCAGGCAA	AGCIGGGGAC	CCAGGGAGAG	5520
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	TACCGGGAAA	GCCAGGCGAG	GATGGGAAAC	CTGGCCTGAA	TGGAAAAAAC	GGAGAACCTG	5640
	gggagggggg	AGANGACGGG	aggaaggagag	agaaaggaga	TTCMGGGGGCC	TCTGGGAGAG	5700
	A DOCUMENTOS	20000000000000	compandormo	CACCTOCTOC	TATOOMYSCA	CCCCPGGGGG	5760
	amage aggam	000000000000000000000000000000000000000	amagagagama	OTTO CONTROL	mmmmorm over	arcochacha	5020
60	CTCCMGGCCT	CCCAGGGCCA	GIGGGCCCIC	CIGGCOMOGG	1111001001	drocondono	5000
00	GCACGGGCCC	CARGOGTGAC	CUTTUGGGGAGA	CIGGATCCAA	MOGGGMGCMG	GGCCTCCCTG	2000
	GAGAGCGTGG	CCTGCGAGGA	CAGCCTGGAA	GTGTGCCGAA	TOTOGRATUGG	TIGGIGGANA	5940
	CTGCTGGCAT	CAAGGCATCT	GCCCTGCGGG	AGATCGTGGA	GACCTGGGAT	GAGAGCTCTG	6000
	GTAGCTTCCT	GCCTGTGCCC	GAACGGCGTC	GAGGCCCCCAA	GGGGGACTCA	GGCGAACAGG	6060
	GCCCCCAGG	CAAGGAGGGC	CCCATCGGCT	TTCCTGGAGA	ACGCGGGCTG	AAGGGCGACC	6120
65	GTGGAGACCC	TOGCCCTCAG	GGGCCACCTG	GTCTGGCCCT	TGGGGAGAGG	GGCCCCCCCC	6180
	accerrecea	cerraceaga	GAGCCTGGAA	AGCCTGGTAT	TCCCCGGGCTC	CCAGGCAGGG	6240
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	C100030101	GGGAGAGGCA	CONTRACTOR	ORGANIAGOSG	maga tagggga	accanacaca	6366
	AACGIGGAGA	ACAGGGCAGA	GATGGCCCTC	CIGGACICCC	IGOVACCCCI	000000000	6360
70	GACCCCCTGG	CCCCAAGGTG	TCTGTGGATG	AGCCAGGTCC	TOGACTETET	GGNUARCNOG	6420
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	AAGGAGACAG	GGGTGTGCCA	GGCATCAAAG	GAGACCGGGG	AGAGCCTGGA	CCGAGGGGTC	6540
	AGGACGGCAA	CCCGGGTCTA	CCAGGAGAGC	GTGGTATGGC	TGGGCCTGAA	GGGAAGCCGG	6600
	апетоськака	TOTALGAGGE	CONCETTERCE	CAGTGGGTGG	TCATGGAGAC	CCTGGACCAC	6660
	chachacca	GCCHCTHCCT	GGCCCTGCAG	GACCCCAAGG	ACCITCION	CTGAAGGGGG	6720
75	CIGGIGCCC	0001011001	0000010010	a accept a const	a component	OCONTROCCO O	cane
15	NOCCIOUAGA	GACHGGACCT	CONSUMERS	accidencing		COMMESCOCIAC	6046
	Trectegace	CUCCGGCCCT	TUAGGCUTTG	TOGGTUCACA	GUGGTUTCCA	CONTRACTO	6840
	GACAAGTGGG	GGAGACAGGG	AAGCCGGGAG	CUCCAGGTCG	AGATOGTGCC	AU TOGAAAAG	6900
	ATGGAGACAG	AGGGAGCCCT	GGTGTGCCAG	GGTCACCAGG	TCTGCCTGGC	CUTGTOGGAC	6960
	CTAAAGGAGA	ACCTGGCCCC	ACGGGGGCCC	CTGGACAGGC	TGTGGTCGGG	CTCCCTGGAG	7020
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	CCAAAGGTYGA	CCGAGGACTG	CCAGGGGCGG	GAGGCGAGAA	GGGTGAAGCT	OGCCGTGCAG	7140
	GGGAGCCCGG	AGACCCTYCGG	GARGATGCTC	AGAAAGGGGC	TOCAGGACCC	AAAGGTTTCA	7200
	2000000000	NOOT ORDOGOG	O'MONT GOLD	COCCECCOCC	TOTOGOGO	CCROCHETCA	7260
	MOGREGACCC	MUCAUTUUGG	U1CCCGGGCT	COUCTOOGCC	#CONTROL OF	CONGREGATION COM	7200
85	AUGGAGATCT	GGGCTCCCT	GGCCTGCCCC	GIGCTCCTCC	1011011000	TICCCGGGTC	/320
00	AGACAGGCCC	TCGAGGAGAG	ATGGGTCAGC	CAGGCCCTAG	TUGAGAGCOGG	GUTCTUUCAG	7380
	GCCCCCCAGG	GAGAGAAGGA	ATCCCAGGAC	CCCTGGGGCC	AUCTGGACCA	CUGGGGTCAG	7440
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		AGGCGAGCGT					7560
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	GTGATGTTGG	GAGTGCAGGA	CTAAAGGGTG	ACAAGGGAGA	CTCAGCTGTG	ATCCTGGGGC	7680
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	AACCTGGTGC	AGCAGGGATC	CCTGGTGACC	COGGATCCCC	AGGAAAGGAT	GGAGTGCCTG	7920
	GTATCOGAGG	AGAAAAAGGA	GATGTTGGCT	TCATGGGTCC	CCGGGGCCTC	AAGGGTGAAC	7980
4.0	GOOGAGTGAA	GGGAGCCTGT	GGCCTTGATG	GAGAGAAGGG	AGACAAGGGA	GAAGCTGGTC	8040
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		GGCCCCTGGC					8160
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20		GTACTCTGAA					8700
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		CTGTGGAGGG					8880
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Seq ID NO: 63 Protein sequence:

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		AA SAQGVRFA					120
		FLPOLARPGV					180
40		TSDFFFFFVND					240
		ONTARSGRAT					300
		YANSIGEAVS					360
		OELGPGOGSV					420
		ILLSWNLVPE					480
45		HEVATPATVV					540
		LVLPGSQTAF					600
		ATRURVANGE					660
		REEGPAAVIV					720
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50	RLOILNASSD	VLRITHVGVT	GATAYRLANG	RSEGGPMRHO	ILPGNTDSAE	IRGLEGGVSY	840
	SVRVTALVGD	REGTPUSIUV	TTPPEAPPAL	GTLHVVQRGE	HSLRLRWEPV	PRACGFLLHW	900
	OPEGGOEQSR	VLGPELSSYH	LDGLEPATQY	RVRLSVLGPA	GEGPSAEVTA	RTESPRVPSI	960
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		VLDGVRGPEA					1080
55	LALGPLGPQA	VQVGLLSYSH	RPSPLFPLNG	SHDLGIILQR	IRDMPYMDPS	GNNLGTAVVT	1140
	AHRYMLAPDA	PGRRQHVPGV	MVLLVDEPLR	GDIFSPIREA	QASGLNVVML	GMAGADPEQL	1200
	RRLAPGMDSV	QTFFAVDDGP	SLDQAVSGLA	TALCQASFTT	QPR PEPCPVY	CPKGQKGEPG	1260
		PGDPGLPGRT					1320
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60	PLGDPGPRGP	PGLPGTAMKG	DKGDRGERGP	PGPGEGGIAP	GEPGLPGLPG	SPGPQGPVGP	1440
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		QGERGPPGLV					1620
65		GRDGEVGEKG					1680
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		RGPPGPQGDP					1800
		PGLRGEQGLP					1860
		DGPKGERGAP					1980
70		GKEGPIGFPG					2040
70		VGEAGRPGER					2100
		GLKGAKGEPG					2160
	PGLSGEQGPP	GPRGPPGPVG	SNGDQGPRGD	RGVFGINGDR	CD COL MODDO	BOGDEGERON B	2220
	AGPEGREGIQ	PPGPSGLVGP	OCCUPATION	COMMONANTO	DECIN CONTROL	PUCCHARGE	2280
75	GPIGAVGLPG	EPGPTGAPGO	QUARGEROUV	GETOKPOOR NO	Dr. (1/CHDON VC	DDG DGDDG	2340
13	GLEGEVGERG	CDPGEDGOKG	ADGDPGANG	PURCHAGENO	DEVOSEGMAG	LCT DCL DCAD	2400
	CHUCEPOORC	PRGEMGOPGP	OCEDAL POOL	CHECKROSIC	pagangguan	DOLLEGILLONE	2460
	apparer non	RGERGEPGIR	GENGUNGEE	DRECTFORM	DODDODAGE	CONGULATIONS	2520
		PRGAKGDMGE					2580
80	CITCHOCOBC	AAGIPGDPGS	DOVINGUEGER	CENCENCENC	DEGLETER OF	KGPGGITGIK	2640
00		RPGLAGHKGE					2700
		FPGPSGNDGS					2760
		PGPAGPRGEK					2820
		VPVLRVSHAE					2880
85		RWYHRAVTGS					2940
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WO 02/086443 Seq ID NO: 64 DNA sequence Nucleic Acid Accession #: NM_006945 Coding sequence: 1-219

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	TGTCCACAGC	CCTGCCCACC	TCAGCAGTGC	CAGCAGAAAT	ATCCTCCTGT	GACACCTTCC	180
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Seq ID NO: 65 Protein sequence: Protein Accession 8: NP_008876

15

20 Seq ID NO: 66 DNA sequence Nucleic Acid Accession #: NM_005629.1 Coding sequence: 639-2546

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	ccccccccc	GAAGGAGAGG	GCGAGGCGCG	CCCGAGCCGC	caccaccacc	GCCACOGCCG	120
	CCGCCGCCAC	CACCGCCACC	GGAGTCGCGG	GCCAGCCGGG	CAGCCTCCGC	GGGCCCCGGC	180
20	caaaacaaaa	accaccacacc	ACAGGCCCCT	GCTCCGGCCG	TCGTTTGCAG	ACCGCGGGGCG	240
30			TTAGGATGAG				300
			CAGGAGCCTC				360
			GGGGGGGGG				420
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35			ccccaccca				
33	CCTCGGGGGCC	CTCCCCCGGTG	CCGCCGGTGC	CCCCCCCCTG	ACCIGCOGCOC	CCCGTGAGGC	600
	GCCGCGACCC	COGCCCGGGCC	GTGCGGCCCG	CCGGGGCCAT	GGCGAAGAAG	AGGGGGGAGA	660 720
	ACGCCATCTA	TAGCGTGTCC	GGCGACGAGA	AGAAGGGCCC	CCTCATCGCG	CCCGGGCCCG	780
	ACGGGGCCCC	GGCCAAGGGC	GACGGCCCCG	TGGGCCTGGG	GACACCCGGC	GGCCGCCTGG	
40	COGTGOCGCC	GCGCGAGACC	TGGACGCGCC	AGATGGACTT	CATCATGTCG	TGCGTGGGCT	840
40	TOGCCGTGGG	CTTGGGCAAC	GTGTGGCGCT	TCCCCTACCT	GIGCTACAAG	AACUGCGGAG	900 960
	GTGTGTTCCT	TATTCCCTAC	GTCCTGATCG	CCCTGGTTGG	AGGAATCCCC	ATTTTCTTCT	1020
	TAGAGATCTC	GCTGGGCCAG	TTCATGAAGG	CCGGCAGCAT	CANTOTCIGG	AACATCTGTC	1020
	CCCTGTTCAA	AGGCCTGGGC	TACGCCTCCA	TGGTGATCGT	CITCIACIGC	AACACCTACT	1140
45	ACATCATGGT	GCTGGCCTGG	GGCTTCTATT ACCTGGAACA	ACCTGGT CAA	COMMONTAL	MCCMCGCIGC	1200
43	CCTGGGCCAC	ATOTOGCCAC	CTGGCCAACC	CICCOMCIG	COLCOMONIC	CI COCCACO	1260
	ANGACTOTOC	CANTGCCAGC	GAGAACAAAG	DOMECTICION	CENGCIIGCI	GMCCGCCGG1	1320
	CCCCTGTCAT	CGMSTTCTGG	GTGACCCTTT	CONTRACTOR	OTCIOGGGGG	CIGGROGIGC	1380
	CMGGGGGCCCT	CAACIGGGAG	AAATCCACGG	GICIGCIOGC	CIGCIGGGIG	CLOGICIACI	1440
50	TCTGTGTCTG	GANGGGGGTC	CTGCTGGTGC	CHANGATOGT	COMCOCOCOC	GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1500
50	CCTACGTGGT	CCTGGTGGTG	COTGACTGGT	GIGGAGIGCI	CERCUTGOC	GCCCTGGHTG	1560
	JEGGGGGGGG	CINICICANO	TTTTCTTACG	CODIGCIGGG	acadaccercano	LCAGCCCTGG	1620
	ATGCGGGGAC	COMMITTIC	AACAACTGCT	PCM1100CC:	CATCATCCTG	COTOTOTO	1680
	1010ECIACAA	CACCUTCHAC	GCTGGCTTCG	MOOTOTOTO	CATCCTGGGG	TTCATGGCTG	1740
55	ACMSTOOGAC	COMMUNICATION OF THE COMMUNICA	TCCAAGGTGG	CAGAGTCAGG	acceaacces	GCCTTCATCG	1800
55	CAGAGGGGGG	COLOGRAPICACO	CIGATOCCAG	TOGOTOTO	cragacracc	CTCTTCTTCT	1860
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	CONTROCTOR	OCTOCTOCO	GCCTCCTACT	ACTITICCTOTE	DEDDDGGGGG	ATCTCTGTGG	1980
	COCTOCTOR	TOCCUCTO	TTTGTCATCG	ATCTCTCTCTAT	COTCACTCAT	GGCGGGATGT	2040
60	ACCTOTOTA	CCTOTTTCAC	TACTACTCGG	CCAGCGGCAC	CACCOTTSCTC	TOGCAGGCCT	2100
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			CCTTGCCCCT				2220
			TTCATCTTCA				2280
	ACAACACCTA	COTTOTACCO	TGGTGGGGTG	AGGCTATGGG	CTGGGCCTTC	GCCCTGTCCT	2340
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	CTCAGGACGC	AGATGTCAGG	GGCCTGACCA	CCCTGACCCC	AGTGTCCGAG	AGCAGCAAGG	2520
	TOGTOGTGGT	GGAGAGTGTC	ATGTGACAAC	TCAGCTCACA	TCACCAGCTG	ACCTCTGGTA	2580
	GOCATAGCAG	CCCCTGCTTC	AGCCCCACCG	CACCCCTCCA	GGGGGCCTGC	CTTTCCCTGA	2640
70	CACTTTTTGGG	GTCTGCCTGG	GGGAGGAGGG	GAGAAAGCAC	CATGAGTGCT	CACTAAAACA	2700
			AACGCCAAAA				2760
	TCCCCCTCCA	COCCTAGOOG	AGCTGGTCCT	AGGCCCCGCC	TAGTGCCCCA	CCCCCACCCA	2820
	CAGTGCTGCA	CTCCTCCTGC	CCCTGCCACG	CCCACCCCCT	OCCCACCTCT	CCAGGCTCTG	2880
	CTCTGCAGCA	CACCCGTGGG	TGACCCCTCA	CCCCAGAAGC	AGCAGTGGCA	GCTTGGGAAA	2940
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	GAGGGGGAGC	AGAACCAAGG	CAAATATTTC	AGCTGGGCTA	TACCCCTCTC	CCCATCCCTG	3060
	TTATAGAAGC	TTAGAGAGCC	AGCCAGCAAT	GGAACCTTCT	GGTTCCTGCG	CCAATCGCCA	3120
	CCAGTATCAA	TIGIGIGAGC	TTGGGTGCGA	GTGCACGCGT	GCGTGAGTAC	GGAGAGTATA	3180
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	TTTCTAAAAA	GAGGAAGGAG	CCCAAACCAT	CCTCTCCTTA	CCACTCCCAT	CCCTGTGAGC	3360
	CCTACCTTAC	COCTCTGCCC	CTAGCCAAGG	AGTGTGAATT	TATAGATCTA	ACTITICATAG	3420
	GCAAAACAAA	AGCTTCGAGC	TGTTGCGTGT	GTGACTCTGT	TGTGTGGATG	TGCGTGTGTG	3480
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	GGGCTGCTAA	CCTGGCCTGC	TCAGGCTTCC	CACCCTGTGC	GGGGCACACC	CCCAGGAAGG	3660
	GACCCTGGAC	ACGCTCCCA	CGTCCAGGCT	TAAGGTGGAT	GCACTTCCCG	CACCTCCAGT	3720

CTTCTGTGTA GENCTITAA CCCACGTTTG TCTGTCACGT COAGTCCCGA GACGGCTGAG 3780
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AAAACC

Seq ID NO: 67 Protein sequence: Protein Accession #: NP_005620.1

31 41 51 10 120 INVHNICPLE KOLGYASAVI VEYCHTYYIM VLANGFYYLV KSFTTTLPNA TCCHTWNTPD 180 CVETERHEDC AMASLAMLTC DQLADRRSPV IEFWENKVLR LSGGLEVPGA LNWEVTLCLL 240 15 CVELTRIBLE CHARLESHIT DUDANTSEEV TERRIBLYONG BOOLSYNON BANKINGEN CHARLESHIT VYFTATFYYY VLVVILVARGY LIPAGADGI YYTRAFDWSLL GSEQWYLDAG TQIFFSYAIG IGALTALGSY HRRHINCYND AITLALING TSFRAGSVYF SILGHMARD GYHISKYABS GPOLAFLAYR BAVTHUWAR HAALFFRHI LIGHDSQFY GUSGFTTGLL DLLBASYYFF FQREISVALC CALCFVIDLS MVTDGGNYFF QLEDYYSASG 300 360 420 480 TILLWOAFNE CYVVAWVYGA DRFMDDIACM IGYRPCPWMK WCWSFFTPLV CWGIFIFNVV 540 20 YYEPLVYNYT YYYPAWGEAM GWAPALSSML CVPLHLLGCL LRAKSTMAER WQHLTQPIWG LHHLEYRAQD ADVRGLTTLT PVSESSKVVV VESVM 600

25 Seq ID NO: 68 DNA sequence Nucleic Acid Accession #: NM_021953.1 Coding sequence: 178-2469

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40		CTGCAGCTAG					660
		AGACCIGIGC					720
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		GGATTGAGGA					1020
		TCCGCCACAA					1080
		TOTCCTTCTG					1140
	CAGGIGITTA	AGCCACTGGA	CCCAGGGTCT	CCACAATTGC	COGAGCACTT	GGAATCACAG	1200
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	GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
	CAGTTCCCGG	TGAACCAGTC	ACTGGTGTTG	CAGCCCTCGG	TGAAGGTGCC	ATTGCCCCTG	1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCC	CATTGCCCCC	1440
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		CCTCCCAGCT					1980
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		CGGAGCCACA					2340
70		ACACAATGAA					2400
//		AGGACCCACT					2460
		GCCCTGCCCT					2520
		CACCCCAAGC					2580
		CCTCCCTGAT					2640
75	CTTGTGTTCC	CCAAGAGTAT	CTGATTCCTC	TGCTGTCCCT	GCCAGGAGCT	GAAGGGTGGG	2700
15		GCAATGGTGA					2760
		CTTACCTTCC					2820
	TCCAAATTAT	CCTCTAATTA	TAAATUTAAU	CTTATTTCCT	TAGATCATTA	TCCAGAGACT	2880 2940
	GOCAGAAGGT	GGGTAGGATG	ACCTGGGGTT	TCAATIGACT	CONTROL	GCTTTTAGTT	3000
80	TTGATAGAAG	TGCAGGGACC	CAGTGCACGG	CARROTTOCAG	GCTGAGGTAC	CIGGATCITG	3060
00		TCCCCGTGTT					3120
	PACEGORIA	TATTGGGTCA	COMMETCAG	CITICUIGGA	NOGATIONATC	CARCTGARGA	3120
	ANSTUTTITG	TATTGGGTCA	COAGTIGAAT	- 100001000	TO A THE A PROPERTY	CHALIDANGC	3240
		TGCCCAGATG					3300
85		GGCTTCCTTA					3360
05	CONCUTGOCT	TGGGTGTGAG	COLLEGERA	ADCICTABOT	ACTORAGE	ACCOUNT OCCUPA	3420
				NACACIMACT	ACTUMATARA	MUCUMMOGTG	3220
	GACCNAAAAA	AAAAAAAAA	AAAA				

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Seq ID NO: 69 Protein sequence:

	Protein Accession #: NP_068772.1											
5	1	11	21 	31 	41 	51 						
	GIKIINHPTM	LKRRRLPLPV PNTQVVAIPN AKRTEVTLET	MANIHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTOPPG	120 180					
10	LSNIQWLREM	SSDGLGSRSI	KQENEEKENC	HLEQRQVKVE	EPSRPSASWQ	NSVSERPPYS	240					
		STERKRMTLK					300					
	ANGKVSFWTI	HPSANRYLTL	DOVEKPLDEG	SPQLPEHLES	QQKRPNPELR	RNMTTKTELP	360					
		LPRVSSYLVP APLSSAGPGK					420 480					
15		APSFKEESSH					540					
13		LPPCVDEPEL					600					
		TPSKSVLPRT					660					
		ESPORLLSSE					720					
		LSKILLDISF										
20												
	Seq ID NO: 70 DNA sequence											
25	Nucleic Acid Accession #: BC006529.1 Coding sequence: 178-2424											
23		11	21	31	41	51						
	ī	11	î*	ĭ	ĩ*	ĭ						
	GGCACGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTCGGCCC	60					
		GGAGCCCGGA					120					
30		GGTCCACACT					180					
	AAAACTAGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCCT	TCCTGTTCAA	240					
	AATGCCCCAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCCTGCCCA	ACAGGAGTCT	300					
	AATCAAGCAG	AGGCCTCCAA	GGAAGTGGCA	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360					
35	ATCAAGATTA	TTAACCACCC ACAGCATCAT	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAAT	420 480					
55		AATTCATCCT					540					
	OGGCCCTCAAA	CCCARACCAG	CTATGATGCC	AAAAGGACAG	AAGTGACCCT	GGAGACCTTG	600					
		CTGCAGCTAG					660					
40		AGACCTGTGC					720					
40		AGTGGCTTCG					780					
	CAAGAGATGG	AGGAAAAGGA	GAATTGTCAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840					
	CCTTCGAGAC	CATCAGCGTC	CTGGCAGAAC	TCTGTGTCTG	AGCOGCCACC	CTACTCTTAC	900 960					
		GGATTGAGGA					1020					
45		TCCGCCACAA					1080					
75	ANTIGCANGO	TCTCCTTCTG	GACCATTCAC	CCCAGTGCCA	ACCICCACTA	GACATTGGAC	1140					
	CAGGTGTTTA	AGCAGCAGAA	ACGACCGAAT	CCAGAGCTCC	GCCGGAACAT	GACCATCAAA	1200					
	ACCGAACTCC	CCCTGGGCGC	ACGGCGGAAG	ATGRAGOCAC	TECTACCACG	GGTCAGCTCA	1260					
60		CTATCCAGTT					1320					
50		CCCTGGCGGC					1380					
	GTCCGCATTG	CCCCCAAGGT	GCTGCTAGCT	GAGGAGGGGA	TAGCTCCTCT	TTCTTCTGCA	1440					
	GGACCAGGGA	AAGAGGAGAA AGGAGGAAGA	ACTCCTGTTT	GGAGAAGGGT	TTTCTCCTTT	GCTTCCAGTT	1500 1560					
	CAGACTATCA	AGAGOCCTCC	ARTCCAGCCT	TOTO CONTROL	CCCCCCCACACTT	TTTCAAAGAG	1620					
55	GLATCATOTO	ACTOCTOGGA	GGATTOGTCC	CANTOTOGO	CCCCAAGACC	CARGARGTCC	1680					
00		TTAGGTCCCC					1740					
	GAGAGGAGGG	AGAGGAGCOG	GTCTCGGAGG	AAACAGCATC	TACTGCCTCC	CTGTGTGGAT	1800					
	GAGCCGGAGC	TGCTCTTCTC	AGAGGGGCCC	AGTACTTCCC	GCTGGGGCCGC	AGAGCTCCCG	1860					
60	TTCCCAGCAG	ACTOCTCTGA	COCTGCCTCC	CAGCTCAGCT	ACTCCCAGGA	AGTGGGAGGA	1920					
60	CCTTTTAAGA	CACCCATTAA	GGAAACGCTG	CCCATCTCCT	CCACCCCGAG	CARATCTGTC	1980					
	CTCCCCAGAA	CCCCTGAATC	CIGGAGGCTC	AUGCCCCCAG	CCAAAGTAGG	GGGACTGGAT	2040					
	TICAGCCCAG	TACAAACCCC GCACCACTCC	CLAGGGTGCC	TUTUACUCCT	TOCCTUACCC	CCITGGGGCTG	2160					
	A TOGATOTCA	AACCCTTAGA	CATGUMANGT	and controls	CONTRACTOR CO.	TCCCTCaGAT	2220					
65	ATAGACGTCC	CCAAGCCAGG	CTCCCCCGGAG	CCACAGGTTT	CTGGCCTTGC	AGCCAATCGT	2280					

CHARTINE MACCITION OF CHINATICS CHOICETTIS GEALUTITIS TOCCHOMIN TRANSCRIPC CONSIGNOUS CHICAGOTTIS CONSIGNOUS CHARTINET TOCCHOMIN TRANSCRIPC CONSIGNOUS CHICAGOTTIS CONSIGNOUS CHARTINET CONSIGNOUS CHICAGOTTIS CONSIGNOUS CHICAGOTTIS CONSIGNOUS CHICAGOTTIS CHICAGOTTIS CONSIGNOUS CONSIGNOU

AAATAGTATA AATTCTCCAA ATTATCCTCT AATTATAAAT GTAAGCTTAT TTCCTTAGAT

CATTATCCAG AGACTGCCAG AAGGTGGGTA GGATGACCTG GGGTTTCAAT TGACTTCTGT TCCTTGCTTT TAGTTTTGAT AGAAGGGAAG ACCTGCAGTG CACGGTTTCT TCCAGGCTGA

OSTACCIGGA TOTTOGOTTO TICACTICAS GGACCOAGAC AASTGGATOT GOTTOCCAGA GTCCTTTTTTG COCTTOCCTG CCACCTCCCC GTGTTTCCAA GTCAGCTTC CTGCAAGAAG

AMATICTIST TAMANASTI TITTGTATTS GGTCAGGAST TGAATTIGG GTGGGAGGAT GGATGGAACT GAAGAAGT GTGGGTGCC MGATGTGGC TATTAGATGT TICTCTGATA

ATGTCCCCAA TCATACCAGG GAGACTGGCA TTGACGAGAA CTCAGGTGGA GGCTTGAGAA

GGCCGRARGG GCCCCTGRCC TGCCTGGCTT CCTTAGCTTG CCCCTCAGCT TTGCRAMGAG 3300 CCRCCCTAGG CCCCACCGG CCCACGGG GTGAGCAGC TTGAGRACAC TAACTACTCA 3360 ATRARAGCGA AGGTGGAARA ARAARAARA ARARAARA

Sec ID NO: 71 Protein sequence: Protein Accession #: AAH06529.1

	1	11	21	31	41	51	
	1	1	1	1	1	1	
_		LKRRRLPLPV					60
5		PNTQVVAIPN					120
		AKRIEVILET					180
		SSDGLGSRSI					240
		STERKRMTLK					300
		HPSANRYLTL					360
10	SYLVPIQFPV	MOSLVLQPSV	KVPLPLAASL	MSSELARHSK	RVRIAPKVLL	AEEGIAPLSS	420
	AGPGKEEKLL	FGEGFSPLLP	VQTIKEEEIQ	PGEEMPHLAR	PIKVESPPLE	EWPSPAPSFK	480
		SQSPTPRPKK					540
	DEPELLIFSEG	PSTSRWAARL	PFPADSSDPA	SQLSYSQEVG	GPFKTPIKET	LPISSTPSKS	600
	VLPRTPESWR	LTPPAKVGGL	DESPVOTEQG	ASDPLPDPLG	LMDLSTTPLQ	SAPPLESPOR	660
15	LLSSEPLDLI	SVPEGNSSPS	DIDVPKPGSP	EPQVSGLAAN	RSLTEGLVLD	TMNDSLSKIL	720
	LDISFPGLDE	DPLGPDNINW	SQFIPELQ				

20 Seq ID NO: 72 DNA sequence Nucleic Acid Accession #: U74612.1 Coding sequence: 178-2583

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	Couring nego	Tellice: 176-	1503				
	1	11	21	31	41	51	
	Ī	1	1	1	1	ì	
25	GGCACGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGGCCCT	GGCTCGGCCC	60
	CCAGGTTGGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
		GGTCCACACT					180
	AAAACTAGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCCT	TCCIGTTCAA	240
20	AATGCCCCAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCCTGCCCA	ACAGGAGTCT	300
30	AATCAAGCAG	AGGCCTCCAA	GGAAGTGGCA	GAGTCCAACT	CTTGCAAGTT	TCCMGCTGGG	360
		TTAACCACCC					420
	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAAGAGAG	TGGCAGTAGT	480
	GGGCCCAACA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
35		CCCARACCAG					660
33	GGACCAAAAC	CTGCAGCTAG	GGATGTGAAT	CTTCCTAGAC	CACCTGGAGC	CCTTTGCGAG	720
	CAGAAAACGGG	AGACCTGTGC AGTGGCTTCG	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCIA	780
		AGGAAAAGGA					840
		CATCAGCGTC					900
40	CCTTCGMGAC	TACAATTCGC	CIGGOMONAC	TCIGIGICIO	AGCGGCCACC	mmmaaaaana	960
70	ATOGCCATGA	GGATTGAGGA	CATCHICAGC	TACTUTABOO	ACCOUNTGRO	accadacting	1020
	ALCIAIRCGI	TCCGCCACAA	CONTINUE	CACCIACATOR	TTOTOCCAN	GACGTCTGCC	1080
		TCTCCTTCTG					1140
	CAGGTGTTTA	AGCCACTGGA	COCAGGGTCT	CCACAATTICC	CCGAGCACTT	GGAATCACAG	1200
45		CGAATCCAGA					1260
		GGAAGATGAA					1320
		TGAACCAGTC					1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCCC	1440
		GGGAACAGGT					1500
50	CGAGATTTTG	GTACACCCAT	CACCAGCTTG	TTTAATTTTA	TCTTTCTTTG	TTTATCAGTG	1560
	CTGCTAGCTG	AGGAGGGGAT	AGCTOCTCTT	TCTTCTGCAG	GACCAGGGAA	AGAGGAGAAA	1620
	CTCCTGTTTG	GAGAAGGGTT	TTCTCCTTTG	CTTCCAGTTC	AGACTATCAA	GGAGGAAGAA	1680
	ATCCAGCCTG	GGGAGGAAAT	GCCACACTTA	GCGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
		GGCCCTCCCC					1800
55		AATCTCCCAC					1860
		TCTCGGAAAT					1920
						GCTCTTCTCA	1980
		GTACTTCCCG					2040
60		AGCTCAGCTA					2100
UU	GAAACGCTGC	CCATCTCCTC	CACCCCCGAGC	AAATCTGTCC	TCCCCAGAAC	CCCTGAATCC	2160
	TGGAGGCTCA	CTGACCCCTT	CAAAGTAGGG	GUACTGUATT	TORGUCONGT	ACADOMOCTCC	2220
		CTCCCCCCT					2340
		TCCCCTTTGG					2400
65	Econocontana	CACAGGTTTC	DOGGOODETCC:	CCCICAGAIA	CTCTCACACA	AGGCCTGGTC	2460
05		TGAATGACAG					2520
	CACCACCACC	CACTOGGCCC	TGACAACATC	AACTGGTCCC	AGPTTATTCC	TGAGCTACAG	2580
	TAGAGCCCTG	CCCTTGCCCC	TGTGCTCAAG	CTGTCCACCA	TCCCGGGCAC	TCCAAGGCTC	2640
		AAGCCTCTGA					2700
70	CCCTGCTGCC	TGATTATGCA	AAAGTAGCAG	TCACACCCTA	GCCACTGCTG	GGACCTTGTG	2760
	TTCCCCCAAGA	GTATCTGATT	CCTCTGCTGT	CCCTGCCAGG	AGCTGAAGGG	TGGGAACAAC	2820
						CTGCCCAGCA	2880
		TTCCCTGATC					2940
		ATTATAAATG					3000
75	AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTICTGTT	CCTTGCTTTT	AGTTTTGATA	3060
		CCTGCAGTGC					3120
	TCACTGCAGG	GACCCAGACA	ACTGGATCTG	CTTGCCAGAG	TCCTTTTTGC	CCCTCCCTGC	3180
	CACCTCCCCG	TGTTTCCAAG	TCAGCTTTCC	TGCAAGAAGA	ARTCCTGGTT	AAAAAAGTCT	3240
00						AAGCAGAGTG	3300
80						CATACCAGGG	3360
		TGACGAGAAC					3420
		CTTAGCTTGC					3480
			TGAGAACACT	AACTACTCAA	TAAAAACCGAA	GGTGGACAAA	3540
85	AAAAAAAAA	AAAAA					
00							

Seq ID NO: 73 Protein sequence: Protein Accession #: AAC51128.1

	WO 02.	/086443					
	1	11	21	31	41	51	
5	GIKIINHPTM LRPQTQTSYD LSNIQWLRKM YMAMIOFAIN	PHTQVVAIPH AKRTEVTLET SSDGLGSRSI STERKRMTLK	QNAPSETSEE NANIHSIITA LGPKPAARDV KQEMEEKENC DIYTWIEDHF	LTAKCKESCS NLPRPPGALC HLEQROVKVE PYFKHIAKPC	SGPNKFILIS EQKRETCADG EPSRPSASWQ WKNSIRHNLS	CGGAPTOPPG BAAGCTINNS NSVSERPPYS LHDMFVRETS	60 120 180 240 300
10	ANGKVSFWTI LGARRKMKPL PKVFGEQVVF KLLFGEGFSP EDSSOSPTPR	HPSANRYLTL LPRVSSYLVP GYMSKFFSGD LLPVQTIKEE PKKSYSGLRS	DQVFKPLDPG IQFPVNQSLV LRDFGTPITS BIQPGREMPH PTRCVSEMLV DPASQLSYSQ	SPOLPEHLES LQPSVKVPLP LFNFIFLCLS LARPIKVESP IQHRERRERS	QQKRPNPELR LAASLMSSEL VLLAEEGIAP PLEENPSPAP RSRRKQHLLP	RNMTIKTELP ARHSKRVRIA LSSAGPGKEE SFKEESSHSW PCVDEPELLF	360 420 480 540 600 660
15	SWRLTPPAKV DLISVPFGNS LDEDPLGPDN	GGLDFSPVQT SPSDIDVPKP INWSQFIPEL	SQGASDPLPD GSPEPQVSGL Q	PLGLMDLSTT	PLOSAPPLES	PORLLSSEPL	720 780
20	Nucleic Ac:	74 DNA sequid Accession id Accession ience: 111-	n #: Eos se	quence			
	1	11	21	31	41	51	
25 30	TCATCCTTCT CTCAAGCTGA ATGACAAGAT TTAGTGCCTG AGAATGAGGA	ACTOGTGACG GAGGTCCATA TGAGAAGCCA TGACAAAAAG TAAGAAGATT	TTATAAAGGA CTTCCCAGCT ATAGGCATGA AGCCTGCTGA GGCACAAATT GATTTTCTG CATGGAGCAG	CTOGCTTTTT TCSACATGTT CGATGATGAA ACCTCGCCGA AGTTTCTGTC	GARAGCARAG TCACARATAC GGAGARCTTC TGTCTTTGAG CTTGCTGGGA	ATGAGCAACA ACCAGACGTG CCCAACTTCC AAAAAGGACA GACATAGCCA	60 120 180 240 300 360 420
	GCCCCACCAA	TOGGCCTCCA	GAGACCCCAG	GAACAATAAA	ATGTCTTCTC	CCACCAGA	***
35	Seq ID NO:	75 Protein					
40	1 MSNTQAERSI KKDKNEDKKI	11 IGMIDMFHKY DFSEFLSLLG	21 TRRDDKIEKP DIATDYHKQS	31 SLLTMMKENF HGAAPCSGGS	41 PNFLSACDKK Q	51 GTNYLADVFE	60
45	Nucleic Ac:	76 DNA seq id Accession uence: 111-	n #: Eos se	quence			
	1	11	21	31	41	51	
50	TCATCCTTCT CTCAAGCTGA ATGGCAAGAT TCAGTGCCTG	ACTOSTGACA GAGGTCCATA TGAGAAGCCA TGACAAAAAG	TTATAAAGSA CTTCCCAGTT ATAGGCATGA AGCCIGCTGA GGCATACATT	CTGGCTTTTT TCGACATGTT CGATGATGAA ACCTCGCCAC	GAAAGCAAAG TCACAAATAC GGAGAACTTC TGTCTTTGAG	ATGAGCAACA ACCOGACGTG CCCAATTTCC AAAAAGGACA	60 120 180 240 300 360
55	CAGACTACCA	CAAGCAGAGC	GATTTTTCTG CATGGAGCGG GAGACCCCAG	CCCCCTCTTC	TGGGGGAAGC	CAGTGATCCA	420
60	Seq ID No: Protein Acc	77 Protein cession #: :	sequence: XP_048124.1	31	41	51	
	ī	Ī	ī"	Ĭ .	Ĭ.	Ĩ	
65	KKDKNEDKKI	DFSEFLSLLG	TGRDGKIEKP DIAADYHKQS	SLLTMMKENF HGAAPC9GGS	PNFLSACDKK Q	GIHYLATVPE	60
	Nucleic Ac:	78 DNA seq id Accession	n #: 273678	.1			
70	Coding sequ	uence: 253-	2433	31	41	51	
	ī	Ī	1	1	Ĭ-	Ĭ	60
	CAGAGAGGGA	CGAACCAGGG	TGGTATATCC TGGAAGCGCC	AGGAGCAGCT	GCAGGGAGCC	CTCACGCGGA	120
75	CCTCGCACCG CCTCCCGCCA	TATGGCCGTA CACCTCGCCT CCATGAACCA	GGGAGCCGCT CGCCTCTCTG CTCGCCGCTC GGCTTTGCCG	GAGAGCGAGA CTCTCCTAGG AAGACCGCCT	AGAGCACGCT CCCCGGCCGC TGGCGTACGA	GCTGCCGGCC GCTGCCACCCG ATGCTTCCAG	180 240 300 360
00	COCKCOCKCC	COSTOCAGGA	CCACCTCATC	ATGRECOUTCA	ACCYCCAGAA	GTCCAAGTCT	420
80	TCCCAGTCGT	CCACCCTGAG	CCACTCCAAT CAGCAGGAGC	CGAGGTTCCA	TGTATGATGG	CTTGGCTGAC	480 540
	GGCTCATGGG	GATATCCGAT	CTACAATGGA GGAGAACTGG	ACCCTCAAGC	GGGAGCCTGA	CAACAGGCGC	600
	ACCACOGGGG	CAGGCAGGGA	CATCTGCTTC	ATGCAGAAAA	TCAAGGCGMG	CCGCACTGAG	660 720
85	CCCGACCTCT	ACTGTGACCC	ACGGGGCACC CTACAGCTIT	CTGCGCAAGG	GCACGCTGGG	CAGCAAGGGC	780 840
	CAGAAGACCA	CTGTGCGCCC	CTACAGCTIT	GCCTCCAAGC	AGGACCCTGT	GTATATCCCG	900

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COCATCTCCT GUAACAAGGA CCTGTCCTTT GGCCACTCTA GGGCCAGCTC CAAGATCTGC ACTIVAÇÃOS TOURATORAS TOURACIDADO ATROCOMAÇÃO CIVERAÇÃO A COMO AGOSTO 1020 CAGGATGAGA AGTACCAGGC CATTOGGGCC TATTACATCC AGCATACCIG CITCCAGGAT GAATCTGCCA AGCAACAGGT CTATCAGCTG GGAGGCATCT GCAAGCTGGT GGACCTCCTC 1140 CGCAGCCCCA ACCAGAACGT CCAGCAGGCC GCGGCAGGGG CCCTGCGCAA CCTGGTGTTC 1200 AGGAGCACCA CCAACAAGCT GGAGACCCGG AGGCAGAATG GGATCCGCGA GGCAGTCAGC 1260 CTCCTGAGGA GAACCGGAA CSCCGAGATC CAGAAGGAG TGACTGGGC GCTCTGGAAC CTGTCTTCCA CTGACGAGCT GAAGGAGGAA CTCATTGCCG ACGCCTGCC TGTTCTGGCC 1380 GACCGCGTCA TCATTCCCTT CTCTGGCTGG TGCGATGGCA ATAGCAACAT GTCCCGGGAA 1440 10 GROGAGICA CHARGETT CTTCAATGC ACAGCINCT TAAGGAACT GARCTCGGCC
GATGCAGCC GCCGACCAT GCGTAACTAC CAAGGCTACT TGATTCCCT CATGGCCTAT
GTCCAGGAACT GTGTAGCGG CAACCACT GAACAAGT CTGTAGAAAA CTGAATGCT 1500 1560 1620 CITYCTCACA ACCICTACA COCCOCTOGAC GCCGAGGTGC CCACCOGCTA COGCCAGCTG GAGTATAACG COCGCAACGC CTACACCGAG AAGTCCTCCA CTGGCTGCTT CAGCAACAAG 1740 15 AGCGACAAGA TGATGAACAA CAACTATGAC TGCCCCCTGC CTGAGGAAGA GACCAACCCC 1800 AAGGGCAGGS GCTCGTTGTA CCATTCAGAT GCCATCCGCA CCTACCTGAA CCTCATGGGC 1860 AAGAGCAAGA AAGATGCTAC CCTGGAGGCC TGTGCTGGTG CCCTGCAGAA CCTGACAGCC 1920 AGCAAGEGGC TGATGTCCAG TGGCATGAGC CAGTTGATTG GGCTGAAGGA AAAGGGCCTG 1980 CCACAAATTG CCCGCCTCCT GCAATCTGGC AACTCTGATG TGGTGCGGTC CGGAGCCTCC 2040 20 CTCCTGAGGA ACATGTCCCG CCACCCTCTG CTGCACAGAG TGATGGGGAA CCAGGTGTTC 2100 COSGAGGTGA CCAGGCTCCT CACCAGCCAC ACTGGCAATA CCAGCAACTC CGAAGACATC 2160 TIGITOTICGG COTGOTACAC TGTGAGGAAC CTGATGGCCT CGCAGCCACA ACTGGCCAAG 2220 CAGTACTTCT CCAGCAGCAT GCTCAACAAC ATCATCAACC TGTGCCGAAG CAGTGCCTCA 2280 CCCAAGGCCG CAGAAGCTGC CCGGCTTCTC CTGTCTGACA TGTGGTCCAG CAAGGAACTG 2340 25 CAGGGTGTCC TCAGACAGCA AGGTTTCGAT AGGAACATGC TGGGAACCTT AGCTGGGGCC 2400 AACAGCCTCA GGAACTTCAC CTCCCGATTC TAAGAAGAGA CTGTCCAAGC AAGTTAGGCT 2460 TOCAGGRAGA TATGACCAG CTGAGRAGC CTCAGGCCTC GCTGGATGG GTTTTCTGTC 2520
CATCCTGTGC AGTATTGGG AAAGTTCACA AGAAACTGAG AAGAAACTTA AAAACTGTGG 250 ATAGTGGAAA GATTTTAGA TITTTTTTT CCTTGGGGAA ACTGGCAGGC AATGGGGGTT 30 2700 AGGGAGGTTG GGGCGGGGG GGCTTTCTTG AGTTAAAGGG GCTTATATGT GATGTCAATA TTTCTTCCTC TGAGAAATGG TATATATATG TGTCTAATGT AAGTGTGTGC ATGCATGTGC 2760 GCGTGCATGT GTGTGTGTG GAGTGTCTTA AAGCATAACC ACAAACTGCA AAAAGCTAGG TAAGCTATTT TGTTGCAGCT CATAAGGTGG TGAAAAGGAC TCTCCTGTGT TTCTTACTCA 2820 2880 TAGGCAAGGA CAACATGTGC TITTIGGTGA GCTGCTCATA ATTCCTGAAA TGTGTGGTGC 35 CAGGGCAAGG GGCCCATCAC TGCAGTCAGG CCCTCAGAGG AGTCCTGCAG GCTTCCTACC 2000 3060 AGTOGTCTCC AAGGGTGCAG GAGTAACTGG GGCTGGGCCA GCCTCCCCCC TTACAAGGCT GCTTTCCAGG AAGGGAGGTC TGGTGTATCT CATGGGAGAA TCTGGGGTGT CTGTAGTGTC ACCCCTCCAG CAGGGCCACA AGGACTGAGG TTGGGTAGGT GTGAGGTTCC AGAGGACAGC 3120 AGGACACTOT CHICATOTT GCCAAATGAG GCCTGCTCAG AGGAGTAGGA GCTGAAAGAT 3240 40 OGTGCCTTCC ACCCTCTTGG GCTGTGTGCC CATCAGAGCA GGCTCAGCCT GCAAAGGCCC 3300 TGCATTCAGA GGTCTTGTAA TCTACTTGTT GCAGGAGAAA GAAGGTAAAA AATGATTTTT 3360 TTANGAAAG CTATTTATT GCAGCTCTTT CCCAAGAGCT GTTCTGGGAA TGGCTGGTCT 3420 TOATATTOTO AGRIGAGAGG GGAACAAGTG GGGCTGGGCA TATACCTATT COGGCTTCTA 3480 GTGGGATGGA GTTGGGGTAT AGAAATTAAC CAGGAAGATG TTTCCACCAA GCCTGCTGTG 45 AGTCHATTGA GOGRGTGTTT GGGTCCCAGG AGACTTGGAC GGGGGGAGTT TGGGTAGACT 3600 AGGAAAGGAA AGTGCCATAT CAGGGTACCG GTACCGGCAA GCTCACATCT CAGCCAGGGG 3660 CCATGCCCA CTTCCCCTGA CCCCAGCTGT CTTGTCTCCA CTCTGTGAAA CCCACAGGGG ATGTGATAAA CAGGGCTATT AGGGGTATCA GCCACGTGGA GCCCCCAGAC TCTGTGCACT 3720 3780 TCAGACCAGC AGCAGCAGGA GGGCTCCCGA GGGCCTTATG AGAAAACCTG TGTGGACATC 50 CCTTGGTGTA CACTAAGACA GAGCAGAGCC CAGCGCTCCC AAGCCTTCCT CCTTCCAGCT 3900 TCTACCTCCA TGCTAGCATT GCTGGTGTTA GAGAGGAATT AACTTCCTGG TCTGTGCCCT 3960 4020 TOTOTAGANG ANTATAAGAT GCTOCTOCTC CTCACCCCTT CTCAGGCCTCC TCCCAAGTCT TOCTOTTOTG CACCACCCC GAGTCCAAAC CCACCTCTTG CCCCAGCATT CAGGCTGGAA 4080 AACACTGATG TOGACTCAGT ATGACAACTG AGATGGGGGA AGCCAGACAT GTGAGGACGC 55 4200 TGTCCTCCGA GAGGTGTCCC CGGCTGTTAG CCAGCTGTGC TGTGGTGCTG TGGGTCTGTC ATACOCTCCC TEGCTECTGT TCACACTGGG AGGCCCACTC CEGGCTCACC TCTCCCTCTC 4260 AGGGACCCAC GTGGGAGCCT GGATCCCTGG ACTGTCCTGG GCATAGGTTT CAGGGGCCTC
CTTTGTTGTC ATCAGAACCC AGAGGAATTC TTCTCCTAAA AAATACGTAT GGCATACCAA 4320 4380 TCTGTGCGGG GCAGTGTCCT AAGCACTTAG ACTACATCAG GGAAGAACAC AGACCACATC 60 CCCGTCCTCA TGCGGCTTAT GTTTTCTGGA GGAAAGTGGA GACACAAGTC CTTGGCTTTA 4500 GGGCTCCCCC GGCTGGGGGC TGTGCAGTCC GGTCAGGGCG GGAGGGGAAA TGCACCGCTG 4560 CATGIGAACC TRACAGGCC AGGGGGATGC COCTTCCCCT TAGCACTACC CTGGCCTCCT 4620
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Seq ID NO: 79 Protein sequence: Protein Accession #: CAA98022.1

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5	RNAYTEKSST DATLEACAGA MSRHPLLHRV	GCFSNKSDKM LQNLTASKGL MGNQVFPEVT CRSSASPKAA	MENNYDCPLP MS9GMSQLIG RLLTSHTGNT	EBETNPKGSG LKEKGLPQIA SNSEDILSSA	WLYFSDAIRT RLLQSGNSDV CYTVRNLMAS	YLNIMGKSKK VRSGASLLSN QPQLAKQYPS	540 600 660 720
10	Nucleic Ac	80 DNA sequid Accession tence: 180-1	#: NM_0065	516.1			
15	1	11	21	31	41	51	
15	GTCAGAGTCG	TCCCCGAGTG CAGTGGGAGT TCGCCACCCG	CCCCGGACCG	GAGCACGAGC	CTGAGCGGGA	GAGCGCCGCT	60 120 180
20	TGGAGCCCAG	CAGCAAGAAG	CTGACGGGTC	GCCTCATGCT	GGCTGTGGGA	GGAGCAGTGC	240
20	TTGGCTCCCT	GCAGTTTGGC CAACCAGACA	TACAACACTG	GCTATGGGGA	GAGCATOCTG	CCCACCACGC	300 360
	TCACCACGCT	CTGGTCCCTC	TCAGTGGCCA	TCTTTTCTGT	TOGGGGCATG	ATTGGCTCCT	420
	TCTCTGTGGG	CCTTTTCGTT	AACCGCTTTG	GCCGGCGGAA	TTCAATGCTG	ATGATGAACC	480 540
25	TGCTGGCCTT	GGGCCGCTTC	ATCATCGGTG	TGTACTGCGG	CCTGACCACA	GGCTTCGTGC	600
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	GCAACAAGGA	CGTCGTCGGCCC	CTGCTGCTGA	GCATCATCTT	CATCCCGGCC	CTGCTGCAGT	720 780
20	GCATCGTGCT	GCCCTTCTGC	CCCGAGAGTC	CCCGCTTCCT	GCTCATCAAC	CGCAACGAGG	840
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35	CTGTCGTGTC	GCTGTTTGTG	GTGGAGCGAG	CAGGCCGGCG	GACCCTGCAC	CTCATAGGCC	1200
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	TACCCTGGAT	GTCCTATCTG	TGGTTCATCG	TOGCTGAACT	CTTTGTGGCC	GGTCCACGTC	1380
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40	GCTTCCAGTA	TGTGGAGCAA CTTCATCTTC	CTGTGTGGTC	REGITICATION	CATCATCTTC	COGACCTTCG	1500 1560
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		VYCGLTTGFV SIIFIPALLQ					180 240
~~	LQEMKEESRO	MMREKKVTIL	ELFRSPAYRQ	PILIAVVLQL	SQQLSGINAV	PYYSTSIFEK	300
75	AGVQQPVYAT	IGSGIVNTAF AIFGFVAFFE	TVVSLFVVER	AGRRTLHLIG	LAGMAGCAIL	NTIALALLEQ	360 420
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60

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75

80

85

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			TCAAAGAATA				480
			TGCTGCTGGC				540
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20			ATCAGACTCA				1320
20	MACO S S VOLUM	CACCAAAAA	AAAAAAAAA	SASSASSAS	220022002	444	
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35	couring seq.	adilee. Els-					
55		11	21	31	41	51	
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			AAAAAAAAGC	0.00.00000	Omeoons 03.3m	man mannaaa	60
							120
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50	CONCELCTOR	COLOCTACAC	ATGTACAACT	TOCANACACC	CATTCACCAG	TGCATGGTTT	780
20	CHICAGOCCA	POGGRADA	CACTCATGGA	MULTIPLE TOTAL	ACTTACABLE AC	CONTRACTOR	840
	CICITGCAAC	MUSCACAGAA	TGGTATCCCT	management CT	ACT THOMANO	macemana.c	900

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	1110.00	mns 4 12					
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50	A						
	0 TD 110	85 Protein					
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55							
33	1	11	21	31	41	51	
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65	KRHMKTHMHK	DEFERREFE	EEEELTESER	UDYGEGLSLE	BALKSVVAKE	GAVVGVGDES	540
•••	RALPDVMOGM	VLSSMOHFSE	AFHOVLGEKH	KRGHLAEAEG	HRDTCDEDSV	AGESDRIDDG	600
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70	QSSKLTRHMK	THOQUOKDVY	KCEICKMPPS	VYSTLEKHMK	KNHSDRVLNN	DIKTE	
	Sea ID NO.	86 DNA sequ	ience				
	Nucleic Ac:	d Accession	n #: XM 035	292.2			
75	Coding sequ	ience: 53-1	576				
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80	GCTCGCTGGG	CCGCGGCTCC	CGGGTGTCCC	AGGCCCGGCC	GGTGCGCAGA	GCATGGCGGG	60
00			CGCTAGCGGC AGAGCGCGGA				120
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	CGCGGAGCTC	GGCACCACCA	TCTCCARATC	GGGCGGCGAC			420
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	TOTOTOCAAT	GCCCTGGCCC	ACTTCTCATT	TGAAGGCACC	AAACTGGATG	TGGGGAACAT	780
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	GCAGATGCTG	TCGTCCGAGG	COGTGGCCGT	GGACTTCGGG	AACTATCACC	TOGGCCTCAT	1020
	GTCCTGGATC	ATCCCCGTCT	TOGTGGGCCT	GTCCTGCTTC	GGCTCCGTCA	ATGGGTCCCT	1080
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0	GNIVLALYSG OTFOMISSPA	VAVDPGNYHL	OVMENT TOUR	VGLSCFGSVN	GSLFTSSRLF	FVGSRECHLP	360
•	STLSMTHPOL	LTPUPSLUFT	CVMTLLYAFS	KDIFSVINFF	SFFNWLCVAL	AIIGMIWLRH	420
	RKPELERPIK	VNLALPVFFI STTVLCOKLM	LACLFLIAVS	FWKTPVECGI	GFTIILSGLP	VYFFGVWHIN	480
5	I I I I I I I I I I I I I I I I I I I	Deer mogram.					
-	Seg ID NO:	88 DNA seq	ience				
	Nucleic Ac-	id Accession	n ∦: 18M_0052 989	268.1			
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5	TCTTTGAGGG	ACTOCTGAGT	GGGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC	240
	TGTCTCTGGT	CTTCATCTTC CAAGGACTTC	CGCGTGCTGG	TGTACCTGGT	GACGGCCGAG	CGTGTGTGGA	300 360
	mmas mas ann	ammanamana.	TOCOL TOTOL	acceptage.	CCTGCSGCTT	ATCCTGGTGA	420
_	CATGCCCCTC	ACTGCTCGTG	GTCATGCACG	TGGCCTACCG	GGAGGTTCAG	GAGAAGAGGC	480
0	ACCGAGAAGC	CCATGGGGAG	AACAGTGGGC	GCCTCTACCT	GAACCCCGGC	AAGAAGCGGG	540
	THE COURT OF THE PARTY OF THE P	GTGGACATAT GTTCCACTCA	TTOTACOOCA	BATATATOOT	CONTRACTOR	GTCAAGTGCC	660
	ACGCAGATCC	ATGTCCCAAT	ATAGTGGACT	GCTTCATCTC	CAAGCCCTCA	GAGAAGAACA	720
-	TTTTCACCCT	ATGTCCCAAT CTTCATGGTG	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC	780
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	COCCOTON CYT	CATIOTOTOTO	GGCTCLGLCL	GTCATOCTCC	TOTOTTACCA	GACCGCCCCC	960
	GAGACCATGT	GAAGAAAACC	ATCTTGTGAG	GOGCTGCCTG	GACTGGTCTG	GCAGGTTGGG	1020
0							1080
U	CATGAGGTAG	GGGCAGGCAA	CAGCTCGACG	CAGACGCTC	AGTTCCCCCT	CTRCTCTCCA	1200
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0	MNWSIFEGLL	SGVNKYSTAF VSHVRLWALQ	GRIWLSLVFI	PRVLVYLVTA	MKVWSDDHKD	PMCNTROPGC	60 120
9	GERROCIANT	VUCSLVPKAS	VDIAPLYVEN	SPYPKYILPP	VVKCHADPCP	NIVDCFISKP	180
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_	DDLL9GDLIF	LGSDSHPPLL	PDRPRDHVKK	TIL			
5							
	Nucleic Ac	90 DNA sequid Accession uence: 26-4	n #: NM 002	391.1			
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	1	1	1	1		 	60
	CUGGCGAAGC	AGCGCGGGCA GCGCTCACCT	COGGGGGGGGGG	CARCUGAGGC	GATARGGTCA	ACACCUTCCT	120
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	GCCCTGCAAC	TGGAAGAAGG GGGGGCACAG	AGTTTGGAGC	CCGCCCAAG	TACAMSTITIG	AGAACTGGGG	300 360
	IGUSTGTGAT	GUGGGACAG	GUNCCHONGT.			, LOCOLOCIA	300

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5	CAATGCTCAG AAAGGCCAAA GCCCCTGGTG CACCAGTGCC ACTCCCCCAGC	/086443 TGCCAGGAGA GCCAAGAAG TCACATGGGG TTCTGTCTGC GCCACGCCTA CCAAAGCAAT AACACTCAA	GGAAGGGAAA CCTGGCCACG TCGTTAGCTT AGTGCCCAAA GTGAGTCCCA	GGACTAGACG CCCTCCCTCT TAATCAATCA GTGGGGAGGG GAGCCCGCTT	CCAAGCCTGG CCCAGGCCCG TGCCCTGCCT ACAAGGGATT TTGTTCTTCC	ATGCCAAGGA AGATGTGACC TGTCCCTCTC CTGGGAAGCT CCACAATTCC	420 480 540 600 660 720 780
10	Sea ID NO:	91 Protein cession #: 1	sequence: P_002382.1				
15	CGAQTQRIRC	11 LLALLALTSA RVPCNWKKEP KAKAKAKKGK	GADCKYKFEN	31 GGPGSBCAEW WGACDGGTGT	41 AMGPCTPSSK KVRQGTLKKA	51 DCGWGFREGT RYNAQCQETI	60 120
20	Nucleic Ac	92 DNA sequ Ld Accession Lence: 98-80	#: NM 005	130.1			
25	1	11	21	31	41	51 .	
	GCTGTGCTCA GCTCTCCTTC GAATGGACTT	CACAGCTGCA GAACAAGGTG CTCCTACTGG CACAGCAAAG	AACGCCCAGC CTGCTCAGGT TGGTCTCAGA	GCTCCTGGTG	AAGATCTGTA GAGGGGAAAA ACTCTGGGCA	ACACCCAGAT	60 120 180 240
30	CAGATGGGCT GGACCATGAA TGAGAGAGTC	TTTTCCTGTG TATTGGAAAC	AGGAGGAGGG TCTTTGCTGG AAGTTGCCCG	CATCTCTCTC CAATCCAACC GAATCTGCGC	AAGGTTGAGT TCATGCCTAA TCACAGAAAG	GCACTCAATT AGCTCAAGGA ACATCTGTAG	300 360 420 480 540
35	TAAGCTAGTC GTCCCCCAGG GACCATGGCC GACTGCCCTG	AGCTCCACTC GAGCACATCA ACCAAAGCTC GAGTTCTGTG	CCGAGTGTGT	GACCACCCCC GAGGACCCA GAGCTCTCTC	AGGAAGGAGA TCTAGCCTAG GATATGGCAA TGCACATTCT	AAACAGAGAT CAGTGACCCA ACCAGAGGAA TCCTCAGCAT	600 660 720 780
40	TGTCGTAAGT TGTGCTTAGT TGGAATTTGC TTCCATGGCC	ACGTCATGCT CCCTCTGTAT GAGTGCAACG CTTATTTTTC CACACAGCTA TTCAGTGCAA	ACTTTAAAGC AAATATTTAA TTGGATGCGA TGTGTTTGAG	TCTCTACAGT ACAAGTTTTG TGTTCAGAGG CAGCGAAGAG	CCCCCCAAAA TATTTTTTGC CTGTTTGCTG TCTTTGAGCT	TATGAACTTT TTTTGTGTTT CAGCATGTAT GAATGAGCCA	900 960 1020 1080 1140
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	Protein Ac	cession #: 1	TP_005121.1				
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55	VTKDQANCRW RSOKDICRYS	FLLLAAQVLL AATEQEEGIS KTAVKTRVCR ATKAPECVED	LKVECTQLDH	EFSCVFAGNP VSSTLFGNTK	TSCLKLKDER PRKEKTEMSP	VYWKQVARNL REHIKGKETT	60 120 180
60	Nucleic Ac	94 DNA sequid Accession sence: 125-	n #: NM 0121	101			
		11 GTGTGTCTCT GTCACCTATC	21 AGTCCTCGTG CTGAACCCCA	31 GTTGCCTGCC GCAAGCCTGA	41 CCACTCCCTG AACAGCTCAG	51 CCGAGACGCC CCAAGCACCC	60 120
65	TGCGATGGAA CCGGAGGCCG TGCCAAGACC CCTGAAGCCA	GCTGCAGATG TCGGGCCCCA ACCAACGGGC GGGGAAGGTA	CCTCCAGGAG GTGGCAGCCT ACGGCGGGGA GGAGCGCCCT	CAACGGGTCG GGAGAATGGC GGCAGCTGAG GTTCGCGGGC	AGCCCAGAAG ACCAAGGCTG GGCAAGAGCC AATGAGTGGC	CCAGGGATGC ACGGCAAGGA TGGGCAGCGC GGCGACCCAT	180 240 300 360
70	GGAAGGCAAG TACCTTTGCC GGTGTCCATC	GTCGAGTCCG AGGTCGCCGT GAAAAGGGCC ATGGAGCCCG CGGTCCAAGT	ACCCAGGGCT ACCTGCGCAA GGGAGACCCG	GCGGAACAGC	TACCCCCGGG	AGCCACCCGT GGAAGCCCAC CCGACACGGG	420 480 540 600 660
75	CAAGCCCCAC CAAGCCCCAC CTTTGAGGCC CCAGACCTGC	GCGGTCAAGT CTGGAGGGCG CGCAAGTGTC ATCTGCTACC	CCTGCCTGGT	GTGCCAGGCC AGACCACCAG CAAGACGATG CCAGGAGCAC	TOUTTCIGGG CIGCTCGAGC GAGCTCITCT AAGAATCATA	AGCTGCATCT CCATCCGGGA GCCAGACCGA GCACCGTGAC	720 780 840 900 960
80	GCTCAAGATC CAAGAGCTTC GGACCTGGAG TGTGGACCAA	ATTGAGATTG ACCACCAATG AAGCAAAAGG GTGAAGGTGA	AGGATGAAGC AGGAAGCCAT AGGAAGTGAG TCATGGATGC	TGAGAAGTGG CCTGGAGCAG GGCTGCGCTG TCTGGATGAG	CAGAAGGAGA AACTTCCGGG GAGCAGCGGG AGAGCCAAGG	AGGACCGCAT ACCTGGTGCG AGCAGGATGC TGCTGCATGA	1020 1080 1140 1200
85	ATTTGGTGCA GCTGGAGGGG ATGCATGCCC		ACATOTOCAA	CATCAGOGAC CCCCCCACCC AGGCAACTTC GGCGGACCTG CTATGTGAAC	AAGGACGACC AGCCGTAACT	ATCATGTCCT TGCTCAATGT TCATTGAGAG	1260 1320 1380 1440 1500

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	COCCUGATOR TOCTOCTGAC	CCTGCTGCTC	TTGCCTTCTA	ACCTACTGTG	CTTGTCTGGG	1980
	TOTAL CONTRACTOR OF THE PROPERTY OF THE PROPER	CACCTGCCCT	CTGCAGCCCT	CTGCCAGCCT	CTTGGGGGGCA	2040
10	GTTCCGGCCT CTCCGACTTC	CCCACTGGCC	ACACTCCATT	CAGACTCCTT	TCCTGCCTTG	2100
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	MEANING COCK	CCCDEADDAD	SPSGPSGSLE	NOTKADGKDA	KTTNGHOGEA	AEGKSLGSAL	60
35	MANAGEMENT OF THE	ACMINIDADET T	QFVESGDDKN	SNYRSMDSME	GKRSPYAGLO	LGAAKKPPVT	120
33	REGERGRANDE	ADDEDUNE TO	SIMEPGETER	MOVED ADVICE.	PERSKSOSEE	VI-CDSCIGNK	180
	PAEKGDVKKS	IF SESKKFIV	STUBLOSTICA	HOLLEDIDE	PARKCOVECK	THELFCQTDQ	240
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40	KOTREQLHSI	SDSVLFLQEF	GALMSNYSLP	PPLPTYHVLL	EGEGLGQSLG	NFKDDLLNVC	
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	VETEVOPESE	GRETKETTOK	NENNLYGIKG	NYTSRVWEYS	SSIGNSDNDL	PVVQGSSSFS	540
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45 Seq ID NO: 96 DNA sequence Nucleic Acid Accession #: NM_080668.1 Coding sequence: 83-841 11

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1-5		VPRVCA KPWA	PDNTLPGISP	PPEKQKRKKK	KMPBILKTEL	DEWAAAMNAE	240
	PEAAEOFDLL	VE					

20	Nucleic Ac:	98 DNA sequid Accession uence: 58-1	n #: Eos sec	quence			
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		GCAGCAGCCC					240
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	AACACUTTTG	AGGGGGGCCATT	CIGIOGUCAG	CCCTCGGGCA	accordence A	CCTGCTCCTG	3780
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,	ATGGAGTTTA GACTTGTGTA	CCACGACTCT	GCTAAACACC	TCCCCGGAAG	GATGGAAGCT	CCTGAAGAAG	414
	ATAGGTTTCA	ACATCGGAGA	CCTCCAGGTT	ATGOCTCATC	TTCCTGATGT	TTGTGTGAAT	426
	CTGATGAAAG AAAATAACAG	CTCTAAAGAT CACAGAGCAT	GTCCCCATAC	AAAGATATCC TRIGCOGTCA	TAGAGACCCA	TCTGAGAGAG	432
)	CAAGTGGACA	GGAGCAGGCAT	GGCTGCTGTT	GTGTCTGCCT	GTAAACAGCT	TCACAGAGCT	444
	GCCCTTCTGC	ATAATATATT	ACCGTCTCAG	TCCACAGATT	TGCATCATTC	TGTTGGCACA	450
	GAACTTCTTT	CCCTGGTTTA	TARAGGCATT	GCCCCTGGAG AGCGGACTTC	ATGAGAGACA TGGAGTTAGC	GTGTCTGCCT	456
	TCTCTAGACC	GTGAGCGCCT	TGTGAGTCTT	CTCCTGAACC	CAGCGGTGCT	GTCCACGGCG	468
5	TCCTTGGGCA	GCTCACAGGG	CAGCGTCATC	CACTTCTCCC	ATGGGGAGTA	TTTCTATAGC	474
	TTGTTCTCAG CTCATGCAGT	CTTCAGTGGA	CACGGAATTA TAATACCAAA	TTGAAAAATC	TGGATCTTGC	CCCCATCTTA	486
	GACCAGAGCT	TCAGGGAGCG	AGCAAACCAG	AAACACCAAG	GACTGAAACT	TGCGACTACA	492
)	ATTCTGCAAC	ACTOGAAGAA	GTGTGATTCA ACTGGCAAAA	TGGTGGGCCA	AAGATTCCCC	TCTCGAAACT	498 504
,	AAAATGGCAG AATACAAGTC	TGCTGGCCTT	CCCTGAAGTC	TTTACAGA	ATATTAGTCT	ACTTGCTGAC	510
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5	TOCATGAAAA	AGTTTCTAGA	TGCATTGGAA	TTATCTCAAA	GCCCTATGTT	CTTGGAATTG	534
	ATGACAGAAG	TTCTTTGTOG	GGAACAGCAG	CATGTCATGG	AAGAATTATT	TCAATCCAGT	546
	TTCAGGAGGA TATGAAATGT	TTGCCAGAAG TCAGGAAGGA	GGGTTCATGT TGACCCCCGC	GTCACACAAG CTAAGTTTCA	TAGGCCTTCT	GGAAAGCGTG	552
	COCTCCCTCC	TCACTCTGCT	GTGGCACTGT	AGCCTGGATG	CTTTGAGAGA	ATTCTTCAGC	558
)	ACARTTGTGG	TGGATGCCAT	TGATGTGTTG CAAGAAGATG	AAGTCCAGGT GGCTACTATA	TTACAAAGCT	AAATGAATCT	564 570
	ACCTTTGATA TCTCGCCTTC	CTCAAATCAC CCAAAGATGA	TGTTCATGCT	AAGGAATCAA	AAATTAATCA	AGTTTTCCAT	576
	GGCTCGTGTA	TTACAGANGG	AAATGAACTT	ACAAAGACAT	TGATTAAATT	GTGCTACGAT	582
5	GCATTTACAG TGTGCAGCAT	AGAACATGGC ACAACTGCGC	AGGAGAGAAT	CAGCTGCTGG	AGAGGAGAAG TCTTCAATGA	ACTITACCAT	588
,	TACCAAGGTT	TTCTGTTTAG	TGAAAAACCA	GAAAAGAACT	TGCTTATTTT	TGAAAATCTG	600
	ATCGACCTGA	AGCGCCGCTA	TAATTTTCCT	GTAGAAGTTG AGAGAAGCAG	AGGTTCCTAT CAAATGGGGA	GGAAAGAAAG TTCAGATGGT	612
	CCTTCCTATA	TTGAAATTAG	GARAGARGCC	GCAGAGAGCAG	CCCTGAGTGA	GGAAATGAGT	618
)	CAATTTGATT	TCTCAACCGG	AGTTCAGAGC	TATTCATACA	GCTCCCAAGA	CCCTAGACCT	624
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	GAGCTGGAGA AAGCACATGC	ACAGAAGCCT	GGGCCCGCCT	CAAGGAGAAG	AGGATTCAGT	GCCAAGAGAT	642
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5	ATCCGTCTCT	TCTTAGCCAA	GCTGCAGCTG	AATACAGAAG GCTGCTTCTG	AGGTCTTTCG	CCCTTACGCG AGGAGAAGGA	654
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	CCAACAGGGG	TCCCTAAAGA	TGAAGTGTTA	GCAAATCGAT	TGCTTAATTT	CCTAATGAAA	672
)	CATGTCTTTC	ATCCAAAAAG GGAAGGATTG	AGCTGTGTTT	AGACACAACC	TTGAAATTAT	AAAGACCCTT	678
•	GGTAAAGATC	CTAATTCTAA	AGACAACTCA	GTAGGGATTC	AATTGCTAGG	CATCGTGATG	690
	GCCAATGACC	TGCCTCCCTA	TGACCCACAG	TGTGGCATCC	AGAGTAGCGA TGTATGCCGC	TGCAGCAGAA	702
	GTTCTAGGAC	TTATACTTCG	ATATOTTATG	GAGAGAAAAA		GGAGTCTCTG	708
5	TGTGAACTGG	TTGCGAAACA	ATTGAAGCAA	CATCAGAATA	CTATGGAGGA	CAAGTTTATT	714
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)	CARGTCATGA	GACATAGAGA	TGATGAAAGA	CAAAAAGTAT	GTTTGGACAT TGAACCCCGT	AATTTATAAG TGTGGAATTC	736
,	ATGATGCCAA	AGTTAAAACC CTTCTACAAC	AGTAGAACTC ATGTAGGGAA	CAAATGTATA	ATATTCTCAT	GTGGATTCAT	750
	GATAATTACA	GAGATCCAGA	AACTGAGACA	GATAATGACT	CCCAGGAAAT	ATTTANGTTG	756
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5	CGAAATTTCT	TATATTCTCC	TARGATAGAA	GIGCACITIT	TAAGTTTAGC	AACAAATTTT	774
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)	CATGACTTCA	CACTGACACA	GACTGCAGAT	GGAAGAAGCT	CATTIGATIG	GCTGACCGGG	810
	AGCAGCACTG	ACCCCCTGGT	CGACCACACC	AGTCCCTCAT	CTGACTCCTT	GCTGTTTGCC	816
	AAAAAAAGGC	TGGGCCTTCC	AGGGGACGAG	GTGGATAACA	AAGTGAAAGG	TGCGGCCGGC	822
5	CGGACGGACC	TACTACGACT	GCGCAGACGG	TTTATGAGGG	ACCAGGAGAA	GAGTGAGTTA	82
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	GACATTCAGA	TCAAGCACAG	CAGCCTCATC	ACCCCGTTAC	AGGCCGTGGC	CCAGAGGGAC	846
	CCAATAATTG	CAAAACAGCT	CTTTAGCAGC	TTGTTTTCTG ATCACTCAAA	GAATTTTGAA AGTTGCTTCA	AGAGATGGAT AGACTTCAAT	851
)	CSTTTTCTTA	CACTGTCTGA	CTCTTTCTTT	CCACCCTTTG	TCTCTTGTAT	TCAGGACATT	864
	AGCTGTCAGC	ACGCAGCCCT	GCTGAGCCTC	GACCCAGCGG	CTGTTAGCGC	TGGTTGCCTG	870
	CCTGCTGAGC	AGCAGCCCCT TGCCTGCCAA	GGGAGTCCGT	CTCCTAGAGG	AGGCTCTGCT	COGCCTGCTG	874
_	AGATGGGTGG	AGCTTGCTAA	GCTGTATAGA	TCAATTGGAG	AATACGACGT	CCTCCGTGGG	881
5	ATTTTTACCA	GTGAGATAGG	AACAAAGCAA	ATCACTCAGA	GTGCATTATT	AGCAGAAGCC	894
	AGAAGTGATT	ATTCTGAAGC	TGCTAAGCAG	TATGATGAGG	CTCTCAATAA	ACAAGACTGG CCTTGACTGT	900
	GINGNIGGIG	MULLUNCALIA	~~CCOMONNO				200

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TACRACCACC TRUCTGAGIG GRANTSCIPT GARACTUTT CTACACCAG TATACACAGT 9120 GAGRACOCC CRIGACITAA TARARTCTG AGTGRACCHT TITATCHGGA ARCRITCTA CCTIACRTGA TCCGCAGCAA GCTGARGCTG CTGCTCCAGG GRGRGCTGA CCAGTCCCTG 9180 CTCACATTTA TTGACAAAGC TATGCACOGG GAGCTCCAGA AGGCGATTCT AGAGCTTCAT 0200 TACAGTCAAG AGCTGAGTCT GCTTTACCTC CTGCAAGATG ATGTTGACAG AGCCAAATAT 9360 TACATTCAAA ATGGCATTCA GAGTTTTATG CAGAATTATT CTAGTATTGA TGTCCTCTTA 9420 CACCAAAGTA GACTCACCAA ATTGCAGTCT GTACAGGCTT TAACAGAAAT TCAGGAGTTC ATCAGCTTTA TARGCARACA AGGCARTITA TCATCTCARG TTCCCCTTAR GAGACTTCTG 9600 AACACCTOGA CAAACAGATA TOCAGATGCT AAAATGGACC CAATGAACAT CTGGGATGAC 10 ATCATCACAA ATCGATGTTT CTTTCTCAGC AAAATAGAGG AGAAGCTTAC CCCTCTTCCA 9660 GAAGATAATA GTATGAATGT GGATCAAGAT GGAGACCCCA GTGACAGGAT GGAAGTGCAA 9720 GACCAGGARG ARGATATCAG CTCCCTGATC AGGAGTTGCA AGTTTTCCAT GAAAATGAAG 9786 ATGATAGACA GTGCCCGGAA GCAGAACAAT TTCTCACTTG CTATGAAACT ACTGAAGGAG CTGCATARAG AGTCAAAAAC CAGAGAGGAT TGGCTGGTGA GCTGGGTGCA GAGCTACTGC 9900 15 COCCTGAGCC ACTGCCGGAG CCGGTCCCAG GGCTGCTCTG AGCAGGTGCT CACTGTGCTG 9960 AAAACAGTCT CTTTGTTGGA TGAGAACAAC GTGTCAAGCT ACTTAAGCAA AAATATTCTG 10020 GCTTTCCGTG ACCAGAACAT TCTCTTCGGT ACAACTTACA GGATCATAGC GAATGCTCTC 10080 AGCAGTGAGC CAGCCTGCCT TGCTGAAATC GAGGAGGACA AGGCTAGAAG AATCTTAGAG 10140 CTTTCTGGAT CCAGTTCAGA GGATTCAGAG AAGGTGATCG CGGGTCTGTA CCAGAGAGCA 10200 20 TTCCAGCACC TCTCTGAGGC TGTGCAGGCG GCTGAGGAGG AGGCCCAGCC TCCCTCCTGG 10260 AGCTGTGGGC CTGCAGCTGG GGTGATTGAT GCTTACATGA CGCTGGCAGA TTTCTGTGAC 10320 CAACAGCTGC GCAAGGAGGA AGAGAATGCA TCAGTTATTG ATTCTGCAGA ACTGCAGGCG 10380 TATCCAGCAC TIGTOGIGA GAAAATGITG AAAGCITTAA AATTAAATTC CAATGAAGCC 10440 AGATTGAAGT TTCCTAGATT ACTTCAGATT ATAGAACGGT ATCCAGAGGA GACTTTGAGC 10500 25 CTCATGACAA AAGAGATCTC TTCCGTTCCC TGCTGGCAGT TCATCAGCTG GATCAGCCAC 10560 ATGGTGGCCT TACTGGACAA AGACCAAGCC GTTGCTGTTC AGCACTCTGT GGAAGAAATC 10620 ACTGATAACT ACCGGCAGGC TATTGTTTAT COCTTCATCA TAAGCAGGA AAGCTATTCC 10680 TTCMAGGATA CTTCTACTGG TCATAAGGAT AAGGAGTTTG TGGCAAGGAT TAAAAGTAAG 10740 TTGGATCAAG GAGGAGTGAT TCAAGATTTT ATTAATGCCT TAGATCAGCT CTCTAATCCT 10800 30 GARCTGCTCT TTAAGGATTG GRGCAATGAT GTAAGAGCTG AACTAGCAAA AACCCCTGTA 10860 ANTARARAA ACRITGARAA RATGIRIGAR AGRATGIRIG CAGCCITGGG IGACCCARAG 10920 GCTCCAGGCC TGGGGGCCTT TAGAAGGAAG TTTATTCAGA CTTTTGGAAA AGAATTTGAT 10980 AMACATETTG GGAAAGGAGG TTCTAAACTA CTGAGAATGA AGCTCAGTGA CTTCAACGAC 11040 ATTACCAACA TGCTACTTTT AAAAATGAAC AAAGACTCAA AGCCCCCTGG GAATCTGAAA 11100 35 GARTGITCAC CCTGGATGAG CGACTTCAAA GTGGAGTTCC TGAGAAATGA GCTGGAGATT 11160 CCCGGTCAGT ATGACGGTAG GGGAAAGCCA TTGCCAGAGT ACCACGTGCG AATCGCCGGG 11220 TTTGATGAGC GGGTGACAGT CATGGCGTCT CTGCGAAGGC CCAAGCGCAT CATCATCCGT 11280 GGCCATGACG AGAGGGAACA CCCTTTCCTG GTGAAGGGTG GCGAGGACCT GCGGCAGGAC 11340 CAGCGCGTGG AGCAGCTCTT CCAGGTCATG AATGGGATCC TGGCCCCAAGA CTCCGCCTGC 11400 40 AGCCAGAGGG CCCTGCAGCT GAGGACCTAT AGCSTTGTGC CCATGACCTC CAGGTTAGGA 11460 TTAATTGAGT GGCTTGAAAA TACTGTTACC TTGAAGGACC TTCTTTTGAA CACCATGTCC 11520 CARGAGAGA AGGIGGETTA CETGAGTGAT CCCAGGGCAC CGCCGTGTGA ATATAAAGAT 11580 45 CTCTTARAGC GGGCCTTCGT GAGGATGAGT ACAAGCCCTG AGGCTTTCCT GGCGCTCCGC 11760 CCCACTTCG CCAGCTCTCA CGCTCTGATA TGCATCAGCC ACTGGATCCT CGGGATTGGA 11820 GACAGACATC TGAACAACTT TATGGTGGCC ATGGAGACTG GCGGCGTGAT CGGGATCGAC 11880 TTTGGGCATG COTTTGGATC CGCTACACAG TTTCTGCCAG TCCCTGAGTT GATGCCTTTT 11940 COGCTAACTC GCCROTTTAT CAATCTGATG TTACCAATGA AAGAAACGGG CCTTATGTAC 12000 50 AGCATCATGG TACACGCACT COGGGCCTTC CGCTCAGACC CTGGCCTGCT CACCAACACC 12060 ATGGATGTGT TTGTCAAGGA GCCCTCCTTT GATTGGAAAA ATTTTGAACA GAAAATGCTG 12120 ARAAAAGGAG GGTCATGGAT TCAAGAAATA AATGTTGCTG AAAAAAATTG GTACCCCCGA 12180 CAGAAAATT GTTACOCTAA GAGAAAGTTA GCAGGTGCCA ATCCAGCAGT CATTACTTGT 12240 GATGAGCTAC TCCTGGGTCA TGAGAAGGCC CCTGCCTTCA GAGACTATGT GGCTGTGGCA 12300 55 CORGRAGOA ANGATCACAA CATTCOTOCC CANGAACCAA ANATOGOCT TTCAGAAGAA 12360 ACTCAGGTAA AGTSCCTGAT GGACCAGGCA ACAGACCCCA ACATCCTTGG CAGAACCTGG 12430 AGAGGATGGG AGCCCTGGAT GGAGGCTGT TGGGAGTCTT TGGAGTGTG 12440 GTTTAAAGAA TCTACTATAC TTTGGTTGGC AGCATTCCAT GAGCTGATTT TCCTGAAACA 12540 CTAAAGAGAA ATGTCTTTTG TGCTACAGTT TCGTAGCATG AGTTTAAATC AAGATTATGA 12600 60 TGAGTAAATG TGTATGGGTT AAATCAAAGA TAAGGTTATA GTAACATCAA AGATTAGGTG 12660 AGGTTTATAG AAAGATAGAT ATCCAGGCTT ACCAAAGTAT TAAGTCAAGA ATATAATATG 12720 TGATCAGCTT TCAAAGCATT TACAAGTGCT GCAAGTTAGT GAAACAGCTG TCTCCGTAAA 12780 TGGAGGAAAT GTGGGGAAGC CTTGGAATGC CCTTCTGGTT CTGGCACATT GGAAAGCACA 12840 CTCAGAAGGC TTCATCACCA AGATTTTGGG AGAGTAAAGC TAAGTATAGT TGATGTAACA 12900 65 TIGTAGAAGC AGCATAGGAA CAATAAGAAC AATAGGTAAA GCTATAATTA TGGCTTATAT 12960 TTAGAAATGA CIGCATIIGA TATTITAGGA TATTITICTA GGTTTTTTCC TITCATTITA 13020 TICICITCIA GITTIGACAT TITATGATAG ATTIGCICTO TAGAAGGAAA COTCTITATI 13080 TAGGAGGGCA AAAATITTGG TCATAGCATI CACTITTGCT ATTCCAATCI ACAACTGGAA 13140 GATACATAAA AGTGCTTTGC ATTGAATTTG GGATAACTTC AAAAATCCCA TGGTTGTTGT 13200 70 TAGGGATAGT ACTAAGCATT TCAGTTCCAG GAGAATAAAA GAAATTCCTA TTTGAAATGA 13260 ATTCCTCATT TOGAGGAAAA AAAGCATGCA TTCTAGCACA ACAAGATGAA ATTATGGAAT 13320 ACAAAAGTGG CTCCTTCCCA TGTGCAGTCC CTGTCCCCCC CCGCCAGTCC TCCACACCCA 13380 AACTGITTCT GATTGGCTTT TAGCTTTTTG TTGTTTTTTT TTTTCCTTCT AACACTTGTA 13440 TTTTGGAGGCT CTTCTGTGAT TTTGAGAAGT ATACTCTTGA GTGTTTAATA AAGTTTTTTT 13500 75

Seq ID NO: 99 Protein sequence:

	TIOCCIII NO	Debbion					
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	Ī	Ī	Ī	1	1	1	
	MAGSGAGVRC	SLLRLQETLS	AADROGAALA	GHOLIRGLGO	ECVLSSSPAV	LALQTSLVFS	60
	RDFGLLVFVR	KSLNSIEFRE	CREEILKFLC	IFLEKMGQKI	APYSVEIKNT	CTSVYTKDRA	120
	AKCKIPALDL	LIKLLQTERS	SRLMDEFKIG	ELFSKFYGEL	ALKKKIPDTV	LEKVYELLGL	180
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	CAHTNVELKK	AALSALESFL	KQVSNMVAKN	YEMHKUKI'ĞA	PMEQFYGIIR	NVDSNNKELS	360

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IAIRGYGLFA GPCKVINAKO VDFMYVELIQ RCKQMFLTQT DTGDDRVYQM PSFLQSVASV 420 LLYLDTUPEV YTPULEHLUV MQIDSPPQYS PKMQLVCCRA IVKVFLALAA KGPVLRNCIS TVHGGIRI CSKPVLDKG PESESEEHRA SGEVRTGENK VPTYKDYVDL FRHLLSSOM 480 540 MOSILADRAF FSVNSSSESL NHLLYDEFVK SVLKIVEKLD LYLRIOTYGE GENGDEAPGV 5 WMIPTSDPAA NLHPAKPKDF SAFINLWEFC REILPEKOAE FFEPWYYSFS YELILQSTRL 660 PLISGFYKLL SITURNAKKI KYFEGVSPKS LKHSPEDPEK YSCFALFVKF GKEVAVKMKQ 720 YKDELLASCL TPLLSLPHNI IELDVRAYVP ALQMAPKLGL SYTPLAEVGL NALEEWSIYI 780 DRUMORYNK DILECTRONI, KYSALSDETK NUMEVSALSE ABOKGENKYV LKHILKKTKNI. 840 SENEAISLEE IRIRUVOMLG SLGGOINKNL LTVTSSDEMM KSYVAWDREK RLSFAVPFRE MKPVIPLDVP LPRVTELALT ASDRQTKVAA CELLHSMVMF MLGKATQMPE GGQGAPPMYQ 960 LYKRTFPVLL RLACDVDOVT ROLYEPLVNO LIHNFTNNKK FESODTVALL EAILDGIVDP 1020 VDSTLRDPCG RCIREPLKNS IKQITPQQQE KSPVNTKSLF KRLYSLALHP NAPKRLGASL ADMNIYPDER EERSLUPOPV FEALVIYMES LALAHADEKS LCTIOOCCDA IDBLCRIIEK 1080 1140 KHVSLNKAKK RRLPROFFPS ASLCLLDLVK WLLAHCGRPQ TECRHKSIEL FYKFVPLLPG 15 NRSPHLWLKD VLKEEGVSFL INTFEGGGCG QPSGILAQPT LLYLRGPFSL QATLCWLDLL 1260 LAALECYNTF IGERTVGALQ VLCTERGSSL LKAVAFFLES IAMEDIIAAR KCFCTGAACH RTSPOGGERY NY SKCTYVVR IMERITILIN TSPEGWKLLK KOLCHTILIMR VLVQTICEPA SIGFHIGUVQ VMAHLPDVCV NLKKALMOSP YKOLLETILE BKITAGSIEE LCAVNLYGFD 1320 1380 1440 ACCUPATION ACCUPATION OF THE STREET OF THE S 1500 20 PSLDLSCKQL ASCLLELAFA FOGLCERLVS LLLNPAVLST ASLGSSQGSV IHFSHGEYFY 1560 SLESETINTE LLKNLDLAVL ELMQSSVDNT KMVSAVLNGM LDQSFRERAN QKHQGLKLAT 1620 THI OWNER OF SHEAFINGER TEMANIALIA KILOTOGGUS PATSHOSPPE VETTYISILA 1680 DTKLDLHLKG OAVTLLPFFT SLTGGSLEEL RRVLEGLIVA HFPMQSREFP PGTPRFMNYV 1740 DCMKKPLDAL ELSOSPMLLE LMTEVLCREQ QHVMEELFQS SFRRIARRGS CVTQVGLLES 25 VYEMPREDDP RLSFTROSFV DRSLLTLLWH CSLDALREFF STIVVDAIDV LKSRFTKLNE 1860 STEDTOITKK MGYYKILDVM YSRLPKDDVH AKESKINOVE HGSCITEGNE LTKTLIKLCY 1920 DAFTENMAGE NOLLERRRLY HOMAYNOMIS VICCVFNELK FYGGFLFSEK PEKNILIFEN 1980 THE KERNYE PURVEYENER KKKYTETEKE ARRAMODED GREYMESLEY LADSTLEEM 2040 SQFDFSTGVQ SYSYSSQDPR PATGRFRRRE QRDPTVHDDV LELEMDELNR HECMAPLTAL 2100 30 VKEMERSLOP POGEEDSVPR DLPSMMKFLH GKLGNPIVPL NIRLFLAKLV INTEEVFRPY 2160 AKHWLSPILO LAASENNOGE GIHYMVVEIV ATILSWTGLA TPTGVPKDEV LANRLINFLM 2220 KHVFHPKRAV FRHNLEIIKT LVECHKOCLS IPYRLIFEKF SOKOPNSKON SVGIQLLGIV 2280 MANDLPPYDP QCGIQSSEYF QALVNNMSFV RYKEVYAAAA EVLGLILRYV MERKNILEES 2340 LCELVAROLK QHQNTMEDKF IVCLMKVTKS FPPLADRFMM AVFFLLPKFH GYLKTLCLEV VLCRVEGMTE LYPQLKSKDF VQVMRHEDDE RQKVCLDIIY KMMPKLKPVE LRELLMPVVE 2400 35 2460 FUSHPETTOR ROMYNILMWI HDNYRDPESE TONDSOEIFK LAKDVLIGGL IDENPGLQLI 2520 IRNFWSHETR LPSNTLDRLL ALMSLYSPKI EVHFLSLATN FLLEMTSMSP DYPNPMFEHP 2580 LSECEFGEYT IDSDWRFRST VLTPMFVETQ ASQCTLQTRT QEGSLSARWP VAGQIRATQQ 2640 OHDFTLTOTA DGRSSFDWLT GSSTDPLVDH TSPSSDSLLF AHKRSERLOR APLKSVGPDF 2700 40 GKKELGLEGD EVDNKVKGAA GETDLIELER REMEDQEKLS LMYARKGVAE QKREKEIKSE 2760 LINKQDAQVV LYRSYRHGDL PDIQIKHSSL ITPLQAVAQR DPIIAKQLFS SLFSGILKEM 2820 DKFKTLSEKN MITCKLLODF NRFLNTTFSF FPPFVSCIQD ISCOHAALLS LDPAAVSAGC LASLOOPVGI RLLEEALLRL LPAELPAKRV RGKARLPPDV LRWVELAKLY RSIGEYDVLR 2880 2940 GIFTSEIGTK OITOSALLAE ARSDYSEAAK QYDEALNKQD WYDGEPTEAE KDFWELASLD 3000 45 CYNHLAEWKS LEYCSTASID SEMPPDINKI WSEPFYGETY LPYMIRSKIK LILGGEADGS 3060 LLTFIDKAMH GELQKAILEL HYSQELSLLY LLQDDVDRAK YYIQNGIQSF MQNYSSIDVL 3120 LHQGRLTKLQ SVQALTEIQE FISFISKQGN LSSQVPLKRL LNTHTNRYPD AKMDPMNIND 3190 DITHROPPL SKIEEKLTPL PEDMSMANDQ DGDPSDRMEV QEQEEDISSL IRSCKFSWAM KMIDSARRQH NFSLAMKLLK ELKKEKKTRD DHIMSWNGSY CRLSHCRSS GGCSDYNLTV LKTYSLLDEN NYSSYLSKNI LAPRQKILL GTTYRIINNA LSSSPACLAE IEBDKARRIL 3240 3300 50 3360 ELSGSSSEDS EKVIAGLYOR APOHLSEAVO AREERAOPPS WSCGPARGVI DAYMTLADFC 3420 DOGLEKKEEN ASVIDSAELQ AYPALVVEKM LKALKLMSNE ARLKFPRLLQ IIERYPEETL 3480 3540 SLMTKEISSV PCWOFISWIS HMVALLDKDQ AVAVQHSVEE ITDNYPQAIV YPPIISSESY SFKDTSTGHK NKEFVARIKS KLDOGGVIOD FINALDQLSN PELLFKDWSN DVRAELAKTP 3600 55 3660 VNKKNIEKMY ERMYAALGDP KAPGLGAFRR KFIQTFGKEF DKHFGKGGSK LLRMKLSDFN DITHMLLLKM NKDSKPPGNL KECSPWMSDF KVEFLENELE IPGQYDGRGK PLPEYHVRIA 2720 OFDERVIVMA SLRRPKRIII ROHDEREHPF LVKGGEDLRQ DQRVEQLFQV MNGILAQDSA 3780 CSORALOLRY YSVVPMTSRL GLIEWLENTV TLKDLLLNYM SQEEKAAYLS DPRAPPCEYK 3840 DULTKMSOKH DVGAYMLMYK GANTETVTS FRKRESKUPA DILKRAFVRM STSPEAFLAL 3900 60 RSHFASSHAL ICISHWILGI GDRHLKNYMV AMETOGVIGI DFGHAFGSAT QFLPVPELMP FRLTROFINL MLPMKETGLM YSIMVHALRA FRSDPGLLTN TMDVFVKEPS FDWKNPEQKM 4020 LKKGGSWIGE INVAEKNWYP ROKICYAKRK LAGANPAVIT CDELLLGHEK APAFRDYVAV 4080 ARGSKDHNIR AQEPESGLSE ETQVKCLMDQ ATDPNILGRT WEGWEPHM

65 Seq ID NO: 100 DNA sequence Nucleic Acid Accession #: NM_000673 Coding sequence: 101-1225

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75					AATGGTGTCC			300
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	CATCATGGGC	TGTAAGT	CAG	CTGGTGCATC	TAGGATCATT	GGGATTGACC	TCAACAAAGA	780
					CACTGAGTGT			840
85	CARACCCATC	AGTGAGG	TGC	TGTCAGAAAT	GACAGGCAAC	AACGTGGGAT	ACACCTTTGA	900
	AGTTATTGGG	CATCTTO	AAA	CCATGATTGA	TGCCCTGGCA	TCCTGCCACA	TGAACTATGG	960
	GACCAGCGTG	GTTGTAG	BGAG	TTCCTCCATC	AGCCAAGATG	CTCACCTATG	ACCOGATGTT	1020

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	GCTCTTCACT	GGACGCACAT	GGAAGGGATG	TGTCTTTGGA	CCTTTGAAAA	GCAGAGATGA	1080
	TGTCCCAAAA	CTAGTGACTG CCATTTAAAA	AGTTCCTGGC	AAAGAAATTT	CTGCTCAATT	CAGGACAAAG	1200
5	CATTYGGAACG	GTOCTGACGT	TTTGAGATCC	AAAGTGGCAG	CAGGTCTGTG	TTGTCATGGT	1320
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	TATABACATT	TARACTCTTG	TGAGCACCTG	GGAATTAGTA	TAATAACAAT	CTTAATATTT	1440
	TTCATTTACA	DEAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	CTATAATTGT	ATCTTTTAAG	AAAACATACA	CTTGGATTTC	1500 1560
10	CAGATATAGC	GTATAAAGAT	ATAGTAAATG	CATCTCCCAG	AGTAATATTC	ACTTAACACA	1620
	TIGARACTAT	TATTTTTTAG	ATTTGAATAT	AAATGTATTT	TTTAAACACT	TGTTATGAGT	1680 1740
	TARCTTGGAT	TACATTTTGA AAAAGATTAA	CCCACCGCCA	CATTTTTCAA	CGATTAGGA	TCATCATTAC	1800
	ATABCTTGGT	GAAACTGAAA	AACTATATCA	TATGGGTACA	CAAGGCTATT	TOCCAGCATA	1860
15	TATTAATATT	TTAGAAAATA ACTTATCATA	TTCCTTTTGT	AATACTGAAT	ATAAACATAG	AGCTAGAGTC	1920
	CCTATTCACT	GTGCTTAGTA	GTGACTCCAT	TTAATAAAA	GTGTTTTTAG	TTTTTAACAA	2040
	CTAAACCG						
20	Sed ID NO:	101 Protein	sequence:				
	Protein Acc	ession #: N	IP_000664				
	1	11	21	31	41	51	
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25	MGTAGKVIKC	KAAVLNEQKQ TGIVESIGEG	PFSIEEIEVA	PPKTKEVRIK	CHACGICRED	DHVIKGTMVS	60 120
	CULADOTTER	TOKOK PVHHF	MUTSTFTEYT	VVDESSVAKI	DDAAPPEKVC	LIGCGFSTGY	180
	GAAVKTGKVK	PGSTCVVPGL SEVLSEMTCN	GGVGLSVIMG	CKSAGASRII	GIDLNKDKFE	KAMAVGATEC	240 300
30	INTERPRESENT	GRTWKGCVFG	GLKSRDDVPK	LVTEFLAKKE	DLDOLITHVL	PEKKISEGFE	360
	LLNSGQSIRT	VLTP			_		
	Sea ID NO:	102 DNA sec	mence				
25	Nucleic Act	d Accession	#: NM_0067	83.1			
35	Coding sequ	ence: 178	36				
	1	11	21	31	41	51	
		GGACGCTGCA	CD COUNTY OF THE	OCCOCONCECS.	A CRANACA CTC	CACCAGCATC	60
40	CCCS SCCSSCT	COLTCACACT	CATCTTTATT	TTCCGAGTCA	TGATCCTAGT	GGTGGCTGCC	120
	CAGGAAGTGT	GGGGTGACGA	GCAAGAGGAC	TTCGTCTGCA	ACACACTGCA	ACCGGGATGC	180
	CTGATCTTCG	GCTATGACCA TCTCCACCCC	AGCGCTGCTG	GTGGCCATGC	ATTTTGGCCTA	CTACAGGCAC	300
45	GARACCACTC	GCAAGTTCAG	CCCACCACAC	AAGAGGAATG	ATTTCAAAGA	CATAGAGGAC	360 420
45	TTTTTTCCGAA	ACAAGGTTCG TCATCTTTGA	AGCAGCCTTT	ATGTATGTGT	TTTACTTCCT	TTACAATGGG	480
	TACCACCTGC	CCTGGGTGTT	GAAATGTGGG	ATTGACCCCT	CCCCCAACCT	TGTTGACTGC	540
	TTTATTTCTA	GGCCAACAGA TGCTTAACGT	GAAGACOGTG	TTTACCATTT	TTATGATTTC	GTGTTTTAGG	660
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	CAGAATGAAA	TGAATGAGCT	GATTTCAGAT	AGTOGTCAAA	ATGCAATCAC	AGGTTTCCCA	780
	AGCTAA						
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33	Protein Acc	ession #: 1	P_006774.1				
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	NDWORT USET	GGVMKHSTSI	CHARACTERI	PRIMITIANIA	OFFUNCTION	PVCNTLOPGC	60
60	KNVCYDHFFP	VSHIRLWALQ	LIFVSTPALL	VAMHVAYYRH	ETTRKFRRCE	KRNDFKDIED	120
	TKKHKVRIEG	SLWWTYTSSI FTIFMISASV	FFRIIFBAAF	MYVPYPLYNC	AHTAMATKCG	IDECEMPAR	180 240
		SGONAITGFP		CIDDLEVCER	KOKANYIYAN	ne workings.	240
65	-						
03	Seq ID NO:	104 DNA sec Ld Accession	ruence 1 %: NM 0204	11			
	Coding seq	lence: 86-5	26				
	1	11	21	31	41	51	
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	GGACCTGGGA	AGGAGCATAG GGAACCTCAC	GACAGGGCAA	GGCGGGATAA	GGAGGGGCAC	CACAGCCCTT	60 120
	ACTGGGCGTC	TTCCCATCGG	CCCCTTCGCC	AGTGTGGGGA	ACGCGGCGGA	GCTGTGAGCC	180
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	ACACCTCAGA	TOCCACTGOG	CGACATGGAA	GGTGATCTGC	ARGAGETGEA	TCAGTCAAAC	420
	ACCIGGGGATA	AATCTGGATT ATGCCAGAAG	TOGGTTCCGG	CGTCAAGGTG	AAGATAATAC	CTAAAGAGGA	480 540
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	CAGCTTTCAC	CAAAAAAAAA	AAAAAA				
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	MLLWCPPQCA PRSPVMESPK SGVKVKIIPK	KKNOOLKVGI	SPVWGTRRSC LHLGSRQKKI EEQPQV	 EPATRVPEVW RIQLRSQCAT	ILSPLIRHGG WKVICKSCIS	HTQTQNHTAS QTPGINLDLG	60 120	
5	Seq ID NO: Nucleic Aci Coding sequ	d Accession	1 #: J04129					
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	TCACCCTGGG AGGACCTGGA	CGTGGCCCTG GCTCCCAAAG	TCAGAGCCAC GTCTGTGGTG TTGGCAGGGA	TCCCGGCCAT	GGACATCCCC CATGGCCATG	CAGACCAAGC GCGACCAACA	60 120 180	
15	CCACCCCCGA AGAAGAAGGT TGGCGAACGA	GGACAACCTG CCTTGGAGAG GGCCACGCTG	CTGAAGGCCC GAGATOGTTC AAGACTGGGA CTCGATACTG	TGCACAGATG ATCCAAAGAA ACTACGACAA	GGAGAACAAC GTTCAAGATC TTTCCTGTTT	AGCTGTGTTG AACTATACGG CTCTGCCTAC	240 300 360 420	
20	AGGACACCAC AGGACGATGA GGTACTTGCT	CACCCCCATC GATCATGCAG GGACTTGAAA CAGACTCCCA	CAGAGCATGA GGATTCATCA CAGATGGAAG CCCTTCCACA TCAGAAGACG	TGTGCCAGTA GGGCTTTCAG AGCCGTGCCG CCTCCAGAGC	CCTGGCCAGA GCCCCTGCCC TTTCTAGCTC AGTGGGACTT	AGGUACUTAT ACCTCOCCU CCTCCTCCC	480 540 600 660 720	
25	TCCTGCTGCA	CACCTGCACC	ATTGCCATGG CTTGGAGCAT	GGAOGCTGCT	CCCTGGGGGC	AGAGTCTCTG	780	
30	Seq ID NO: Protein Acc	107 Protein ession #: 2	n sequence: NAA60147					
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35	WENNSCVEKK	VLGEKTGNPK	SMAMATNNIS KPKINYTVAN RPLPRHLWYL	EATLLDTDYD	NPLFLCLQDT	EDNLEIVLHR TTPIQSMMCQ	60 120	
40	Nucleic Ac	108 DNA sed id Accession mence: 48-7	#: Eos se	quence				
70	1	11 -	21 GCCGCCCGCC	31	41 CRONGCONTO	51 -	60	
45	GTCTGATCCA TCATGAAAGG	GAAGGCCAAG	CTGGCAGAGC AAGGGCGAGG	AGGCCGAACG AGCTCTCCTG	CTATGAGGAC CGAAGAGOGA	ATGGCAGCCT	120 180	
	TTGAGCAGAA	AAGCAACGAG	GTGGGCGGCC GAGGGCTCGG	AGGAGAAGGG	GCCCGAGGTG	CGTGAGTACC	240 300	
	GOCACCTCAT	CAAGGAGGCC	CTCCAGGGCG GGGGACGCCG	AGAGCCGGGT	CTTCTACCTG	AAGATGAAGG	360 420	
50	ACTORGOOGG	GECAGCCTAC	GCCGAGGTGG CAGGAGGCCA	TOGRACATCAG	CAAGAAGGAG	ATGCCGCCCA	480 540	
	CCARCCCCAT	concernance	CTGGCCCTGA	ACTITICCGT	CTTCCACTAC	CACATCGCCA	600 660	
	TGCACACCCT	CAGOGAGGAC	TCTCTGGCCA TCCTACAAAG	ACAGCACCCT	CATCATGCAG	CTGCTGCGAG	720	
55	AGCCCCAGAG	CTGAGTGTTG	GCCGACAACG CCCGCCACCG	CCCCGCCCTG	CCCCCTCCAG	TCCCCCACCC	780 840	
	TOCCOSAGAGG	ACTAGTATGG	GGTGGGAGGC AGGGACTGGC	CCCACCCTTC	TCCCCTAGGC	GCTGTTCTTG	900 960	
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00	CTGCCCCTGC	TGCCTCTGAT	CGTAGGAATT	GAGGAGTGTC	COGCCTTGTG	GCTGAGAACT	1140	
	CGCGCGCGCCC	AGTGCAAGAC	GATGGGTGTG CGAGATTGAG	GGAAAGCATG	TCTGCTGGGT	GTGACCATGT	1260	
65	Seg ID NO:	TAAAGTTOCC 109 Protein ession #+ 1	CTGTGACACT n sequence: NP_006133.1	С				
70	1	11	21	31	41	51		
70	MERASLIQKA	KLAEQAERYE	DMAAFMKGAV	EKGEBLSCEE	RNLLSVAYKN	VVGGQRAAWR	60	
75	T.KWKGDAABA	LARVATGOOK	VREYREKVET KRIIDSARSA AMADLHTLSE	YORAMDISKK	EMPPTNPIRL	AGDAESRVFY GLALNFSVFH TADNAGEEGG	120 180 240	
80	Nucleic Ac:	110 DNA se id Accession Lence: 407-	n #: NM 0000	595				
ou	1	11	21	31	41	51		
	 CACGAGTTGG	TTTGGGAGCT	GCCAGTCTCC	TOGGAGGATC	GCAGTCAGCA	GAGCAGGGCT	60	
85	anacererosa	COTACCACCA	GNGCCTGCGC	ATCTGGAGGC	AGCATGTCCA	AGAAAGGGAG CCTTCGAGGA	120 180	
33	CACACTGCGG	CGGCTGCGTG	AGGCCTTCAA TGGGCCACTT	CTGAGGGGGGG	ACGOSGCCGG	CCGAGTTCCG	240 300	

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	CGTGCTGGCC	CAGGACCTGC	ATAAGCCAGC	TTTCGAGGCA	GACATATCTG	AGCTCATCCT	360
	TTGCCAGAAC	GAGGTTGACT	ACCCTCTCAA	GAACCTTCAG	GCCTGGATGA	AGGATGAACC	420
	ACGGTCCACG	AACCTGTTCA	TGAAGCTGGA	CTCGGTCTTC	ATCTGGAAGG	AACCCTTTGG	480
	CCTGGTCCTC	ATCATCGCAC	CCTGGAACTA	CCCATTGAAC	CTGACCCTGG	TGCTCCTGGT	540
5	COSCACOCTO	CCCCCCACGGA	ATTGCGTGGT	GCTGAAGCCG	TCAGAAATCA	GCCAGGGCAC	600
	AGAGAAGGTC	CTGGCTGAGG	TGCTGCCCCA	GTACCTGGAC	CAGAGCTGCT	TTGCCCTGGT	660
	CCTCCCCCCA	CCCCACCACA	CAGGGCAGCT	CCTACACCAC	ABOTTOGACT.	ACATCTTCTT	720
	CLOSCOOR	CCCCTGCMGM	GCAAGATTGT	CATCACTOCT	CCCACCAAGC	ACCTGACGCC	780
	CNUNOSSNSC	0010010100	GCAAGAACCC	CULTURAL COMO	CACCACCARCE	CCCTONCOCC	840
10	OF COMMONDO	GAGC1GGGGG	CCTGGTTCTG	CIGCIACISIG	COCCONCIONCI	GCGMCCCCCC	900
10	GACCGTGGCC	AACCGCGTGG	GCCCCGAGAT	CINCILCONI	GUCGGGCCNGN	CCIGCGIGGC	960
	CCCTGACTAC	GTCCTGTGCA	GCCCCGAGAT	GCAGGAGAGG	CIGCIGCCG	CCCIGCNONG	
	CACCATCACC	CGTTTCTATG	GCGACGACCC	CCAGAGCTCC	CUAAACCTGG	GCCGCATCAT	1020
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	GAGCGTGGAC	GAGGCCATCA	AGTTCATCAA	CCGGCAGGAG	AAGCCCCTGG	CCCTGTACGC	1260
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	CCACAGTGGG	ATGGGCCGGT	ACCACGGCAA	GTTCACCITC	GACACCTTCT	CCCACCACCG	1440
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	GTGAGCGTCC	CACCORCCTC	CARCGGGTCA	CACAGAGAAA	CCTGAGTCTA	GCCATGAGGG	1620
	GCTTATGCTC	CCAACTCACA	TIGITCCTCC	AGACCGCAGG	CTCCCCCAGC	CTCAGGTTGC	1680
	TOGRACTORC	ACATGACTOC	ATCCTGCCTG	CCAGGGCTGC	AAAGCAAGGT	CTTYGCTTCTA	1740
25	TCTGGGGGAC	CCTCCTCCAC	AGAGGCCGAG	AGGCCCGCAGA	ACATGCCAGG	TGTCCTCACT	1800
	27.00000000	MOCOCO ATTO	CAGCCCTTTG	COCTOTOTO	CAGGGTTGGC	CAGGCCCAGT	1860
	CACCCOACCC	CECCUANTIC	GGAAAATACA	GEOCCETTOCC	TTCTTAGGGG	CATCAGOCCT	1920
	CACAGGGGGA	GIGICACCCI	CCCTCCAGGC	OTOGGGTOGG	OCCUPATION OF C	ACACCICCAC	1980
	UNACCOULTUR	00000010000	AACTGCACCA	act officers	CCCCACCCAT	COTOTOACAT	2040
30	TICCACCICI	GCCCCATCCC	ACCCCTCTGG	THE CACA COOSE	*CCCCAGGGAT	CACCCACAGO	2100
50	CCCACACTGG	TCTCTGCACC	CTGGGGTTTG	ar mar cooc	ACCCT GCACT	mms amagas a	2160
	AGCTCCATCC	ACTOGGAAAA	CIGGGGTTIG	CATCACTOCA	CIGCACAGIG	GTTGCTGGAA	2220
	CTGGGGGCAA	GTCCCTTGAC	TTCTCTGAGC	CTCAGITICC	OTTO TO	CACATAGAAG	2280
	CCAAAATGGA	GTCACTTATG	CCMMACTUM	ATAMARIOUA	G1C0000000	CHCHINGHNO	2340
35	CCCTCACACA	CACATGCCCG	TAACAGGATT	TATCACCOMO	ACACGCCIGC	ATGAGCTGCA	2400
33	AGACACAGGG	CGTATGGAAA	AGCACGTCCT	CAAAGACIGI	AGTAT TOCAG	ATGMOCTOCA	2460
	CATGCTTACC	TACCACGGCC	GTCTCCACCA	GAMMACCATC	GCCADACTCCT	GCGMICAGCI	
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					AAGCACTCAT	AGCCCAGATA	2580
40	GGAATCCTCT	GCTCCTCCCA	AATAAATTCA	TCTGTTC			
40							
		111 Protei					
	Protein Acc	cession #: 1	NP_000686				
45	1	11	21	31	41	51	
	}	1		1	1	1	
	MKDEPRSTNL	FMKLDSVFIW	KEPFGLVLII	APWNYPLNLT	LVLLVGTLPA	GMCVVLKPSE	60
	ISOCTEKVLA	EVLPQYLDQS	CPAVVLGGPQ	ETGQLLEHKL	DYIFFTGSPR	VGKIVMTAAT	120
	KHLTPVTLEL	GGKNPCYVDD	NCDPQTVANR	VANFCYFNAG	QTCVAPDYVL	CSPEMQERLL	180
50	PALOSTITRE	YCDDPOSSPN	LGRIINOKOF	ORLEALLGCG	RVAIGGQSNE	SDRYIAPTVL	240
	VDVOETEPVM	QEBIFGPILP	IVNVQSVDEA	IKPINRQEKP	LALYAFSNSR	QVVNQMLERT	300
	SSGSFGGNEG	FTYISLLSVP	FOGVGHSGNG	RYHCKFTFDT	FSHHRTCLLA	PSGLEKLKEI	360
		QLLRWGMGSQ					
55	Sec ID NO:	112 DNA sec	wence				
			n #: NM_0044	156			
		lence: 58-2					
	1	11	21	31	41	51	
60	ī	ī	Î.	1	1	1	
	GAATTCCGGG	CGACGCGCGG	GAACAACGCG	ACTCGGCGCG	CGGGACGAAG	AATAATCATG	60
	GGCCAGACTG	GGAAGAAATC	TGAGAAGGGA	CCAGTTTGTT	GGCGGAAGCG	TOTAAAATCA	120
	GAGTACATGC	GACTGAGACA	GCTCAAGAGG	TTCAGACGAG	CTGATGAAGT	AAAGAGTATG	180
	TTTAGTTCCA	ATCGTCAGAA	AATTTTCCAA	AGAACGGAAA	TCTTAAACCA	AGAATGGAAA	240

65 CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG 200 CAGGORAGEA TACAGGORAT GACATGOTTA ACTITETERS GOTCATTOG GEGGARMAG GAGGOTTOGO TACAGGORAT GACAGGOTTA COLARIZANA TACAGGORAT ANGONATO CITAGATAG GAGAGATTA COLARIZANA TACAGGORAT ANGONATO CITAGATAGA GACATAGAA ACTAGATAG GAGAGAGAA TETAGATAG GAGAGAGAT GATAGAAGA ACTAGATAGA ACTAGATAG GAGAMAGAA GAGAGAGA GAGAGAGA CANTONCOT CITAGAAGA ARAMAATAGAA ACTAGATAGA GAGAMAGAA GAGAGAGA GAATGAGAGA GAGAGAGAA ATAGAAGAA ACTAGATAGA GAAMAGAAGA GAGAGAGA GAATGAGAGA GAGAGAGA GAGAGAGAA AGAAGAAGA GAGAGAGAA GAGAGAGAA GAATGAGAGA GACAGATAGAAGAA ACTAGAGAGA GAGAGAGAA GAGAGAAA GAATGAGAGAAGAAGAA GAATGAGAAGAA GAACGAGAA 360 420 540 70 600 660 720 780 GARAGATATA ARGARCTURE CORRESPOND CTCCCRGGGG CACTICCTCC TGRATGTACC 75 CCCARCATAG ATGGACCAAA TGCTBAATCT GTTCAGAGAG AGCAAAGCTT ACACTCCTTT 900 CATACGCTT TCTGTAGGC ATGTTTAAA TATGACTXCT TCTGCACTCC TTTTCATGCA ACACCCACAC CTTATAAGCC GAAGAACAC GAAGAACAC GAAGAACAC GAAGAACAC ACCACATTT ACCACGATT GAGGGAACA AAGGACTT GCGCGGCAC CACGGTGGG 1080 CGGATAAAGA CCCCACCAAA ACGTCCAGGA GGCCGCAGAA GAGGACGGCT TCCCAATAAC 80 AGTAGCAGGC CCAGCACCCC CACCATTAAT GTGCTGGAAT CAAAGGATAC AGACAGTGAT AGGGAAGCAG GGGCTGAAAC GGGGGGAGGG AACALTATGAT AGGAGAAGAA AGGAGAAGAA CATGAAACTT CGAGCTCCCC TGAAGCAAAT TCTCGGGTGTC AAACACCAAT AAAGATGAAG 1200 1260 UNIDAMACET UMACCOTT TURANCARAT "UTCOGNITO" MACRICANT MAGRITANA 1320
CENARATUTO ACCOTTORIA GARACTORIA STRUCTURO CHIMAGOTTO ANTATTINO, 1300
GEOCHAPITO CONCETTANE TURCHATTET INTOCATTO CHIMAGOTTANI TORONOCONA 1440
ANCHERIANO ACCONTRACTA TURCHATTET INTOCATTO CHIMAGOTTANI TORONOCONA 1440
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COTORIGINA CONTRACTO TUCCHACIONA ANAMARICAN ANCHERIA TORONOCONA 1540
CONTROCARA ANAMARICANI CARACTORICANI ACCONTRACTO ANCHERIA 1540 1320

80

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WO 02/086443 COCTOTIGATE ATCCACCOCA COCTTGTGAC AGTTCGTGCC CTTGTGTGAT AGCACAAAAT 1680 TTTTGTGAAA AGTTTGTCA ACTAGTTCA GAGGTGCAAA COGGGTGCCGG 1740 TCCAAAGCAC AGTGCAACAC CAAGCAGTGC COGTGCTACC TOGGTGTCCG AGAGTGCTGA 1800 CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATTGGG ACAGTAAAAA TGTGTCCTGC 1960 AAGAACTOCA GTATTCAGOG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG 1920 GCAGGCIGGG GGATTTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980 TOTOGAGAGA TTATTTCTCA AGATGAAGCT GACAGAAGAG GGAAAGTGTA TGATAAATAC ANCHORAGE TECHTICAR CTIGARCAT GATTITOTIC TIGATECARC COCCARGOGT ARCARATEC GITTIGGARA TCATTCOGFA ANTOCARACT COCTATIGARA AGTTATGATO GITTAGOGTC ATCACAGGAT MOSTATTITT GCCARGAGAG CCATCCAGA TGCAGGAGAGA 2100 2160 10 2220 CTGTTTGTTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCGG CATCGAAAGA 2280 GRAATGGAAA TCCCTTGACA TCTGCTACCT CCTCCCCCTC CTCTGAAACA GCTGCCTTAG 2340 CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAAATTCTG 2400 ARTITOCHAR GURCUGURAG ARTARUTURU AGUARUGAGU TURARARUCA ACTUUTURUU 2460 15 GCCTTCTCAC CACCIGCAA GTCTTTTGTA CCACTGAATT TTTGCAATAA TGCACTATGG 2520 TACATTTTC AACTTTGAAT AAAGAATACT TGAACTTGAA AAAAAAAAA AAAAAA Seg ID NO: 113 Protein sequence: 20 Protein Accession #: NP 004447 51 MOQTOKKSEK GPVCWRKRVK SEYMBLRQLK RFRRADEVKS MFSSNRQKIL ERTEILNQEW 25 KORRIGPVHI LTSVSSLRGT RECSVTSDLD FPTQVIPLKT LNAVASVPIM YSWSPLQONF 120 MURDRIVLHN IPYMODEVLD ODGIFIEBLI KNYDGKVEGD RECGFINDRI FVELVMALGO 180 YNDDDDDDDD DDPEREEKQ KOLEDHRDDK ESRPPRKPPS DKILEAISSK FPDKGTAEEL KEKYKELTEG OLDGELPPSC TPNIDGPNAK SVORBOSLHS PHTLFCRRCF KYDCFLHPFH 240 ATPHTYKRKN TETALDNKPC GPQCYQHLBG AKEFAAALTA ERIKTPPKRP GGRRRGRLPN 260 30 420 NSSRPSTPTI NVLESKOTOS DREAGTETGG ENNOKEREEK KDETSSSSEA NSRCQTPIKM KONTERDENU ENGGERASME DVIJCTYVIN FCATABLICT KTCROUVEFR VKESSIJAPA 480 PAEDVDTPPR KKKRKHRIMA AHCRKIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPCVIAQ NFCEKFCQCS SECONRFPGC RCKAQCNTKQ CPCYLAVREC DPDLCLTCGA ADHINDSKNVS 600 CKNCSIORGS KKHLLLAPSD VACWGIFIKD PVQKNBFISE YCGEIISQDB ADRRGKVYDK 660 35 YMCSFLPNLN NDFVVDATRK GNKIRPANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720 ELFVDYRYSO ADALKYVGIE REMEIP Seg ID NO: 114 DNA sequence Nucleic Acid Accession #: NM_001827 **4**0 Coding sequence: 96-335 21 31 AGTOTOGGG GAGTTOTIGG CROGGCTGGA CGTGGTTTTG TCTGCTGCGC CCGCTCTTCG COCTCTCGTT TCATTTTCTG CAGCGCGCCA CGAGGATGGC CCACAAGCAG ATCTACTACT 120 OGGACHAGTA CTTOGACGAA CACTACGAGT ACCOSCATOT TATGITACCC AGAGGAACTT CCAAAACGACT ACCTGAATGT ACCAAAACGAA TATGITACCC AGACGAACA CTTGAGTGTC AACACGAATCT AGACGAAGAA CTTGAGTGTC CATTACATGT TTCATGAGCC AGAACCAACA ATTCTTCTTC 180 AMCHANTET MODITIONITE CHITAGNING THOMSEND MARCHANG MILITHINI
TRANSCRICE THITCOMAIN AR CHAONAN ANTOMOTT MICHOGONO CONTUMENT
TITTOMATT "MINOTRAIN CHIGARIANA GOTAGIARTIC ANTOMANA CHAONANTO AGRANICIT TAGANANTOT
AMATOMAT CHICAGNING CONTUNINTET CHICAGNING GOSTICATIC CHICAGNING GOSTICATIC CHICAGNING AGGITCHAT
TITCOMITA GOMOTHOG THOMSENDA TOTTINGAN AMARTICIT CHICAGNING
TITCOMITA GOTOCHITT GOTTITAGNI AMARTICIT CHICAGNING
TITCOMITA GOTTITAGNING
TITCOMITA GOT 360 50 420 480 TATGTTGCAT TTARARARA ARARAA 55 Seq ID NO: 115 Protein sequence: Protein Accession #: NP_001818 60 MAHKOIYYSD KYFDEHYEYR HVMLPRELSK QVPKTHLMSE EEWRRLGVOO SLGWVHYMIH PREPARE OF THEFT Seg ID NO: 116 DNA sequence 65 Nucleic Acid Accession #: CAT cluster

21 TOMOROPICA TORGECACTY OGRCTCTTGA GCCACCTCTG GGGGTGGAGT CTCTCTCCTG

GCATCTGGAC CCTTGGTGCT ATCGACGAAG CTTGGGTGGG GCTCTTAGCT GCTATGTGCA

AGAGGTGTGT TCCAGGGAAA GCCCCTATCT CTCTGCAGAG GTCAAGTGAA AGCGACGGCC

GCAGCCAACA GAGTTCAAAA TGCAGGCTTG GAAAGTACAG GGGGCTCTGT GGAGGATGGG ARGUACTGAT CCACATTCCC ACCAGGAAGT TTAGCAGAAC CCCCGCGTGC CAACTGGACC CCTTGGAAGG ACCTGGCTCA GGCTGGACCA CCTCTTGAGA GGGAGGAGCT CTGGATTTGA

TCAAGAATTC TTTGCTGAGC ATGGTGCCTC ATGCCTATAA TACCAACACT TTGGGAGGCC

ILMANDRA IL JIMATINEE ARGENECITE ARUGINERIA RICCARDAT TRASARGENE TRASARGENE ARCHITERIA RICCARDAT TRASARGENE CARRESTORIA RICCARDAT RICCAR

TTTGAGTGC CATTOGGTA GAAGGAAAG ACGTTTACAC CGAGAATAG TCTGTGTTGC

CACAGACCTT GTCCTTCTTC CTTCTGGAAA GTGTTTCCTC TGCTGCTACT GCTCATGAGA CTCTTCCCCC TCCCTCTCCC AGGGACCAA AGGGCTTTCT ACCACACCCT TTCTTGCCCC

COGCCTCCCA TGTC:GCTGT GCCTTTGTAC TCAGCAATTC TTGTTTGCTC CATTATCTTC

CAGCOOGATA CAGAGTGAAT AGTTAACCAC ACTTAGGTCA AATAGGATCT AAATTTTTGT TCCTGCTCCC TGTAAGAGG CCAGTGTTTG TGTGTTGCAA GCAGCCTTGG AATAGTAACT

PCT/US02/12476

120

180

260

420

480 660

720

780 840

960

1020

WO 02/086443 CTTCTCTTT GTTGGGATC TGGCCACCAA GTTCCAGAAT GATACACGGA TCAGTGCAGA 1200
AGTTCATCAG GCTCTCGGAC CTTAGGGCTG TTGGAGARGG CTTCAGCAC AGGACTGATG
GTGAAGGCTC GTGTTCTCA TCCTCAGCTT TCTTTGCTTC GATCATACA AGGAATACAT 1270 TTOGAAGGGC AAAAATGAA CACTGTOGTT CATTGCAGCC GTGTTTTGTG ACACAGATGC 1380 5 ACASTCTGCT GYGRACACCT TCTCTCAMST GGCATTTGGG AGTCCATGCC AGATCATGGT GCTTCATGAG AGACTGACAG CTATCAGGGG TTGTGGCACT TAGTGAGGAC TCTCCTCCCC 1440 1500 CASTSTOTEC TGATGACACA TACACACCTS ACASTAGCTT GAGTCTTCTC TGTTCCTTTT 1560 ACTOTTAGE CAACATACAC ATGATTTAAA ACCOTTTCTA AATATCTATC ATGGTTCATC 1620 CTTGTCCAAA TGCAGAGTCA GAGCTATTTG TACTTCATTA TTATTTCCAA GGCGAATAGT 10 TOGETTTETT TITGEAAAAA TAATTAAAGT TITTGTATGT TGCAAAAAA AAAAAAAAAAA 1740 ADDCAADAAA Sen ID NO: 117 DNA semience Nucleic Acid Accession #: BC012178.1 15 Coding sequence: 204-2285 41 51 CTTCTCTCCC GCGGCGCTGG GGCCCGCGCT CCGCTGCTGT TGCTCCATTC GGCGCTTTTC 20 TOGOGGOTGG CTCCTCTCCG CTGCCGGCTG CTCCTCGACC AGGCCTCCTT CTCAACCTCA 120 GCCCGCGGGG CCGACCCTTC CGGCACCCTC CCGCCCCGTC TCGTACTGTC GCCGTCACGG 180 240 CTOCIAGGAG CCTTAAGGAT GGCCACCACC ACTATGAAGG AGCTGTTGTC ATTCTGGATG 300 CTGGTGCTCA GTACGGGAAA GTCATAGACC GAAGAGTGAG GGAACTGTTC GTGCAGTCTG 360 25 AAATTTTCCC CTTGGAAACA CCAGCATTTG CTATAAAGGA ACAAGGATTC CGTGCTATTA 420 TCATCTCTGG AGGACCTAAT TCTGTGTATG CTGAAGATGC TCCCTGGTTT GATCCAGCAA 480 TRITCACTAT TOGCARGOCT GITCITGGAA TITGCTATOS TATGCMGATG ATGATAAGG TATTIGGAGG TACTIGTGCAC AAAAAAAGGT TOGAGGARAGA TOGAGTITATIC ANCATTAGTG TOGATTAATCA ATGTTCATTA TICAGGGGGC TICAGGARAGA AGAAGTTGIT TICCTTACAC 540 600 30 ATGGAGATAG TGTAGACAAA GTAGCTGATG GATTCAAGGT TGTGGCACGT TCTGGAAACA 720 TAGTAGCAGG CATAGCAAAT GAATCTAAAA AGTTATATGG AGCACAGTTC CACCCTGAAG 700 TTGGCCTTAC AGADALTGGA AAAGTANTAC TGAAGANTT CCTTTATGAT ATAGCTGGAT GCAGTGGAAC CTCAACCGT CAGAACAGGA ACATTGGAGT ATTGGAGTAG ATCAAGAACAG AGATGAGGC ATCAAAAGT TTGGTTTTAC ACAGTTGGA ACAGTTGAACACA ACAGTTGTA 840 900 35 CAGCTTTGCT AAATCGTGCT TTGAACCAAG AACAAGTCAT TGCTGTGCAC ATTGATAATG 1020 GCTTTATGAG AAAAGGAGAA AGCCAGTCTG TTGAAGAGG CCTCAAAAAG CTTGGAATTC AGGTCAAAGT GATAAATGCT GCTCATTCTT TCTACAATGG AACAACAACC CTACCAATAT 1080 1140 AGGITGARAGI GETTARATGCI GCICATICIT TCITACHIG ARCAGAGAC CIRCARIAT CAGATGARGA TAGARCCCCA COGRARAAGAA TTAGCARAAC GITARATATG ACCACARGIC CTGARGAGAA AAGRARATC ATTGGGGATA CITITGITIA GATTGCCARI GARGITATTG 1200 1260 GRGAARTGAA CTTGAAACCA GAGGAGGITT TCCTTGCCCA AGGITACTITA CGGCCTGATC TARTIGAAAG TOCATCCCTT GITGCAAGTG GCAAAGCTGA ACTCATCAAA ACCCATCACA 1380 ATGACACAGA GCTCATCAGA AAGTTGAGAG AGGAGGGAAA AGTAATAGAA CCTCTGAAAG ATTTTCATAA AGATGAAGTG AGAATTTTOG GCAGAGAACT TGGACTTCCA GAAGAGTTAG 1440 1500 TITCCAGGCA TCCATTTCCA GGTCCTGGCC TGGCAATCAG AGTAATATGT GCTGAAGAAC 1560 45 CTTATATTTG TAAGGACTTT CCTGAAACCA ACAATATTTT GAAAATAGTA GCTGATTTTT 1620 CTGCAAGTGT TAAAAAGCA CATACCCTAT TACAGGGAGT CAAAGCCTGC ACAACAGAAG AGGATCAGGA GAAGCTGATG CAAATTACCA GTCTGCATTC ACTGAATGCC TTCTTGCTGC 1600 1740

AGTARTARAC TICTIGITOT ATTARAA

60 Seq ID NO: 118 Protein sequence:
Protein Accession #: AAH12178.1

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65 MALCNGDSKL ENAGGDLKDG HHHYEGAVVI LDAGAQYGKV IDRRVRELFV QSEIFPLETP AFAIKEQGFR AIIISGGPNS VYAEDAPWFD PAIPTIGKPV LGICYGMQMM NKVFGGTVHK 120 KSVREDGVFN ISVUNTCSLF RGLQKESVUL LTHGDGVDKV ADGFKVVARS GNIVAGIANE SKKLYGAOFH PEWSLTENGK VILKNFLYDI AGCSGTFTVO NRELECIREI KERVGTSKVL 180 240 VLLSGGVDST VCTALLNEAL NOSOVIAVHI DNGFMRKRES QSVESALKKL GIQVKVINAA 300 70 HSPYNGTTIL PISDEDRIPR KRISKTINNT TSPESKRKII GDTFVKIANE VIGENNLKPE EVPLAGGTLR FOLIESASLV ASGKAELIKT HHNDTELIRK LREEGKVIEP LKDFHKDEVR 420 ILGRELGLPE ELVSRHPFPG PGLAIRVICA EEPYICKDFP ETNNILKIVA DPSASVKKPH 480 TLLQRVKACT TEEDQEKLMQ ITSLESLRAF LLPIKTYGYQ GDCRSYSYYC GISSKDEPDW ESLIFLARLI PRKCHNYNRV VYIFGPPVKE PPTDVTPTFL TTGVLSTLRQ ADFEAHNILR 540 600 75 ESGYAGKISO MPVILTPLHF DRDPLQKQPS CQRSVVIRTF ITSDFMTGIP ATPCNEIPVE VVLKMVTEIK KIPGISRIMY DLTSKPPGTT EWE

CASTTARARA TOTAGGTOTO CAGGGGRACT GTCGTTCCTA CAGTTACGTG TGTGGGATCT CCAGTAAGG TGTACCTGGC AGCTTATTTTCT GGCTAGGCTT ATACCTGGCA GGTTACAGG GTTGTTTATA TATTTGCCC CACCAGTAAA GAACCTGCTA

CAGATOTTAC TCCCACTTTC TTGACAACAG GGGTGCTCAG TACTTTACGC CAAGCTGATT

TTGAGGCCCA TARCATTCTC AGGGAGTCTG GGTATGCTGG GAAAATCAGC CAGATGCCGG

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GATCTOTOGT TATTCGAACC TITATTACTA GTGACTTCAT GACTGGTATA CCTGCAACAC

CTGGCAATGA GATCCCTGTA GAGGTGGTAT TAAAGATGGT CACTGAGATT AAGAAGATTC

CTGGTATTTC TCGAATTATG TATGACTTAA CATCAAAGCC CCCAGGAACT ACTGAGTGGG

Seq ID NO: 119 DNA sequence

80 Nucleic Acid Accession #: NM_006500.1 Coding sequence: 27..1967

1860

1920

1980

2040

2100

2160

3220

WO 02/086443 TEATETTEES TETTEGGECAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300 TOACCTTOTA GGACAGAGG GCTACTCTOG CCCTGACTCA AGTCACCCCC CAAGACGAGG 360 GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG TOTACARAGO TODOGRAGAS CORRACATOS AGGTCARCOS COTOGGCATO COTOTGARCA 480 GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCCTCAAG 540 TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAGT 600 CCTCCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC TOGTTARAGA AGACARAGAT GCCCAGTTTT ACTGTGAGCT CARCTACOGG CTGCCCAGTG GGAACCACAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCCG ACAGAAAAAG 700 10 TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 940 GITTGGCTGA TGGCAACCCT CCACCACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA 900 GOGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCCT GGTGCTGGAG CCTGCCCGGA 960 ACGAACACAG TGOGCOCTAT GAATGTCAGG CCTGGAACTT GGACACCATG ATATCGCTGC 1020 TGAGTGAACC ACAGGAACTA CTGGTGAACT ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080 15 CCCCTGAGAG ACAGGAAGGC AGGAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140 ACCTCGACTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAAAG GGGCCTGTGC 1200 TTCAGTTGCA TGACCTGAAA CGGGAGGCAG GAGGCGGCTA TCGCTGGGTG GGGTCTGTGC 1260 CCACCATACC CGGCCCGAAC CGCACACAGC TGGTCAAGCT GGCCATTTTT GGCCCCCCTT GCATGGCATT CAAGGAGAG AAGGTGTGGG TGAAAGAGAA TATGGTGTTG AATCTGTCTT 20 GTGAAGCGTC AGGGCACCCC CGGCCCACCA TCTCCTGGAA CGTCAACGGC ACGGCAAGTG 1440 AACAAGACCA AGATCCACAG CGAGTCCTGA GCACCCTGAA TGTCCTCGTG ACCCCGGAGC 1500 TOTTGGGAGC AGGTGTTGAA TICACGGCCT CCAACGACCT GGGCNAANAC ACCATGCATCC TCTTCCTCGG GCTGGTCAAC TTAACGACCC TCACACCAGA CTCCAACCAA ACCACTGGCAC CCTCATACCA GAGCAACAG CACCTCCACA GAGGAAAGC 1560 1680 25 TOCCOCAGOC GGAGAGCOGG GGCGTGGTCA TCGTGGCTGT GATTGTGTGC ATCCTGGTCC 1740 1800 TOGCOGTGCT GGGCGCTGTC CTCTATTTCC TCTATAAGAA GGGCAAGCTG CCGTGCAGGC GCTCAGGGAA GCAGGAGATC ACGCTGCCCC CGTCTCGTAA GACCGAACTT GTAGTTGAAG 1860 TTAAGTCAGA TAAGCTCCCA GAAGAGATGG GCCTCCTGCA GGGCAGCAGC GGTGACAAGA GGGCTCCGGG AGACCAGGGA GAGAAATACA TCGATCTGAG GCATTAGCCC CGAATCACTT 1980 30 CAGCTCCCTT CCCTGCCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG 2040 CCTCCRAAGG GACTAGAGAG AAGCCTCCTG CTCCCCTCAC CTGCACACCC CCTTTCAGAG 2100 GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCGCCTT TCAGGGACCA GTCCACCAC ATTCCCTCA GGGACCACCA GGCTCATCCC AAGCGAGGAC CGGACCGGGT AGGAAGAT CCTGCAGAAC GGGTTTTTC TTTACACA TTATGGTGT 2160 2220 2280 35 ARATACCTGG CTCCTGCCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTGG TTTCCTGCCC 2340 CALAGGETGG CTTCCACCAT CCAGGTGCAC CACTGRAGTG AGGACACACC GGRGCCAGGC 2400 GCCTGCTCAT GTTGAAGTGC GCTGTTCACA CCCGCTCCGG AGAGCACCCC AGCGGCATCC 2460
AGAAGCAGCT GCAGTGTTGC TGCCACCACC CTCCTGCTG CCTCTTCAAA GTCTCCTGTG 2520 ACATTTTTC TTTGGTCAGA AGCCAGGAAC TGGTGTCATT CCTTAAAAGA TACGTGCCGG 2580 40 GGCCAGGTGT GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GGCGGGCGA 2640 TCACAAAGTC AGGACGAGAC CATCCTGGCT AACACGGTGA AACCCTGTGT CTACTAAAAA 2700 TACAAAAAAA AATTAGCTAG GGGTAGTGGT TGGCACCTAT AGTCCCAGCT ACTCGGAAGG 2760 CTGAAGCAGG AGAATGGTAT GAATCCAGGA GGTGGAGCTT GCAGTGAGCC GAGACCGTGC CACTGCACTC CAGCCTOGGC AACACAGOGA GACTCOGTCT OGAGGAAAAA AAAAGAAAAG 2880 45 ACCCCTACCT GCCGTGAGGA AGCTGGGCGC TGTTTTCGAG TTCAGGTGAA TTAGCCTCAA 2940 TOCCOGTGIT CACTTGCICC CATAGCCCTC TIGATGGATC ACGTRAAACT GAAAGGCAGC 3000 GGGGAGCAGA CARAGATGAG GTCTACACTG TCCTTCATGG GGATTARAGC TATGGTTATA 3060 THAGGACCAR ACTTCTACAA ACCAAGCTCA GOGCCCCAAC CCTAGAAGGG CCCAAATGAG
AGAATGCTAC THAGGATGG ARACCAGGC CTGGCTAGAG CTTCGGTGT GTGTCTGT 3120 50 CTGTGTGTAT GCATACATAT GTGTGTATAT ATGGTTTTGT CAGGTGTGTA AATTTGCAAA 3240 3300 PTAAT TGTCCCAGAA AATCATACAT TGCTTTTTTA TTCTACATGG GTACCACAGG 3360 ANGERTAGE CONCORDANCE TACANCERA ANGERTAGEA ANGESTITUTE ACTUGUESCAGE 3420 3480 AGAGATCAGG GGTTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG 55 CTACCCTACT TTTCAGCAGC AAAACGTCCC GTATGACGCA GCACGAAGGG CCTGGCAGGC 3540 TOTTAGCAGG AGCTATGTCC CTTCCTATCG TTTCCGTCCA CTT

Seq ID NO: 120 Protein sequence: Protein Accession #: NP 006491.1

60

31 41 51 ī 65 MGLPRLVCAF LLAACCCCPR VAGVPGEABO PAPELVEVEV GSTALLKCGL SOSOGNLSHV DWFSVHKEKR TLIFRVRQGQ GQSEPGEYEQ RLSLQDRGAT LALTQVTPQD ERIFLCQGKR 120 PROCEURIOL RVYKAPEEPN ICVNPLGIPV NSKEPEEVAT CVGRNGYPIP QVINVKNGRP 180 LKEEKNRYHI OSSOTVESSG LYTLOSILKA OLVKEDKDAQ FYCELNYRLP SGNHMKESRE VTVPVPYPTE KVWLEVEPVG MLKEGDRVEI RCLADGNPPP HPSISKQNPS TREASSETTN 70 DNGVLVLEPA RKEHSGRYEC QAWNLDTMIS LLSEPQELLV NYVSDVRVSP AAPERQBGSS 360 LTLTCEAESS QDLEFQMLRE ETDQVLERGP VLQLHDLKRE AGGGYRCVAS VPSIPGLMRT OLVKLAIPGP PHMAFKERKV WVKENMVLNL SCEASGHPRP TISWNVMGTA SEQDQDPQRV 420 480 USTINVLVTP ELLETGVECT ASNDLGRNTS ILFLELVNLT TUTPOSNTTT GLSTSTASPH TRANSTSTER KLPEPPSKGV VIVAVIVCIL VLAVLGAVLY FLYKKKLPC RRSCKQEITL 75 PPSRKTELVV EVKSDKLPEE MGLLQGSSGD KRAPGDQGEK YIDLRH

Seq ID NO: 121 DNA sequence Nucleic Acid Accession #: NM_018306

Nucleic Acid Accession #: NM_0183 Coding sequence: 60-671

85

Seq ID NO: 125 DNA sequence Nucleic Acid Accession #: NM_004994.1 Coding sequence: 20..2143

	WO 03	2/086443 TCAACTCTAT	aas as maama	amaan an aan	COURS COOPER	CCCCA ATCAC	360
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5	GGGCCTTGCT	GGTGTGTTAT	CACTATTACG	CAGACTGGTT	CATGTCTCTT	GOOGTCOGCC	540 600
3	TGCTCACCTT	CGCCTCCCTG	GAAACCGTTG	GCATCTACTT	COGACTAGTG	COCTTCACCA	660
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13	GGCAGGAAAA	TGATCATCAG	AAACTAAATG	GCAGCCAGGC	ATGGGGGGCTC	ACGACTGTAA	1260
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20	CGACAGAGCA	AGATOGTTTC	TCTAAAATT	INCONTCHNO	CCACIGORGI	CCHOCCIGOO	2300
	Sec ID NO:	122 Protein	semience:				
25	Protein Ac	cession #: 1	NP_060776				
	1	11	21	31	41	51	
	ī	Ī.	Ī	1	i"	Ĩ.	
20	METSASSSOP	QDNSQVHRET	EDVDYGETDF	HKQDGKAGLF	SQEQYERNKS	SSSSFSSSSS	60
30	SSSSSSSSS	GPGHGEPDVL FHFVLLCFAI	KDELQLYGDA	PGEVVPSGES	GLRRRGSDPA	SGEVEASQLR	120 180
	RENIKKODEF HSVLOGFIPL	FORFRLTGFR	KTD	ADWFMSLGVG	LLTPASLBIV	GIIFGLVIKI	180
35	Seq ID NO:	123 DNA sei id Accession	quence				
55	Coding sec	uence: 243.	.896	-			
						51	
	1	11	21 	31	41	51 I	
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	CCTTCCTGCG	TOOGCACCTG	GCCCCGCGCGCG	CCCCTCTCGG	GCGTCCGGCT	TCCGGCGTCC	120
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	ATTTGTCCAA GTTTTCAAGC	CTTTTTGCCT	GTTCTCATTT	GCTATCATCG	GCCGCACAGT	GAAGATGGAG	600
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	TATGCCAATG	GAACAAGATG GACTGTACAT	AAGTATAAAT	CAGTATATAA	GAATGTGATT	CTACAAGTTC	780 840
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	TTCTTCTAGA	ATTAATTACT	TITATCITIT	GTCTTCATTT	GTGGCCAAAA	TTATGTTTAC	1020
	TAGAGGAAAT	TTGGGATCAT	CAGATGCCAT	TICCARANTO	THETGUTCTA	TABATTAATC	1080
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65	CAGCTAATTG	GAAGGGTGAG GAAGGGTGAG	ACARANGTTA GOGGGAGGAT CACTACAGCC	OGCTTGAACC TGGGCGACAG	TGGGAGGCOG AACGAGACCC	AGGTTCCAGA TGTCTCCAAA	1440 1500 1560
65	ACCCTGTCTC CAGCTAATTG GAGCCAAGAT GGAAAAACAA	GAAGGGTGAG CGCACCACTG AAAAGAAGAA	GOOGGAGGAT CACTACAGCC TANAATAATT	GCTGGGGCTG CGCTTGAACC TGGGCGACAG TGGATGAAAA	TGGGAGGCGG AACGAGACCC TCATGTTTAT	AGGTTCCAGA TGTCTCCAAA TTAAATAGTA	1440 1500 1560 1620
65	ACCOMMENTO CAGCHARTIG GAGCCAAGAT GGAAAAACAA ATGTCATGAG	TACTAAAAAT GAAGGGTGAG CGCACCACTG AAAAGAAGAA ACTATTAAAG	ACAAAAGTTA GOOGGAGGAT CACTACAGCC TAAAATAATT ATGTGCCAGA	GCTGGGGCTG CGCTTGAACC TGGGCGACAG TGGATGAAAA GTTTCAATGA	TGGGGGGCG TGGGAGGCCG AACGAGACCC TCATGTTTAT AAATCATTAA AAATTATTGA	TCTGTAGTCC AGGTTCCAGA TGTCTCCAAA TTAAATAGTA AGTAGGACAG TTATTCCTTA	1440 1500 1560 1620 1680
	ACCCTGTCTC CAGCTAATTG GAGCCAAGAT GGAAAAACAA ATGTCATGAG CTAAGAAATT ACGCACTCC	TACTABABAT GARGGTGAG CSCACCRCTG AAAAGAAGAA ACTATTABAG AATATTABTA A TTCTCCTTT	ACARANGTTA GOOGGAGGAT CACTACAGCC TANANTARTT ATGTGCCAGA TANANATTATI F ACATTTTATI	GCTGGGGCTG CGCTTGAACC TGGGCGACAG TGGATGAAAA GTTTCAATGA TGATAATCTT ATGTTTCTT	TGGTGGGCA TGGGAGGCOG AACGAGACCC TCATGTTTAT AAATCATTAA AAATTATTGA T TGAATATAT	TCTGTAGTCC AGGTTCCAGA TGTCTCCAGA TTAGATAGTA AGTAGGACAG TTATTCCTTA AATTGGCAGA	1440 1500 1560 1620 1680 1740 1800
65 70	ACCOMPTOTO CAGCTAATTG GAGCCAAGAT GGAAAACAA ATGTCATGAG CTAAGAAATT ACGCCACTCG	TACTABARAT GARGGTGAG COCACCACTG ARANGARGAA ACTATTARAG AATATTRATA A TTCTCCTTT G BARCTGRGT	ACARAGTTA GOSGAGGAT CACTACAGCC TAXAATAATT ATGTGCCAGA TAAAAATTAT T ACATTTTAT A CTAAGATTA	GCTGGGGCTG CGCTTGAACC TGGGCGACAG TGGATGAAAA GTTTCAATGA TGATAATCTT C ATGTTTCTT G GTACAGAGTT	GTGGTGGGCA TGGGAGGCCC AACGAGACCC TCATGTTTAT AAATCATTAA AAATTATTGA I TGAATATAT A TGTCAGGAA	TCTGTAGTCC AGGTTCCAGA TGTCTCCAAA TTAAATAGTA AGTAGGACAG	1440 1500 1560 1620 1680 1740 1800
	ACCOMPTOTO CAGCTAATTG GAGCCAAGAT GGAAAACAA ATGTCATGAG CTAAGAAATT ACGCCACTCG	TACTABABAT GARGGTGAG CSCACCRCTG AAAAGAAGAA ACTATTABAG AATATTABTA A TTCTCCTTT	ACARAGTTA GOSGAGGAT CACTACAGCC TAXAATAATT ATGTGCCAGA TAAAAATTAT T ACATTTTAT A CTAAGATTA	GCTGGGGCTG CGCTTGAACC TGGGCGACAG TGGATGAAAA GTTTCAATGA TGATAATCTT C ATGTTTCTT G GTACAGAGTT	GTGGTGGGCA TGGGAGGCCC AACGAGACCC TCATGTTTAT AAATCATTAA AAATTATTGA I TGAATATAT A TGTCAGGAA	TCTGTAGTCC AGGTTCCAGA TGTCTCCAGA TTAGATAGTA AGTAGGACAG TTATTCCTTA AATTGGCAGA	1440 1500 1560 1620 1680 1740 1800
	ACCOMPTOTO CAGCTAATTO GAGCCAAGAT GGAAAAACAA ATSTCATGAG CTAAGAAATT ACGCACTCC GGACTTGAT TIGGCATTT	TACTABAAT GAAGGTGAG GGCACCACTG AAAAGAAGAA ACTATTAAAG AATATTAATA A TTCTCCTTT G AAACTGAGT T AAATAAAGT	ACARAMETTA GOOGAGGAT CACTACAGCC TAMAMEATT ATGTGCCAGA TAMAMATTAT I ACATTTATA CTAMAMATTAT I GTACATGAA	GCTGGGGCTG CGCTTGAACC TGGGCGACAG TGGATGAAAA GTTTCAATGA TGATAATCTT C ATGTTTCTT G GTACAGAGTT	GTGGTGGGCA TGGGAGGCCC AACGAGACCC TCATGTTTAT AAATCATTAA AAATTATTGA I TGAATATAT A TGTCAGGAA	TCTGTAGTCC AGGTTCCAGA TGTCTCCAGA TTAGATAGTA AGTAGGACAG TTATTCCTTA AATTGGCAGA	1440 1500 1560 1620 1680 1740 1800
70	ACCCTGTCC CAGCTAATTG GAGCCAAGAT GGAAAAACAA ATGTCATGAG CTAAGAAATT ACGCATTCAT TTGCCATTT TTGCCATTT	TACTARARAT GAAGGTGAG GGCACCACTG AARAGAAGAA ACTATTARATA A TTCTCCTTT G ARACTGAGT T ARATARAGT 124 Protei:	ACARAMGTTA GCGGGAGGAT CACTACAGGC TAAATAATTA ATGTGCCAGA TAAAAATTAT T ACATTTATA CTAAGATTTA GTACATGAA	GCTGGGGCTG CGCTTGAACC TGGGCGACAG TGGATGAAAA GTTTCAATGA TGATAATCTT C ATGTTTCTT G GTACAGAGTT	GTGGTGGGCA TGGGAGGCCC AACGAGACCC TCATGTTTAT AAATCATTAA AAATTATTGA I TGAATATAT A TGTCAGGAA	TCTGTAGTCC AGGTTCCAGA TGTCTCCAGA TTAGATAGTA AGTAGGACAG TTATTCCTTA AATTGGCAGA	1440 1500 1560 1620 1680 1740 1800
	ACCCTGTCC CAGCTAATTG GAGCCAAGAT GGAAAAACAA ATGTCATGAG CTAAGAAATT ACGCATTCAT TTGCCATTT TTGCCATTT	TACTABAAT GAAGGTGAG GGCACCACTG AAAAGAAGAA ACTATTAAAG AATATTAATA A TTCTCCTTT G AAACTGAGT T AAATAAAGT	ACARAMGTTA GCGGGAGGAT CACTACAGGC TAAATAATTA ATGTGCCAGA TAAAAATTAT T ACATTTATA CTAAGATTTA GTACATGAA	GCTGGGGCTG CGCTTGAACC TGGGCGACAG TGGATGAAAA GTTTCAATGA TGATAATCTT C ATGTTTCTT G GTACAGAGTT	GTGGTGGGCA TGGGAGGCCC AACGAGACCC TCATGTTTAT AAATCATTAA AAATTATTGA I TGAATATAT A TGTCAGGAA	TCTGTAGTCC AGGTTCCAGA TGTCTCCAGA TTAGATAGTA AGTAGGACAG TTATTCCTTA AATTGGCAGA	1440 1500 1560 1620 1680 1740 1800
70	ACCCTGTCC CAGCTAATTG GAGCCAAGAT GGAAAAACAA ATGTCATGAG CTAAGAAATT ACGCATTCAT TTGCCATTT TTGCCATTT	TACTARARAT GAAGGTGAG GGCACCACTG AARAGAAGAA ACTATTARATA A TTCTCCTTT G ARACTGAGT T ARATARAGT 124 Protei:	ACARAMGTTA GCGGGAGGAT CACTACAGGC TAAATAATTA ATGTGCCAGA TAAAAATTAT T ACATTTATA CTAAGATTTA GTACATGAA	GCTGGGGCTG CGCTTGAACC TGGGCGACAG TGGATGAAAA GTTTCAATGA TGATAATCTT C ATGTTTCTT G GTACAGAGTT	GTGGTGGGCA TGGGAGGCCC AACGAGACCC TCATGTTTAT AAATCATTAA AAATTATTGA I TGAATATAT A TGTCAGGAA	TCTGTAGTCC AGGTTCCAGA TGTCTCCAGA TTAGATAGTA AGTAGGACAG TTATTCCTTA AATTGGCAGA	1440 1500 1560 1620 1680 1740 1800
70	ACCCTFTCTC CAGCTAATTO GAGCCAAGAT GAAAAACAA ATGTCATGAG CTAAGAAATT ACGCACTCC GACTTGAT TTGCCATTT Seq ID NO: Protein Ac	TACTABAAT GAAGGTGAG CSCACCACTG AAAAGAAGAA ACTACTAGAA AATATTAATA A TTCTCCTTT T AAATAAAGT 124 Proteicession #: .	ACAAAMATTA GOOGGAGGAT CACTACAGCC TAAAATAATT ATGTGCCAGA TAAAAATTAT T ACAATTTAT T GTACATGAA T GTACATGAA T SEQUENCE: AAH22542	GCTGGGGTTG GGCTGAACC TGGGCGACAG TGGATGAAAA TGATAATCTT C ATGATTCTT C ATGATTCTT C ATGATTCTT C ATGATTCTT C ATGATTCTT	GTGGTGGCA TGGGAGGCG AACGAGACCC TCATGTTTAT AAATCATTAA AAATCATTAA AAATCATTAA AAATCATTAA A TGTCAGGAA A AAAAA	TOTOTAGTOC AGGITTCAGA TOTOTCAAA TOTAGTAGA TOTAGTAGA TATAGTAGA AGTMOGAAA AATTOGTAA AATTOGCAAA ACAACTCAGA	1440 1500 1560 1620 1680 1740 1800 1860
70 75	ACCCTTTCTC CAGCTAATTG GAGCCAAGAT GAARACCAA ATTSCATTGAG CTAAGAATTC OGACTTGAT TTGCCATTT Seq ID NO: Protein AC	TACTABAAT GAAGGTGAG GCACCACTG AAAAGAAGAA ACTATTAAAG AATATTAATA A TTCTCCTTT GAAACTAGAT TAAATAAAGT 124 Protei ccssion *: . 11 VLKDGFHRDL	ACAAAMATTA GOSGGAGGAT CACTACAGCC TAAAATAATT ATGTSCCAGA TAAAAATTAT T ACAATTTAT T GTACATGAA I Sequence: AAH22542 21 LIKVKPGESI	GCTGGGGTG GGCTGAACG TGGGCGACAG TGGATGAATGA TGATAATCTT C ATGTTTCTT G GTACAGGGT C ARAAAAAAA	GTGGTGGCA AACGAGACCC TCATGTTTAT AAATTATTGA TTGAATATTAT AAATTATTGA T TGAATATATA A TGTCAGGAA A TAAAAA 41	TCHTHATICE AGGTTCCAMA TGTGTCCAMA TGTAGTCAMA AGTMGGACAG TTATTCCTTA ACMACTCAGA ACMACTCAGA	1440 1500 1560 1620 1680 1740 1800
70	ACCCTETCTC CAGCTAATTO GAGCCAAGAT GAAAAACAA ATGTCAATGAA CTAAGAAATT ACCCACTCC GGACTGAT TYGCCATTT Seq ID NO: Protein Ac 1	TACTABAAH GAAGGTTGAG GCACCACTG AAAAGAAGAA ACTATTAAAG AATATTAATG AAACTGAGTT G AAACTGAGT 124 Protei cession *: . 11	ACAAMGTTA GOSGGAGGAT CACTACAGGC TAMAATAATT ATGTGCCAGA TAMAAATTAT A CTAAGATTT T GTACATGAA II SEQUENCE: MAH22542 21 LIKVKPGESI LSKESEVLIY EMISPETUS F	GCTGGGGTCG GGGTGAACC TGGGCGACAG TGGATCAATCT G GTAATCTT G GTACAGAGT C AAAAAAAAA 31. EDLHTCRLLI ARRDSQCLDC KKTLEFPILK	GTGGTGGCA TGGGAGGCOG AACAGGCOC AACAGACCC TCAGGTTAA AAATTATTGA T TGGATATGA T TGGATATA A TGTCAGGAAC A AARAA 41	TOTOTAGICA AGGITCCAGA TOTOTCCAAA TIAAATAGTA AGTMGGCAAG THATTCCTTA AAATGGCAAA ACAACTCAGA 51 DPYELASLRE THEFTS TOTOTAGA	1440 1500 1560 1620 1620 1680 1740 1800 1860
70 75	ACCCTETCTC CAGCTAATTO GAGCCAAGAT GAAAAACAA ATGTCAATGAA CTAAGAAATT ACCCACTCC GGACTGAT TYGCCATTT Seq ID NO: Protein Ac 1	TACTABAAT GAAGGTGAG GCACCACTG AAAAGAAGAA ACTATTAAAG AATATTAATA A TTCTCCTTT GAAACTAGAT TAAATAAAGT 124 Protei ccssion *: . 11 VLKDGFHRDL	ACAAMGTTA GOSGGAGGAT CACTACAGGC TAMAATAATT ATGTGCCAGA TAMAAATTAT A CTAAGATTT T GTACATGAA II SEQUENCE: MAH22542 21 LIKVKPGESI LSKESEVLIY EMISPETUS F	GCTGGGGTCG GGGTGAACC TGGGCGACAG TGGATCAATCT G GTAATCTT G GTACAGAGT C AAAAAAAAA 31. EDLHTCRLLI ARRDSQCLDC KKTLEFPILK	GTGGTGGCA TGGGAGGCOG AACAGGCOC AACAGACCC TCAGGTTAA AAATTATTGA T TGGATATGA T TGGATATA A TGTCAGGAAC A AARAA 41	TOTOTAGICA AGGITCCAGA TOTOTCCAAA TIAAATAGTA AGTMGGCAAG THATTCCTTA AAATGGCAAA ACAACTCAGA 51 DPYELASLRE THEFTS TOTOTAGA	1440 1500 1560 1620 1620 1740 1800 1860

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	1 110 02	11	21	31	41	51	
	AGACACCTCT	GCCCTCACCA	1	1		magnagama am	60
	GGGCTGCTGC	TTTGCTGCCC	CCAGACAGGG	CCAGTCCACC	CTTGTGCTCT	TCCCTGGAGA	120
5	CCTGAGAACC	AATCTCACCG	ACAGGCAGCT	GGCAGAGGAA	TACCTGTACC	GCTATGGTTA	180
		GCAGAGATGC					240 300
	GOGRACOOCA	CTGTCCCTGC	TCCCAGACCT	GGGCAGATTC	CAAACCTTTG	AGGGCGACCT	360
1.0	CAAGTGGCAC	CACCACAACA	TCACCTATTG	GATCCAAAAC	TACTCGGAAG	ACTTGCCGCG	420
10		GACGACCCT					480 540
	CACCTTCACT	OGCGTGTACA GGGTATCCCT	GCOGGGAOGC TOOMOOGAA	AGACATOGTC COLOGGGCTC	CYGGGACAG	COTTTTCCTCC	540 600
	TGGCCCCGGC	ATTCAGGGAG	ACGCCCATTT	CGACGATGAC	GAGTTGTGGT	CCCTGGGCAA	660
16	GGGCGTCCTG	GTTCCAACTC	GGTTTGGAAA	CGCAGATGGC	GOGGCCTGCC	ACTTCCCCTT	720
15	CATCTTCGAG	GGCGGCTCCT ACCACGGCCA	ACTOTOCCTG	CACCACCGAC	GGTCGCTCCG	ACCCCTACCCA	780 840
	GAGACTCTAC	ACCOGGGACG	GCAATGCTGA	TGGGAAACCC	TGCCAGTTTC	CATTCATCTT	900
	CCAAGGCCAA	TCCTACTCCG	CCTGCACCAC	GGACGGTCGC	TCCGACGGCT	ACCCCTCGTG	960
20	CGCCACCACC	GCCAACTACG ATGGGGGGGCA	ACCGGGACAA	GCTCTTCGGC	TTCTGCCCGA	CCCGAGCTGA	1020
20	CCCTAACCAC	TACTOGACCT	GTACCAGCGA	GGGCCGGGA	GATGGGGGGCC	TCTGGTGCGC	1140
	TACCACCTCG	AACTITGACA	GOGACAAGAA	GTGGGGGCTTC	TGCCCGGACC	AAGGATACAG	1200
	TTTGTTCCTC	GTGGCGGCGC	ATGAGTTCGG	CCACGCGCTG	GGCTTAGATC	ATTCCTCAGT	1260
25	GCCGGAGGCG	CTCATGTACC GGCATCCGGC	ACCIPATION	CTTCACTGAG	GRACCTGAGC	CACCATAAGGA	1320 1380
20	AACCACCACC	ACACCGCAGC	CCACGGCTCC	CCCGACGGTC	TGCCCCACCG	GACCCCCCAC	1440
	TGTCCACCCC	TCAGAGCGCC	CCACAGCTGG	CCCCACAGGT	CCCCCCTCAG	CTGGCCCCAC	1500
	AGGTCCCCCC	ACTGCTGGCC	CTTCTACGGC	CACTACTGTG	CCTTTGAGTC	CGGTGGACGA	1560
30	CARCOTTUCARC	GTGAACATCT	CATTOTOTO	COCCOMMENTS	AGCCGGCCGC	AGGGCCCCTT	1680
50	CCTTATCGCC	GACAAGTGGC	CCGCGCTGCC	CCGCAAGCTG	GACTCGGTCT	TTGAGGAGCC	1740
	GCTCTCCAAG	AAGCTTTTCT	TCTTCTCTGG	GCGCCAGGTG	TGGGTGTACA	CAGGCGCGTC	1800
	GGTGCTGGGC	CCGAGGCGTC	TGGACAAGCT	GGGCCTGGGA	GCCGACGTGG	CCCAGGTGAC	1860
35	GTTGGAGTG	AAGGCGCAGA	TRRTTGRATTCC	CORGREGOTIC	AGCGAGGTGG	ACCGGATGTT	1980
-	CCCCGGGGTG	CCTTTGGACA	CGCACGACGT	CTTCCAGTAC	CGAGAGAAAG	CCTATTTCTG	2040
	CCAGGACOGC	TTCTACTGGC	GCGTGAGTTC	CCGGAGTGAG	TTGAACCAGG	TGGACCAAGT	2100
	OGGCTACGTG	ACCTATGACA GTAAATCCCC	A CTROCKA COL	ACCOMMISSION	ACCACCCACT	TTGCCGGGTT	2160
40	CAAACTGGTA	TTCTGTTCTG	GAGGAAAGGG	AGGAGTGGAG	GTGGGCTGGG	CCCTCTCTTC	2280
	TCACCTTTGT	TTTTTTTTGG	AGEGTTECTA	ATAAACTTOG	ATTCTCTAAC	CTTT	
	Sea ID NO.	126 Protein	o comiones.				
	Protein Acc						
45		cession #: 1	NP_004985.1				
45	Protein Acc			31	41	51	
45	1 MSLWOPT,VLV	11 LLVLGCCFAA	SP_004985.1	PPODLRTNLT	DROLABEÝLY	RYGYTRVAEM	60
	1 MSLWQPLVLV RGESKSLGPA	11 LLVLGCCFAA	NP_004985.1 21 PRORQSTIVL PETGELDSAT	PPGDLRTNLT LKAMRTPRCG	DRQLAEBYLY VPDLGRFQTF	RYGYTRVAEM EGDLKWHHHN	60 120
45 50	1 MSLWQPLVLV RGESKSLGPA ITYWIONYSE	11 	NP_004985.1 21 PRORQSTIVL PETGELDSAT FARAFALKSA	PPGDLRTNLT LKAMRTPRCG VTPLTPTRVY	DRQLABEYLY VPDLGRFQTF SRDADIVIOF	RYGYTRVAEM EGDLKWHHEN GVAEHGDGYP	120 180
	1 	11 	NP_004985.1 21 PRORQSTIVL PETGELDSAT FARAFALWSA DAMPDDDELW	FPGDLRTNLT LKAMRTPRCG VTPLTFTRVY SLGKGVVVPT	DRQLABEYLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC	RYGYTRVAEM EGDLKWHHHN GVAEHGDGYP HFPFIFEGRS	120 180 240
	1 MSLWQPLVLV RGESKSLGPA ITYWIQNYSE FDGKDGLLAH YSACTIDGRSDG	11 	21	FPGDLRTHLT LKAMRTPRCG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMCG	DRQLABBÝLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF NSAGELCVFP	RYGYTRVAEM EGDLKWHHHN GVASHGDGYP HFPFIFEGRS PFIFGGGSYS FTFLGKEYST	120 180 240 300 360
50	1 	11 LLVLGCCFAA LLLLQKQLSL DLPRAVIDDA AFPFGFGIQG DGLPWCSTTA YRWCATTANY LWCATTANY	21 PRQRQSTLVL PETGELDSAT FARAFALWSA DAHFDDDELW NYDTDDRFGF DRDKLFGFCP SDKWGFCPD	FPGDLRTHLT LKAMRTPRCG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMCG OGYSLPLVAA	DRQLABBYLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF NSAGELCVPP HBFGHALGLD	RYGYTRVAEM EGDLKUHHHN GVAEHGDGYP HFPFIFEGRS PPIFGGGYS FTFLGKEYST HSSVPEALMY	120 180 240 300 360 420
	1 MSLWQPLVLV RGSSKSLGPA ITYWIQNYSE FDGKDGLLAH YSACTIDGRS ACTIDGRSG CTSEGRGDGR PMYRFIBGPP	11 LLVLGCCFAA LLLLQKQLSL DLPRAVIDDA AFPPGPGIQG DGLPWCSTTA YENCATTANY LHKDDVNGIR	21 PRQRQSTLVL PETGELDSAT FARAFALWSA DAHFDDDELW NYDTDDRFGF DRDKLFGFCPD RDKKGFCPD HLYGPRPEPE	PPODLRTNLT LKAMRTPRCG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMCG QOYSLPLVAA PRPPTTTTPQ	DRQLABEYLY VPDLGRFQTF SRDADIVIQF RPGNADGAAC GNADGKPCQF MSAGELCVFP HSPGHALGLD PTAPPTVCPT	RYGYTRVAEM EGDLKWHHEN GVAEHGDGYP HFPFIFEGES PFIFQGGSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER	120 180 240 300 360 420 480
50	MSLWQPLVLV RGESKSLGPA ITWIQNYSE FDGKDGLLAH YSACTIDGRS ACTIDGRSDG CTSEGRGDGR PMYRFIESDP PTAGPTGPPS	11	NP_004985.1 21 PRORQSTLVL PETGELDSAT FARAFALWSA DAHFDDDELW MYDTDDRFGF DRDKLFGFCP SDKWGFCPD HLYGPRPEPE PSTATVPLS	PODLATMLT LKAMATPROS VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMCG QQYSLPLVAA PRPPTTTTPQ PVDDACNVNI	DRQLABBYLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF MSAGELCVFP HBFGHALGLD PTAPPTVCPT FDAIABIGNO	RYGYTRVAEM RYGYTRVAEM GOLKWIHHIN GVAEHGGYP HFPFIFEGRS PFIFOGQSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW	120 180 240 300 360 420
50	MSLWQPLVLV RGESKSLGPA ITYWIQNYSE FDGKDGLLAH YSACTIDGRSD CTSEGRGDG PMYRFIBGPP ETAGPTGPPS RFSEGRGSRP LDKLGLGADV	11	NP_004985.1 21 PRQRQSTLVL PETGELDSAT FARAPALMSA DAHPDDDELM NYDTDDREGF DRDKLFGFCP SDKKWGFCPD ELYOPFEPE PSTATTVELS PALPRKLDSV	FPGDLRTHLT LHAMRTPRCG VTPLITFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMCG QOYSLPLVAA PRPPTTTTPQ FVDDACNVNI PLWRFDVKAQ	DRQLABEYLY DRQLABEYLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF MSAGELCVFP HSPGHALGLD PTAPPTVCPT FDAIABIGNQ FFSGRQVWVY MVDPRSASEV	RYGYTRVAEM RYGYTRVAEM GVAEHGDGYP HFPFIFEGRS PFIFOGOSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	120 180 240 300 360 420 480 540
50	MSLWQPLVLV RGESKSLGPA ITYWIQNYSE FDGKDGLLAH YSACTIDGRSD CTSEGRGDG PMYRFIBGPP ETAGPTGPPS RFSEGRGSRP LDKLGLGADV	11	NP_004985.1 21 PRQRQSTLVL PETGELDSAT FARAPALMSA DAHPDDDELM NYDTDDREGF DRDKLFGFCP SDKKWGFCPD ELYOPFEPE PSTATTVELS PALPRKLDSV	FPGDLRTHLT LHAMRTPRCG VTPLITFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMCG QOYSLPLVAA PRPPTTTTPQ FVDDACNVNI PLWRFDVKAQ	DRQLABEYLY DRQLABEYLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF MSAGELCVFP HSPGHALGLD PTAPPTVCPT FDAIABIGNQ FFSGRQVWVY MVDPRSASEV	RYGYTRVAEM RYGYTRVAEM GVAEHGDGYP HFPFIFEGRS PFIFOGOSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	120 180 240 300 360 420 480 540
50	MSLWQPLVLV MSLWQPLVLV MSLWQPLVLV MGESKSLGPA ITYMIQMYSE FDGKUGLLAH YSACTIDGRSDG CTSEGRGDGR MYRRTBGPP FTAGPTGPPS FFSGRGGRP LDKLGLGADV THDVFQYREK Seq ID NO:	11	MP_004985.1 21 PRORQSTIVL PETGELDSAT FARAFALWSA NYDTDDREGF DRDKLFGFCP SDKKWGPCPD HLYGPREPE PALFRKLDSV RGNKLLFSG RVSSRSELWQ	FPGDLRTMLT LKAMRTPRG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFUVAA PRPPTTTTPQ PVDDACNVNI PEBPLSKKLP RLMRFDVKAQ VDQVGYVTYD	DRQLABEYLY DRQLABEYLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF MSAGELCVFP HSPGHALGLD PTAPPTVCPT FDAIABIGNQ FFSGRQVWVY MVDPRSASEV	RYGYTRVAEM RYGYTRVAEM GVAEHGDGYP HFPFIFEGRS PFIFOGOSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	120 180 240 300 360 420 480 540
50	MSLWQPLVLV RGESKSLGPA ITYNIQNYSE FDGKDGLLAH XSACTIDGRSDG CTSEGRGDAR PMYRFIBGPP FTAOPTOPPS FFSEGRGGRP LDKLGLGADV THDVFQYREX Seq ID NO: Nucleic Ac:	11	NP_004985.1 21 PRORQSTIVL PETGELDSAT FARAFALMSA AMHFDDDELW NYDTDDREP DRDKLFGFCP SDKKKGFCFD FSTATTVFLS FALFRKLDSV RGKKLLFSGR RVSSRSELWQ Quence a #: NM_0041	FPGDLRTMLT LKAMRTPRG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFUVAA PRPPTTTTPQ PVDDACNVNI PEBPLSKKLP RLMRFDVKAQ VDQVGYVTYD	DRQLABEYLY DRQLABEYLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF MSAGELCVFP HSPGHALGLD PTAPPTVCPT FDAIABIGNQ FFSGRQVWVY MVDPRSASEV	RYGYTRVAEM RYGYTRVAEM GVAEHGDGYP HFPFIFEGRS PFIFOGOSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	120 180 240 300 360 420 480 540
50 55 60	MSLWQPLVLV RGESKSLGPA ITYNIQNYSE FDGKDGLLAH XSACTIDGRSDG CTSEGRGDAR PMYRFIBGPP FTAOPTOPPS FFSEGRGGRP LDKLGLGADV THDVFQYREX Seq ID NO: Nucleic Ac:	11	NP_004985.1 21 PRORQSTIVL PETGELDSAT FARAFALMSA AMHFDDDELW NYDTDDREP DRDKLFGFCP SDKKKGFCFD FSTATTVFLS FALFRKLDSV RGKKLLFSGR RVSSRSELWQ Quence a #: NM_0041	FPGDLRTMLT LKAMRTPRG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFUVAA PRPPTTTTPQ PVDDACNVNI PEBPLSKKLP RLMRFDVKAQ VDQVGYVTYD	DRQLABEYLY DRQLABEYLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF MSAGELCVFP HSPGHALGLD PTAPPTVCPT FDAIABIGNQ FFSGRQVWVY MVDPRSASEV	RYGYTRVAEM RYGYTRVAEM GVAEHGDGYP HFPFIFEGRS PFIFOGOSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	120 180 240 300 360 420 480 540
50	MSLWQPLVLV RGESKSLGPA ITYNIQNYSE FDGKDGLLAH XSACTIDGRSDG CTSEGRGDAR PMYRFIBGPP FTAOPTOPPS FFSEGRGGRP LDKLGLGADV THDVFQYREX Seq ID NO: Nucleic Ac:	11	NP_004985.1 21 PRORQSTIVL PETGELDSAT FARAFALMSA AMHFDDDELW NYDTDDREP DRDKLFGFCP SDKKKGFCFD FSTATTVFLS FALFRKLDSV RGKKLLFSGR RVSSRSELWQ Quence a #: NM_0041	FPGDLRTMLT LKAMRTPRG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFUVAA PRPPTTTTPQ PVDDACNVNI PEBPLSKKLP RLMRFDVKAQ VDQVGYVTYD	DRQLABEYLY DRQLABEYLY VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF MSAGELCVFP HSPGHALGLD PTAPPTVCPT FDAIABIGNQ FFSGRQVWVY MVDPRSASEV	RYGYTRVAEM RYGYTRVAEM GVAEHGDGYP HFPFIFEGRS PFIFOGOSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	120 180 240 300 360 420 480 540
50 55 60	MSLWOPLVLV RGESKSLGPA ITYNIGWYSE POGKOGLLAH YSACTIDGRSD CTSEGREDGR FMYRFIEGPP FTAOPTGPPS FAGORGRP LDKLGLGADV THDVFQYREX Seq ID MO: Nucleic Ac: Coding sequ	11 LLVLGCCFAA LLLLGKQLSL LLLLGKQLSL LLLLGKQLSL LLPRAVIDDA AFPDRPGIO DGLPWCSTTA YRNCATTANY LHKGATTANY LHKGATTANY AGPTGPFTAG QGPFLIADKN AQVTGALRSA AYFCQDRFYW 127 DNA sei d Accessiouence: 32-6	MP_004985.1 21 PROMOSTIVL PROMOSTIVE PRO	PPODLATHLT LIKAMATERCG VTPLITFTRVY SLGKGVVVPT CPSERLYTRD TRADSTWOOG QOYSLEDVAA PRPFITTPQ PVDDACNNIP PEBLISKLP RLWRFDVKAQ VDQVGYVTYD 81	DRQLAESYLY VPDLGREGTF SRDADIVIGE REGRADIVIGE REGRADGAC GNADGKECOF MSAGELCVPP HEFCHALGLD FTAPFTVCFT FDAIAELGE FFSGRQVMVY MVDPRSASEV LLQCPED	RYGYTRVABM EGDLKWHHHN GVABHGDGYP HFFPIFEGRS PFIFEGRSYST HSSVPEALMY GPTVHFSER LYLFKDGKYM TGASULGPRR DRMFFGVPLD	120 180 240 300 360 420 480 540 600 660
50 55 60	MSLWOPLVLV RGESKSLGPA ITYMIGNES FDGKOGLLAH YSACTIDGES ACTIDGESDG CTSEGREDG CTSEGREDG TSEGREDG TSEGREDG TABGES LDKLGLGABU Seq ID NO: Nucleic Ac: Coding sequ	DESSION #: 1 11 LLVLGCCFAA LLLLQKQLSL LLLLQKQLSL LLLLQKQLSL LLLLQKQLSL LLLQKQLSL LLLQKQLSL AFFAGGIQG DALPKGSTX-X YRNCATTANY LHKCDWAGIR AGFGGPFAG AGFGGPFAG 127 DNA sed d Accessio	RP_004985.1 21 PROROSTIVL PETGELDSAT FARRALMSA DAMFDDDELM NOVIDDREGE DEDKLFGFCF DEDKLFGFCF DEDKLFGFCF DEDKLFGFCF DEDKLFGFCF DEDKLFGFCF RCMCLFSGG RVSSRSELMQ TUENCE 1 #: NM_00417 21 TCARACCOCGA	FPGDLRTNLT LKAMRTPRCG VTPLITFTRVY SLGKGVVVPT CPSRRLYTRG UTADSTVWGG CGYSLFLVAA PRPPTTITPG VUDDACNVNI FEBELSKKLF, ELWRFDVKAQ VDQVGYVTYD 81 31 GATGCTGAAC	DRQLABEYLY VPDLGRFQTF SRDADIVIQF SRDADIVIQF SRDADIVIQF SRDADIVIQF SRDADIVIQF SRDADIVIQF MSAGELCVFP HEFGHALGLD FTAPFTVGF FTAPFTVGF FTAPFTVGF FTAPFTVGF SRQVWVY ILQCPED 41 AAAGTQCTGT	RYGYTRVABY EGGLKMHHHN GVASHGGYP HPFPIFDGR PFIFUGKYST HSSVDEALMY GPPTWHSEL LYLFKDGKYN TGASVLGPR DRMFFGVPLD 51	120 180 240 300 360 420 480 540 660
50 55 60 65	1	DESSION #: 1 11 LLVLGCCFAA LLLJCKGLES DLPRAYIDDA APPORGIOD DLPRAYIDDA APPORGIOD DLPRAYIDDA APPORGIOD LENCATTANY LENCATTANY DLENCATTANY APPORGIOD ARPTORPTA APPORGION APPORGION APPORGION 127 DNN seid d Accessio. 11 11 1 CCTAGGGGAGA	RP_004985.1 21 1 PROROSTIVIL PROROSTIVIL PROROSTIVIL DATADDELSA TORROSTORI PROROSTIVIL PRO	PPODLATHLT LKAMATPROO VTPLIFFREY SLOKGVVVPT CPSERLYTED GYSLFLYAM RPPITITPQ PVDDACNVNI PEBPLSKKLP RLWARDVKAQ VDQVGYVTYD 31 31 31 GATGCTGAAC GCTGGGGCTG	DRQLABEYLY VPDLGRFQTF SRDADIVIQF RFQRADDAC GNADGHCQF HEFGHALGLO FTAPFTVCP FDATABLGNQ MVDPRSASEV ILQCPED 41	RYGYTRVABM EGDLKWHHHM GVASHGDGYP HFPFIFGGS PFIFLGKSYST HSSVPEALMY GPFTWHSER LYLFKDGKYM DRMFFGVPLD 51 CCCGGCTGGG CCTCTGGGGCTC	120 180 240 300 360 420 480 540 600 660
50 55 60	1	DESSION #: 1 11 11 12 LLVLGCCFAA LLVLGCCFAA AFPERGIOLO DLFRAVIDDA AFPERGIOLO DLFRAVIDDA AFPERGIOLO DLFRAVIDDA AFPERGIOLO DLFRAVIDDA AFPERGIOLO LEMCOMPSIL AGATISHEP LEMCOMPSIL AGATISHEP LEMCOMPSIL AFFERGIEFE 127 DNA SEE CETAGGGGAA CETAGGGAA CETAGGAA CETAGGGAA CETAGGAA CETAGGGAA CETAGGGAA CETAGGGAA CETAGGAA CETAGGGAA CETAGGAA CETAGGAA	RP_004985.1 21 1 PRQRQSTLVL PRQRQSTLVL PRQRQSTLVL PRQRQSTLVL PRQRALMSA NOTIDDEFOF DRDKNAFGCED HIVOGRAPHE PSTATUPLS P	PEPODLATHLI LKAMATPRO VTPLIFTRIY SIGNOVVER CSERLYTRO TRADSTYMOS PREPFITTE PUDDACIVAL PEPEPLESKLE RLMRPDVKAQ VDQVGYVTYD 31 GATGCTGAAC GCTGGTGGGCTG GCTGGTGGGCTG GCTGGTGGGCTG	DOGLABEYLY VPDLORROTT VPDLORROTT REGINDORAC GRADORECUP REGINDORAC REGINDORA	FYGYTRVAEM EGDLKWHINHIN GOLKWHINHIN GYARSHODEY HFPFIFORS FFILIGKEYST HSSVPEALM GOPTVHFSER LYLFKOGKYS TGASVLGPRE DRMFFGVPLD 51 CCCGGCTGGG CCCGGCTGGG GTCTGGGGTC AGCATGAGAA AGGGTACT	120 180 240 300 420 480 600 660
50 55 60 65	MSLWQPLVLV RESSISJOPA RESSISJOPA TITWIQNYSS FOOKDOLLAR YSACTIONS FOOKDOLLAR YSACTIONS THOUTONEDO CTSBCROCDA FOOKDOLLAR THOUTONEDO THOUTONED THOUTONED THOUTONED THOUTONED THOUTONED THOUTONED THOUTONED THOUTONED THOUTONED THOUTONED T	11 11 12 11 12 11 12 12 13 14 14 14 14 14 15 16 16 16 17 16 17 16 17 17 17 17 17 17 17 17 17 17 17 17 17	RP_004985.1 21 1 PROROSTIVIL P	FOODLATHLT LAXMSTPROD VPELTPRIVE SLOSGVVVPT CPSELYTAD TRADSTYMO, OYSLELVAA PREPTITE PREPLEKKIL RIMREDVKAQ VDQVGYVTD 31 GROGOGGGG GCGGGGGGGGGGGGGGGGGGGGGGGGGG	DOGLABETLY VPILISPOTE SERADIVIDE SERADIVID	RYGYTEVASM EGDLAGHHM GADLAGHHM GADLAGHHM GAVASHODAY HPFITEDGS FITEGGSYS HSSVPSALMY GAPTURGSYS DEMPFQVPLD 51 CCCGGCTGGG CTCTGGGGTC GACCATGGATACTT AGCATGGATA	120 180 240 360 420 480 600 660
50 55 60 65	1	DESSION #: 1 11 12 LLVLGCCFAA LLVLGCCFAA AFPEGGIGO DLFRAVIDDA AFPEGGIGO DLFRAVIDDA AFPEGGIGO DLFRAVIDDA AFPEGGIGO LLKLGCMGISTA YENGCATTAN YENGCATTAN AVGTGATAN AVGTGATAN 127 DNA SEE CCTMGGGAA AGGGGGATA CCCTTGGGCA AGGCGTGGGGAA AGGGGGTGGGAAAGTGGGGAA AGGGGGATGACGCTTGGGAAAGTGGGGAA AGGGGGATGACGCTTGGGAAAGTGGGGAA AGGGGGATGACGGTAGGAAAGTGGGGAA AGGGGGATGACGCTTGGGAAAGTGGGGAAAAGTGGGGAAAAGTGGGAAAAGTGGGAAAAGTGGGAAAAGTGGGAAAAGTGGGAAAAAGTGGGAAAAGTGGGAAAAGTGGGAAAAGTGGGAAAAGTGGGAAAAGTGGGAAAAAGTGGGAAAAGTGGGAAAAGTGGGAAAAAGTGGGAAAAAGTGGGAAAAAGTGGAAAAGTGGGAAAAAGTGGAAAAGTGGGAAAAAGTGGAAAAAA	RP_004985.1 21 1 PRQRQSTIML PRQRQSTIML PRQRQSTIML PRQRQSTIML PRQRAMSA MODIDDREFF DRAFFALMSA MODIDDREFF SNEWGRCED HIVOGREBEP STATUPLS PSIATUPLS TURNING TURNI	FPODLATHLT LAXMSTPROO VPTLTFTSTV SLGKGVVVPT SLGKGVVVPT SLGKGVVVPT SLGKGVVVPT SLGKGVVVPT SLGKGVVVPT FPUDACHVM FPUDACH	DOGLABETLY VPDLGRFOTF SERDALIVE SERDALIVE RESUNDENCE RESUNDE RESUNDENCE RESUNDE RESUNDENCE RESUNDENCE RESUNDENCE RESUNDENCE RESUNDENCE RESUNDE	RYGYTEVABM EGDLAMBHEN GOLAMBHEN GOLAMBHEN GOLAMBHEN GOLAMBHEN HPFIFERS PFIFLORS FFIFLORS FFIFLORS FFIFLORS FFIFLORS GPTVHFSE LULRHOOKYN TOASULDER CCCOCTOOL CCCOCTOOL CCCOCTOOL CCCTGGGGCTC ACCNTGRIGHA AAOTGTACTI CAGTGSCCAA	120 180 240 360 420 420 440 540 660 660
50 55 60 65 70	1 MSLWOPLVLV MSLWOPLVLV MSLWOPLVLV MSCHSSLIGHA TYMACONE MSCHSSLIGHA MSCH	Dession #: 1 LILLANGECEAN LILLANGIS. LILLANGIS. LILLANGIS. LILLANGIS. LILLANGIS. LILLANGIS. LILLANGIS. LILLANGIS. APPOPOJOO DOSLIPPOSTTA YENCATTANY LIKCATTSNY LIKCA	RP_004985.1 Temporary Pemperatura Pem	PEPODLATHLT LAXMSTPROS VPTLPTRY SLGKGVVVPT SLGKGVVPT SLGKGVPT SL	DOGLABETLY VPDLGRFOTF SERDAIVIGE	RYGYTRVABM EDDLWHHIBM GOLWHHIBM GOLWHHIBM GOWASHODEV HPFFIFOGAS FFIFIGASS FF	120 180 240 360 420 420 480 540 660 660
50 55 60 65	1 MSLWQPLVLV MSLWQPLVLV RGESSELGFA TYPKIQNIE TYPKIQNIE TYPKIQNIE SCHOOL SCHOO	Dession #: 1 LILL/MUNICOFPAR	RP_004985.1 21 ROGROTIMIL PROGROTIMIL PROG	FOOLERILIT LAXMETPRO VPELIFFRY SLOKOVVPT SLOKOV SLOKOV SLOKOVPT SLOKOV SLOK	DOGLABETLY VPDLORPOTE SENDAL TYLO SENDAL T	RYGYTEVABM EGDLMGHBH GOLMGHBH GOLMGHBH GOLMGHBH GOLMGHBH GOLMGHBH HPFIFEGR FFIFUGGS'F FFIFUGGS'F FFIFUGGS'F FFIFUGGS'F FFIFUGGS'F CARVAGGA GPTVHFBR LUTPEGGAV TOASVLGPR DRMFGVPLD 51 CCCGCCTGGG CTCTGGGCT CACCTGGGGCT AAGTTTCA AGTTGCAA CCCTTACAGG TOATTTCA GGTGGCCAT CAGTTGCCA TTTCTGAAC CCCTTACAGG TOATTTCA GGATGCCTT CATACAGG TOATTTCA	120 180 240 300 360 420 480 540 660 660 120 180 240 360 360 420 480
50 55 60 65 70	1 MEMORPHATE M	LIVIDOCEPAN LILUVIDOCEPAN LILUVIDOCEPAN LILUVIDOCEPAN LILUVIDOCEPAN LILUVIDOCEPAN LILUVIDOCEPAN LILUVIDOCEPAN LILUVIDOCEPAN LILUVIDOCEPAN LIVUVIDOCEPAN LIVU	RP_004985.1 21 21 PROROSTIML PROR	PRODURTHLIT LAGMETPRO VPELIFFRY SLORGYVEP SLORGYVEP TRADSTYMCO GOYSLEVAN PREPTITE PO PUDOLYMIT PEBPLESKLIP SLORGYVEP	DOGLABETLY VPDLORPOTE SENDLIVING SENDLIV SE	REGITEVABN EDDLWHHEN GOANSHOEDE, GOANSHOEDE, HPFFIFORS PFIFORS PFIFORS FFIFORS	120 180 240 360 420 480 540 660 660 120 180 240 360 420 420 360 420 660
50 55 60 65 70	1 MELMOPPLYLV MELMOPPLYLV MELMOPPLYLV MELMOPPLYLV MELMOPPLYLV MELMOPPLYC MELMOPPLY	Dession #: 1 LULIOCEPAN LULIONISE LUCATTENIP LUCATTE	RP_04985.1 PROGRISTIVIL PETGELISAT PETGELIS	FOOLARTHLE LAGMETPRO VPENTRY SLONGVVEP TRADETWOO TRADETWOO TRADETWOO TRADETWOO TRADETWOO TRADETWOO TRADETWOO TRADETWOO TRADETWO TRADETWOO TRADETWO	DOGLASETLY VPDLORROTE SERBLY V	RYGYTRVABM EDDLWHUBBIN EDDLWHUBBIN EDDLWHUBBIN EDDLWHUBBIN EDDLWHUBBIN EDDLWHUBBIN EDDLWHUBBIN EPFIFORS ENDLWHUBBIN EDDLWHUBBIN EDDLWHU	120 180 240 300 360 420 480 540 600 660 120 180 360 420 480 360 420 480 660
50 55 60 65 70 75	1	LLVLGCCFAA LLLLQRQLSL LDFRAVIDDA LDFRAVIDDA AFFRORIO AFFR	RP_004985.1 PROROSTIVIL PRIVELISAT PRAFFALMS MINITODERGE PRAFFALMS MINITODERGE NOTITIONERGE PSTATTULS PSTAMMAND RESEARCH RESEARC	FOOLATHLE LAGMETPRO VPELTPREV SLOROVVEP COSSELVINE SLOROVVEP TRADSTING OCTSELVINE SLOROVVEP TRADSTING SLOROVVEP TRADSTING SLOROVVEP TRADSTING SLORE SL	DEGLAREFLY VPDLGREGTE VPDLGREGTE REGRADIACO	RYGYTRVABM EGDIAMHEN GYASHODYS EGDIAMHEN GYASHODYS EGDIAMHEN GYASHODYS PPITPAGES PPITPAGES PPITPAGES ESPTIGES E	120 180 240 360 360 420 480 600 660 660 120 180 240 360 360 360 420 480 660 720 720
50 55 60 65 70	1 MSLMOPTVILV MSLM	LILIVIGOCEPAN LILIVICOCEPAN LILIVIGOCEPAN LI	RP_004985.1 FROROSTINIL PROGRISTINIL PROG	PRODURTILIT LAGMETPRO VPEINTRY SIGNOWN PF COSERLY TIME SIGNOWN PF COSERLY TIME PREPITTE PG PUDDACNIVAL PEPPLTATE PG PUDDACNIVAL SIGNOWN PF COSERLY SIGNOWN PF PUDDACNIVAL SIGNOWN PF PU	DOGLASETLY VPDLORPGTF SENDAL TYPE SENDAL T	STATEMENT OF THE STATEM	120 180 240 360 360 420 480 540 600 660 120 180 240 300 420 480 540 600 660 720 780 840
50 55 60 65 70 75	1 MSLMOPTVILV MSLM	LIVLOCCFAA LILLUVLOCCFAA LILLU	FP_004985.1 FROROSTIVIL TOALCOOOLA TOA	PRODLETHLT LAMMETPRO VPELTETRY SLOSSYVEY SLOSS	DOGLARBELLY VPDLARROTE VPDLARROTE SENDLIVIAGE GNADURCO HASCHLAGL PTAPPTVCT FDATAGE HASCHLAGL FTSGROWN WDPSASSEV LIQCPED 41 AMAGGGGT CTTAGTCGG GTTAGTCGG G	RYGYTRVABM EDDLWHUBHN GYASHGOYP HIP PI TUGGS	120 180 240 360 360 420 480 600 660 600 600 600 600 600 600 600 720 480 600 720 780 840 840 840 840 900
50 55 60 65 70 75	MSLWOPTVILV MSLWOPTVILV MSLWOPTVILV MSLWOPTVILV MSSLWOPTVILV MSSLWOPTV	III ILIVIGOCEPAN LLILIQUOLISI LLIVIGOCEPAN LLILIQUOLISI LUPRAVITIDA APPROPRIO LUPRAVITIDA APPROPRIO LUPRAVITIDA APPROPRIO LUPRAVITIDA APPROPRIO LUPRAVITIDA APPROPRIO LUPRAVITIDA LUPRAVITIDA APPROPRIO LUPRAVITIDA LUPRAVITID	FP_004985.1 FROROSTINIL A : IM _0041 TOARACCOCKA TOARACCA ACCARGAGA ACCARGAGA ACCARGAGA ACCARGAGA ACCARGAGA ACCARGAGA COTTCARACCA ACCARGAGA ACCARGAGA ACCARGAGA ACCARGAGA ACCARGAGA COTTCARACCA COCCCACACCA ACCARGAGA ACCARGAGA COCCCACACCA COCCACACCA COCCACAC COCCACACCA COCCACAC COCCACAC COCCACAC COCCACAC COCCACAC COCCACAC COCCACAC	PRODLETHLT LANMETPROO VPILIPERVY VPILIPERVY PROPLETTER GREENLY TO THAN DETAILS GREENLY TO THAN DETAILS STREETLY TO PUDDALEVAL PUDDALEVAL STREETLY TO PUDDALEVAL STREETLY TO PUDDALEVAL STREETLY TO SUPPLIFIED STREETLY TO SUPPLIFIED SU	DOGLASEFLY VPDLGREGTE VPDLGREGTE SEDDLYIG BOOLSEGE BANDLYIG BANDLY	RYGYTRVABM EGDIAMHENI GONASHIGHTS GONASHIGHTS FFIFIGHTS	120 180 240 360 360 420 480 540 600 660 120 180 240 300 420 480 540 600 660 720 780 840
50 55 60 65 70 75	MSLMODIVLY MSLMODIVLY MSLMODIVLY MSSLMODIVLY MSSSSSIGN ITHNIGNISS PROMODILLS MICHAEL M	LLVIGOCEPAN LLLLAMONISE LLVIGOCEPAN LLLLAMONISE LLVIGOCEPAN LLLLAMONISE LLVIGOCEPAN LLLLAMONISE LLVIGOCEPAN LLLLAMONISE LLVIGOCEPAN LLVIGOCEPAN LAMONISE LAMONISE LLVIGOCEPAN	FP_001985.1 PROGROSTINL PRTOELDSAT PROGROSTINL PRTOELDSAT PROGROSTINL PROGROSTINL PROGROSTINL PROGROSTINL PROGROSTINL PROGROSTINL PROGROSTIN PROGROST	PRODLETHLT LANMETPROO VPILIPERVY VPILIPERVY PROPLETTER GREENLY TO THAN DETAILS GREENLY TO THAN DETAILS STREETLY TO PUDDALEVAL PUDDALEVAL STREETLY TO PUDDALEVAL STREETLY TO PUDDALEVAL STREETLY TO SUPPLIFIED STREETLY TO SUPPLIFIED SU	DOGLASEFLY VPDLGREGTE VPDLGREGTE SEDDLYIG BOOLSEGE BANDLYIG BANDLY	RYGYTRVABM EGDIAMHENI GONASHIGHTS GONASHIGHTS FFIFIGHTS	120 180 240 360 360 420 480 600 660 600 600 600 600 600 600 600 720 480 600 720 780 840 840 840 840 900
50 55 60 65 70 75	MELWOPTULV MELWOPTULV MELWOPTULV MESSASJIGA ITYMIQNYSS POROCILLA ITYMIQNYSS POROCILLA COTSIGNATION MICHAEL MIC	III ILIVIGOCEPAN LLILIQUOLISI LLIVIGOCEPAN LLILIQUOLISI LUPRAVITIDA APPROPRIO LUPRAVITIDA APPROPRIO LUPRAVITIDA APPROPRIO LUPRAVITIDA APPROPRIO LUPRAVITIDA APPROPRIO LUPRAVITIDA LUPRAVITIDA APPROPRIO LUPRAVITIDA LUPRAVITID	FP_004985.1 FRGRGSTINL FRTGELIGAT FRTGELIGA	PRODLETHLT LANMETPROO VPILIPERVY VPILIPERVY PROPLETTER GREENLY TO THAN DETAILS GREENLY TO THAN DETAILS STREETLY TO PUDDALEVAL PUDDALEVAL STREETLY TO PUDDALEVAL STREETLY TO PUDDALEVAL STREETLY TO SUPPLIFIED STREETLY TO SUPPLIFIED SU	DOGLASEFLY VPDLGREGTE VPDLGREGTE SEDDLYIG BOOLSEGE BANDLYIG BANDLY	RYGYTRVABM EGDIAMHENI GONASHIGHTS GONASHIGHTS FFIFIGHTS	120 180 240 360 360 420 480 600 660 600 600 600 600 600 600 600 720 480 600 720 780 840 840 840 840 900

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1	11	21	31	41	51	
1	1	1	1	1	1	
MLNKVLSRLG	VAGOWRFVDV	LGLEEESLGS	VPAPACALLL	LFPLTAQHEN	FRKKQIEELK	60
			NODKLGFEDG			120
			FILFNNVDGH	LYELDGRMPF	PVNHGASSED	180
TLLKDAAKVC	REFTEREOGE	VRFSAVALCK	AA			

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10 Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_000213

10		d Accession sence: 127-5		13			
	1	11	21	31	41	51	
15	caccoacaca	CTGCAGCCCC	ATCTCCTAGC	GCAGCCCAG	GCGCGGAGGG	AGOGAGTOOG	60
	CCCCGAGGTA	GGTCCAGGAC	GGGCGCACAG	CAGCAGCCGA	GGCTGGCCGG	GAGAGGGAGG	120 180
	AAGAGGATGG	CAGGGCCACG	CCCCAGCCCA	TGGGCCAGGC	ACCOCCACT	AGCCTTGATC GAAGAGCTGC GTTCAGGGAC GAGCATCGTG CCTGCGGCGC GCGGCATTTT CATGGACTTC	240
	ACCORDING TO	TOTOTOGGAC	TANGGACTIGG	GCCTACTGCA	CAGACGAGAT	GTTCAGGGAC	300
20	COCCGCTGCA	ACACCCAGGC	GGAGCTGCTG	GCCGCGGGCT	GCCAGCGGGA	GAGCATCGTG	360
	GTCATGGAGA	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TTGACACCAC	CCTGCGGGGG	420
	AGCCAGATGT	CCCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGGTGAGGA	CATGGACITC	480
	TOCALCTOCA	TGTTTGAGCC	TCTGGAGAGC	CTCAAGAAGA	TGGGGGCAGAA	CCTGGCTC3G	600
25							
	AGCGTCCCGC	AGACGGACAT	GAGGCCTGAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720 780
	COCCCCTTCT	CCTTCAAGAA	CTCACCCACC	CTGACAGAAG	CTGAGGGGGG	GTTCCGGAAT	840
	ATCCTGCAGG	CAGCTGTGTG	CACGAGGGAC	ATTGGCTGGC	GCCCGGACAG	CTTCGATGCC CACCCACCTG	900
30							
	GGCATCATGA	GCCGCAACGA	TGAACGGTGC	CACCTGGACA	CCACGGGCAC	CTACACCCAG	1020
	TACAGGACAC	AGGACTACCC	CACCAACTAC	TOCTATAGET	ACTACCAGA	CONTCACACC	1140
	TATTTCCCTG	TCTCCTCACT	GGGGGTGCTG	CAGGAGGACT	CGTCCAACAT	CGTGGAGCTG	1200
35	CTGGAGGAGG	CCTTCAATCG	GATCOGCTCC	AACCTGGACA	TCCGGGCCCT	CAAGCACAAC GCTTCACACC CGTGGAGCTG AGACAGCCCC TGGGTCCTTT	1260
	CGAGGCCTTC	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGAOGAGGAC	TGGGTCCTTT	1320
	CACATCCGGC	ACCITOTOCCA	GOTTOCOGRA	CACCACAAGC	GCARCATCCA	TGAGCACGTG TCTGAAACCT	1440
	TOTTTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
40						GTGCGGACAG	
	TGTGTGTGCA	GCGAGGGCTG	GAGTOCCCAG	ACCTGCAACT	GCTCCACCGG	CTCTCTGAGT	1620
	CACATTCAGC	ACTOTOTOTO	CTACGGGGAA	GGCCGCTACG	AGGGTCAGTT	CTGCGAGTAT	1740
	GACAACTTCC	AGTGTCCCCG	CACTTCCGGG	TTCCTCTGCA	ATGACCGAGG	TOTOTORATT TOGOGASTRE CTGCGASTAT ACGCTGCTCC TCCCCTCAGC CTGTGASTOT GATCAACTAC CCAGGCTTGG CAAGATGGTG CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC	1800
45	ATOGGCCAGT	GTGTGTGTGA	GCCTGGTTGG	ACAGGCCCAA	GCTGTGACTG	TCCCCTCAGC	1860
	AATGCCACCT	GCATCGACAG	CAATGGGGGC	ATCTGTAATG	GACGTOGCCA	CIGIGAGIGI	1920
	TOGGGGATCC	ACCOGGGCCT	CTGCGAGGAC	CTACGCTCCT	GCGTGCAGTG	CCAGGCGTGG	2040
	GGCACCGGCG	AGAAGAAGGG	GCGCACGTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGGTG	2100
50	GACGAGCTTA	AGAGAGCOGA	GGAGGTGGTG	GTGCGCTGCT	CCTTCCGGGA	CGAGGATGAC	2160
	GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCCAA	COCCCTGCTC	2220
	CTCCTCCTCC	TGCGGCTCCT	GGCCCTGCTA	CTGCTGCTAT	GCTGGAAGTA	CAMGGATGAC CAGCACTGCT CCCCCTGCTC CTGTGCCTGC GGGCTTTAAG CACGCCCATG CAACAACATG GGTGCCCTAC TGACACTCGG CAGCCAGATC	2340
	TGCAAGGCCT	GCCTGGCACT	TCTCCCGTGC	TGCAACCGAG	GTCACATGGT	GGGCTTTAAG	2400
55	GAAGACCACT	ACATGCTGCG	GGAGAACCTG	ATOGCCTCTG	ACCACTTGGA	CACGCCCATG	2460
	CIGCGCAGCG	GGAACCTCAA	TCATGCCGCC	MCCATCAACC	CCACAGAGCT	GGTGCCCTAC	2580
	GOGCTGTCCT	TGCGCCTQGC	CCGCCTTTGC	ACCGAGAACC	TGCTGAAGCC	TGACACTCGG	2640
	GAGTGCGCCC	AGCTGCGCCA	GGAGGTGGAG	GAGAACCTGA	ACGAGGTCTA	CAGGCAGATC	2700
60	TOOGGTGTAC	ACAAGCTOCA	GCAGACCAAG	TTCCGGCAGC	AGCCCAATGC	CAGGEAGATE COGGECCTG GGTGGCCCCC CCAGGAGGGC CGACGAGAAG COGCCGCCTG GCAGCCTGAG	2760
	CTGAAGCTTA	CACAGAGAAGCA	GGTGGGGGG	AGGGCCTTCC	ACGACCTCAA	GCCGGCCCCC	2880
	GGCTACTACA	CCCTCACTGC	AGACCAGGAC	GCCCGGGGCA	TGGTGGAGTT	CCAGGAGGGC	2940
15	GTGGAGCTGG	TGGACGTACG	GGTOCCCCTC	TTTATCCGGC	CTGAGGATGA	CGACGAGAAG	3000
65	CAGCTGCTGG	TGGAGGCCAT	COACGTGCCC	GCAGGCACTG	CCACCCTCGG	GCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	3120
	TTCTCGGTCA	GCCGCGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGTCCTGGAC CAACOGGGAC	3180
	GGCGGGAAGT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACOGGGAC	3240
70							
/0	GTGAAGCTCC	TGGAGCTGCA	AGAAGITGAC	COCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TYGGGCCAGCCA	GGTCCGCCGT CCACTCCACC GATGTTGTCA TAAGGCCGCT GGGGTACAGG	3420
	ACCATCATCA	TCAGGGACCC	AGATGAACTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
	TCACAGCCAC	CCCCTCACGG	CGACCTGGGC	GCCCCGCAGA	ACCCCAATGC	TAAGGCCGCT	3540
75	GGGTCCAGGA	AGATCCATTT	CAACTGGCTG	COCCCTTCTG	GCAAGCCAAT	CAGCAAGCTG	3600
13						GGTGTGCGCC	
	GTGCCCAGCG	AGCCAGGGGG	TCTGGCCTTC	AATGTOGTCT	CCTCCACGGT	CEACUAGGA GACCENCTE CTGCTATGGC TGACAACCCT CTACACGTG CCTGGCCACC GGACGCCAG CTCCCATCG	3840
80	AGCTGGGCTG	AGCCGGCTGA	GACCAACGGT	GAGATCACAG	CCTACGACGT	CTGCTATGGC	3900
30	CIGGTCAACG	AIGACAACCG	TGAGARCCTT	COCATGAGA	AGCCCTACCG	CTACACCGTG	4020
	AAGGCGCGCA	ACGGGGCCGG	CTGGGGGGCCT	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
	CAGCCCAAGA	GGCCCATGTC	CATCCCCATC	ATCCCTGACA	TCCCTATCGT	GGACGCCCAG	4140
85	AGCGGGGAGG	ACTACGACAG	CTTCCTTATG	TACAGOGATG	ACCTTCTACG	CTCTCCATCG	4200
0.0						TGCTGCTGCC	
	TATGGCACCC	ACCTGAGCCC	ACACGTGCCC	CACCGCGTGC	TANGCACATO	CTCCACCCTC	4380

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GACACGCCCA CCCGCCTGGT GTTCTCTGCC CTGGGGCCCA CATCTCTCAG AGTGAGCTGG CAGGAGCOGC GGTGCGAGCG GCCGCTGCAG GGCTACAGTG TGGAGTACCA GCTGCTGAAC 4620 GGCGGTGAGC TGCATCGGCT CRACATCCCC AACCCTGCCC AGACCTCGGT GGTGGTGGAA 4680 GACCTCCTGC CCAACCACTC CTACGTGTTC CCCGTGCCGG CCCAGAGCCA GGAGGCTGG GGCCGAGAGC GTGAGGGTGT CATCACCATT GAATCCCAGG TGCACCCGCA GAGCCCACTG 4740 4800 TOTOCCCTGC CAGGCTCCGC CTTCACTTTG AGCACTCCCA GTGCCCCAGG CCCGCTGGTG 4860 TTCACTGCCC TGAGCCCAGA CTCGCTGCAG CTGAGCTGGG AGCGGCCACG GAGGCCCAAT 4920 10 GOOGLATATES TEGGETACET GETGLECTET GAGATGGECC AAGGAGGAGG GECAGECACE 4080 GCATTCOGG TGGATGGAGA CAGCCCGAG AGCCGGCTGA CCGTGCCGGG CCTCAGCGAG AACGTGCCCT ACAGTTCAA GTTCCAGGC AGGACCACTA AGGGCTTCGG CCTCAGCGAG GAGGCATCA TCACCATAG TTCCAG GTCCAGGAC CAGGACCACTA CAGGCCTTCGG GCCAGAGGGC GAGGCATCA TCACCATAG 5040 5100 GOOGGGCTCT TCCAGCACCC GCTGCAAAGC GAGTACAGCA GCATCACCAC CACCCACACC 5220 15 AGGGCACCG AGCCCTTCTT AGTGGATGGG CCGACCCTGG GGGCCCAGCA CCTGAAGGCA GGGGCCTCC TCACCCGGCA TGTGACCCAG GAGTTTGTGA GCCGGACACT GACCACCGG GGAACCCTTA GCACCACAT GGACCAACAG TTCTTCCAAA CTTGACCGCA CCCTGCCCCA 5280 5340 5400 COCCOGCCAT GTCCCACTAG GOGTCCTCCC GACTCCTCTC COGGAGCCTC CTCAGCTACT 5460 CCATCCTTGC ACCCCTGGGG GCCCAGCCCA CCCGCATGCA CAGAGCAGGG GCTAGGTGTC 5520 20 TOCTGGGAGG CATGAAGGGG GCAAGGTCCG TCCTCTGTGG GCCCAAACCT ATTTGTAACC 5580 AMAGAGCTGG GAGCAGCACA AGGACCCAGC CTTTGTTCTG CACTTAATAM ATGGTTTTGC 5640 A CTYC

Seq ID NO: 130 Protein sequence: Protein Accession #: NP 000204

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	EVFEPLESPV	DLYILMDFSN	SMSDDLDNLK	KMOONLARVL	SQLTSDYTIG	FGKFVDKVSV	180
			FSFKNVISLT				240
	QTAVCTRDIG	WRPDSTHLLV	FSTESAFHYE	ADGANVLAGI	MSRNDERCHL	DITGTYTQYR	300
35			PIFAVINYSY				360
			LRTEVTSKMF				420
			SDGLKMDAGI				480
			QPCLREGEDK				540
			QCVCEPGWTG				600
40			IHPGLCEDLR				660
			TYSYTMEGDG				720
			ACLALLPCCN				780
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			VHKLQQTKFR				900
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			ITIIKEQARD				1020
			PVEGELLFQP				1080
			IIRDPDBLDR				1140
			YWIQGDSESE				1200
50			SEPGRLAFNV				1260
			RMLLIENLRE				1320
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			THLSPHVPHR				1440
			PTRLVFSALG				1500
55			LPNHSYVPRV				1560
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Seq ID NO: 131 DNA sequence Nucleic Acid Accession #: BC004372 Coding sequence: 132..2231

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			GACAGACACC				900
			ACCATTTCAA				960
			TGGAACCCAA				1020
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5	WO 02/086443 CCCATTCGAC AACAGGGA GGACAACACC AAGCCCAG CCATGGGACG AGGTCATC CCCTTCAGC TACTGCAA CTCTTCAAT GACAACGC TGGAAGAAGA TAAAGACC TCACAGGTGG AAGAAGAC	AG GACAGTTCCT AA GCAGGAAGAA AT CCAAACACAG AG CAGAGTAATT AT CCAACAACTT	GGACTGATTT GGATGGATAT GTTTGGTGGA CTCAGAGCTT CTACTCTGAC	GTTCAACCCA GGACTCCAGT AGATTTGGAC CTCTACATCA ATCAAGCAAT	ATCTCACACC CATAGTACAA AGGACAGGAC CATGAAGGCT AGGAATGATG	1320 1380 1440 1500 1560 1620 1680
10	ATACCTETCA TRACCEAC AGACTGGGTC CTTTGGAG GTTCCTTATC AGGAGACC GATCTGAATG GACACCC GTCCTATAAG GACACCC TGCCTTTGAT TOTTGCAG	AC ACGAAGGAAA TT ACTGCAGTTA AA GACACATTCC AC TCACATGGGA AA ATTCCAGAAT	GCAGGACCTT CTGTTGGAGA ACCCCAGTGG GTCAAGAAGG GGCTGATCAT	CATCCCAGTG TTCCAACTCT GGGGTCCCAT TGGAGCAAAC CTTGGCATCC	ACCTCAGCTA AATGTCAATC ACCACTCATG ACAACCTCTG CTCTTGGCCT	1740 1800 1860 1920 1980 2040
15	ANAMOTROT GATCAACA ACGGAGAGGC CAGCAAGT CTCCAGACCA GTTTATGA TTGGGGTGTA ACACCTAC TAGGGGGGG TGGGACAC TTTTTAGCAT ANAMITTT	GT GGCAATGGAG CT CAGGAAATGG CA GCTGATGAGA AC CATTATCTTG TT AACAGATGCA	CTGTGGAGGA TGCATTTGGT CAAGGAACCT GAAAGAAACA ATGTGCTACT	CAGAAAGCCA GAACAAGGAG GCAGAATGTG ACCGTTGGAA GATTGTTTCA	AGTGGACTCA TCGTCAGAAA GACATGAAGA ACATAACCAT	2100 2160 2220 2280 2340
20				AUGUOUT		
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25	1 11	21	31	41	51	
30	NDKFWWHAAW GLCLVPLS PTMAQMEKAL SIGFETCR ASAPPEEDCT SVIDLPNA GSSERSSIS GGYIFYIF DERDRHLSFS GGGIDDDE MIDVDRNGTT AVEGNMIE	YG FIEGHVVIPS FD GPITITIVNS ST VHPIPDEDSE DP ISSTISTES EA HPPLIHHENS	: IHPNSICAAN : DGTRYVQKGE : WITDSTDRIP : AFDHTKQNQD : BEEETPHSTS	NTGVYILTSN YRTNPEDIYP ATSTSSNTIS NTQWNPSHSN TIOATPSSTT	TSQYDTYCFN SNPTDDDVSS AGMEPNEENE PEVLLQTTTR EETATQKBQW	60 120 180 240 300 360
35	FORRWHBGYR OTFREDSH GHQAGRRHDM DSSHSTTL KDHPTTSTLT SSNRNDVT FGVTAVTVGD SNSNVNRS TPQIPENLII LASLLALA	QP TAMPNTGLVE GG RRDPNHSEGS LS GDQDTFHPSC LI LAVCIAVNSS	DLDRTGPLSM TTLLEGYTSH GSHTTHGSES RROGOKKKLV	TTQQSNSQSP YPHTKESRTP DGHSHGSORG	STSHEGLEED IPVTSAKTGS GANTTSGPIR	420 480 540 600 660
40	SKSQEMVHLV NKESSETE Seq ID NO: 133 DNA Nucleic Acid Access Coding sequence: 15	DQ FMTADETRNI sequence ion #: NM_002	QNVDMKIGV			
45	Couring sequence: 13	0-733				
50	1 21 CGAGGTTCGG GTCGTGGG GCGGAGGGAA GGAGCTAC AGCCGAGCGC ATGATACTTC CACTGAGA TITCTCTTCC TGAGCAAG	GA GTAGCOGCOG GC CGCGCCCCCA AT ACAGACGAGG AA ATTAAAACAC	AGAGGCCGCG TGGCGGCCGC CCAACCATGA TGGAAGAAGA	GAGCCAGOGA CAAGGACACT CCCTCAGTTT TGAAGAGGAA	CGACCGACCC CATGAGGACC GAGCCAATAG CTTTTTAAAA	60 120 180 240 300
55	TOCGGGCAAA ACTGTTCC GCACTGGTGA CGTCAAGC GGAGGGACAA GACCCTGA AGCCCAACGC AGGTAGCG AGTGCCCCAA GCCAGAGC	GA TTTGCCTCTG TC CTGAAGCACA AG ATCTGTGCCA AC CGTGCCTGGC TG CTGGCCATCC	AGAACGATCT AGGAGAAAGG AACCACTACAT TCTGGAACAC GCTTCCTGAA	GCCAGAATGG GGCCATCGGC CACGCCGATG CCACGCTGAC TGCTGAGAAT	AAGGAGCGAG CTCCTCATGC ATGGAGCTGA TTCGCCGACG GCACAGAAAT	360 420 480 540 600 660
60	TCARAACAA GTTTGAAG CAGGCAAAAA TGATCATG AGGAGACCAA GGAGGATG TCTCTTTCCT TTCCTTTT ATTCTTTCAT TTTTACAA	CC GAAAAAGTGG CT GAGGAGAAGG TT TAAAAAATTI	CGGAAAAGCT AATAAATCGT TACCCTGCCC	AGAAGCTCTC CTTATTTTAT CTCTTTTTCG	TOGGTGAAGG	720 780 840
65	Seq ID NO: 134 Prot Protein Accession &	ein sequence: : NP_002873				
70	1 11 MAAAKUTHED HOTSTENI ENDLPEWEER GIGDVKLI VWNITADFAD ECFKPELI AEKLEALSVK EEFKEDAE	KH KEKGAIRLLA AI RFLNABNAQE	RRDKTLKICA	NHYITPMMEL	KPNAGSDRAW	60 120 180
75	Seq ID NO: 135 DNA Nucleic Acid Access Coding sequence: 27	ion #: NM_00	0077.2			
80	1 11 	AC GGCGTCCCCI	TGCCTGGAAA	GATACOGCGG	TCCCTCCAGA	60 120
85	GGATTTGAGG GACAGGGT GGGCTGGCTG GTCACCAG GGAGAGCAGG CAGCGGGC GCCTGGGCT GACAGGG GCTGCTGGAG GCGGGGG GGTCATGATG ATGGGCAG	CG GAGGGGCTC AG GGTGGGGCGC TG CGGGGAGCAC TG CCACGGCCGC TGCCCAACGC	TTCCGCCAGC ACCGCGTGCG CATGGAGCCG GGCCCGGGGT ACCGAATAGT	ACCGGAGGAA CTCGGCGGGCT GCGGCGGGGA CGGGTAGAGG TACGGTCGGA	GAAAGAGGAG GCGGAGAGGG GCAGCATGGA AGGTGCGGGC GGCCGATCCA	180 240 300 360 420 480

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10	AGCACTCACG GAAGCTGTCG	CCCCACTACC AAGAAAAACA CCCTAAGOGC ACTTCATGAC GTCACACTGC ATTCACTC	ACATTCATGT AAGCATTTTG	GGGCATTTCT TGAACTAGGG	TGTTGGAGTT TGCGAGCCTC AAGCTCAGGG	GCAGCCTCCG GGGTTACTGG	960 1020 1080 1140 1200
15	Seq ID NO: Protein Acc	136 Protein	n sequence: P_000068.1				
20	1 MEPAAGSSME ELLLLHGAEP LGHRDVARYL	11 PSADWLATAA NCADPATLTR RAAAGGTRGS	21 ARGRVEEVRA PVHDAAREGF MHARIDAABG	31 LLEAGALFNA LDTLVVLHRA PSDIPD	41 PNSYGRRPIQ GARLDVRDAW	51 VMMMGSARVA GRLPVDLAER	60 120
25	Nucleic Ac:	137 DMA sed id Accession pence: 104	1 #: NM_058	196.1			
30	į.	11	21	31	41	51	
35	GCCCCCACCC CCGAGTGCCG TCTCACCCGA GCACCGGGCC	TCTGCTTGGC TGGCTCTGAC GAGCTGCTGC CCCGTGCACG GGGGCGCGGC CTGGGCCATC AACCATGCCC	CATTCTGTTC TGCTCCACGG ACGCTGCCCG TGGACGTGCG	TCTCTGGCAG CGCGGAGGCTTC GGAGGGCTTC CGATGCCTGG	AACTGCGCCG CTGGACACGC GGCCGTCTGC	TGGGCAGOGC ACCCCGCCAC TGGTGGTGCT CCGTGGACCT CGGGGGGGCAC	60 120 180 240 300 360 420
40	CTACAGGGCC AATAGAGCTT TAAATGTCCA CGCTTCTGCC	AGAGGCTCTG ACAACTGCCC TTAAAAATGT TTTATATCAT TTTTCACTGT	AGAAACCTCG CCGCCACAAC CCTGCCTTT TTTTTATATA GTTGGAGTTT	GGAAACTTAG CCACCOCGCT AACGTAGATA TTCTTATAAA TCTGGAGTGA	TTCGTAGTT TARGCCTTCC AATGTAAAA GCACTCACGC	TCATTTAGAA CCCACTACCG AGAAAAACAC CCTAAGOGCA	480 540 600 660 720
45	AGCATTTTGT	GGCATTTCTT GAACTAGGGA AGAACCAAAG	AGCTCAGGGG	GGTTACTGGC	TTCTCTTGAG	TCACACTGCT	780 840
50	Seq ID NO: Protein Ac	138 Protei	n sequence: NP_478103.1				
55	1 MMMGSARVAE RLPVDLAEEL	11 LLLLHGAEPN GHRDVARYLR	21 CADPATIATRP ARAGGTRGSN	31 VHDAARBOFL HARIDAABGP	41 DTLVVLHRAG SDIPD	51 ARLDVRDAWG	60
60	Nucleic Ac	139 DNA sei id Accession mence: 272-	n #: NM_058	3197.1			
ου	1	11	21	31	41	51	
65	TCCTCCGAGC GGATTTGAGG GGGCTGGCTG	GGCGACTTCA ACTCGCTCAC GACAGGGTCG GTCACCAGAG CAGCGGGCGG	GOTGTGCCAC GGCGTCCCCT GAGGGGGCTC GGTGGGGGCG CGGGGAGCAG	TGCCTGGAAA TTCCGCCAGC ACCGCGTGCG CATGGAGCCG	ACCGGAGGAA CTCGGCGGCT GCGGCCGGGA	TCCCTCCAGA GAAAGAGGAG GCGGAGAGGG GCAGCATGGA	60 120 180 240 300
70	GCCGGCGGCG GGCTCGGGTA TAGTTACGGT CGGGCGACTC CCGGAAAAAG	GGGAGCAGCA GAGGAGGTGC CGGAGGCCGA TGGAGGACGA GGGAGGCTTC	TGGAGCCTTC GGGCGCTGCT TCCAGGTGGG AGTTTGCAGG CTGGGGAGTT	GGCTGACTGG GGAGGCSGGG TAGAAGGTCT GGAATTGGAA TTCAGAAGGG	CTGGCCACGG GCGCTGCCCA GCAGCGGGAG TCAGGTAGCG GTTTGTAATC	COGCGGCCCG ACGCACCGAA CAGGGGATGG CTTCGATTCT ACAGACCTCC	360 420 480 540 600
75	TCCTGGCGAC ACAGATCTCT TCATGATGAT ACTGCGCCGA TGGACACGCT	GECCTGGGGG CGAATGCTGA GGGCAGCGCC CCCCGCCACT GGTGGTGCTG CGTGGACCTG	GAAGATCTGA CGAGTGGCGG CTCACCGGAC CACCGGGCCG	CAAGGAAGAG AGGGGGGAAC AGCTGCTGCT CCCTGCACGA GGGCGCGGGT	GAATGAGGAG ATATTTGTAT GCTCCACGGC GGTGCCCGG GGACGTGCGC	TAGATGGAAG GCGGAGCCCA GAGGGCTTCC GATGCCTGGG	720 780 840 900 960
80	GOGOGGCTGC CCTCAGACAT	GGGGGGGCACC CCCCGATTGA	AGAGGCAGTA AAGAACCAGA ACAGGGCCAC	ACCATGCCCG GAGGCTCTGA	GATAGATGCC GAAACCTCGG GCCACAACCC	GOGGAAGGTC GAACTTAGAT ACCCCGCTTT	1020 1080 1140
85	TGTAAAAAAG ACTCACGCCC GCTGTCGACT	ATTTAGAAAA CACTACCGTA AAAAACACCG TAAGCGCACA TCATGACAAG ACACTGCTAG	TTCATGTGGG CATTTTGTGA	CATTCTTGC ACTAGGGAAG	GAGCCTCGCA CTCAGGGGGG	TGGAGTGAGC GCCTCCGGAA TTACTGGCTT	1260 1320 1380 1440 1500

WO 02/086443 TTCATTCATT CACTC

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Seq ID NO: 141 DNA sequence

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20		AGGGAAGGGG					180
		GTCTGCAGTT					240
						GCGCAGGTTC	300
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		GGCTCACGGG					420
25						AAGACCAGGT	480
						CCCAGCCCAA	540
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	GGACACGCTG	GTGGTGCTGC	ACCGGGCCGG	GGCGCCGCTG	GACGTGCGCG	ATGCCTGGGG	660
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30						COGAAGGTCC	780
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						ACCCCCCTTT	900
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		CACTACCGTA					1020
35		AAAAACACCG					1080
		TARGCGCACA					1140
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		ACACTGCTAG	CAAATGGCAG	AACCAAMGCT	CANATANANA	TAAAATAATT	1260
40	TTCATTCATT	CACTC					

Seq ID NO: 142 Protein sequence: Protein Accession #: NP_478102.1

40

45	1	11	21	31	41	51	
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Seq ID NO: 143 DNA sequence Nucleic Acid Accession #: NM_018131 Coding sequence: 412..1107

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60		AACTCACAGA					180
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	TCTGCTGCAA	CCTCACGAAT	TGCTGAACTT	GAAAGCAAAA	CCAATACACT	CCGTTTATCA	360
	CAGACTGTGG	CTCCAAACTG	CTTCAACTCA	TCAATAAATA	ATATTCATGA	AATGGAAATA	420
65		ATGCTCTGGA					480
		AAGGACTTTT					540
		TCCCACAGCA					600
		GTTACAACGA					660
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70	CAAAAAGAAG	TTCACAATTT	AAATCAGCTG	TTGTATTCAC	AAAGAAGGGC	AGATGTGCAA	780
	CATCTGGAAG	ATGATAGGCA	TAARACAGAG	AAGATACAAA	AACTCAGGGA	AGAGAATCAT	840
		GAAAACTTGA					900
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75		AATTGCATGT					1080
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		GARARCAGAG					1200
		CTGGTGGAAT					1260
	CGATCTGCTT	GICCATGIGG	AATACTGTTC	AAAGTAGCAA	AATAAGTATT	TCTTTTGATA	1320
80	TTAAAAGATT	CANTACTGTA	TTTTCTGTTA	CCTTGTGGGC	ATTTTGAATT	ATATATTTCA	1380
	CATTITGCAT	AAAACTGCCT	ATCTACCTTT	GACACTCCAG	CATGCTAGTG	AATCATGTAT	1440
	CTTTTAGGCT	GCTGTGCATT	TCTCTTGGCA	GTGATACCTC	CCTGACATGG	TTCATCATCA	1500
	GGCTGCAATG	ACAGAATGTG	GTGAGCAGCG	TCTACTGAGA	TACTAACATT	TTGCACTGTC	1560
	ARAATACTTG	GTGAGGAAAA	GATAGCTCAG	GTTATTGCTA	ATGGGTTAAT	GCACCAGCAA	1620
85	GCAAAATATT	TTATGTTTCG	GGGGTTTTGA	AAAATCAAAG	ATAATTAACC	AAGGATCTTA	1680
	ACTGTGTTCG	CATTTTTTAT	CCAAGCACTT	AGANANCCTA	CAATCCTAAT	TTTGATGTCC	1740
	ATTGTTAAGA	GGTGGTGATA	GATACTATTT	TTTTTTCATA	TTGTATAGCG	GTTATTAGAA	1800

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	CACACAACTC	TTTTCTTGAT TGTTCTGCGC TTTCTCTTAT	ACGARACAGT GTTATCTGGC	GCTTACCATT ATCTGTTTGA AGTAACTGTA	GGCATAATCT	CATTAGCACA	1860 1920 1980
5	TTCTGCTTAG ATTGACAGTA TTTGTTTGTC	CTARARTIGT TTITAGTTAT TGARCAGGTA TTCTARCATG	TAAAATAAAC TTTTGGCATT TTTTTATACA	TTTAATAAAC CTTAAAGCTG TGCTTTTTGT GGCTACTGTA	CCATGTAGCC GGCAATGTAA AAACCAAAAA	CTCTCATTIG TGATCAGATC CTTTTAAATT	2040 2100 2160 2220
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20	DVQHLEDDRH	KTEKIQKLRE	ENDIARGKLE	EEKKRSEELL ILKELRKARK	SQVQSLYTSL	LKQQEEQTRV	180
20				THERMAN	MINITERIA		
25	Nucleic Ac:	145 DNA sec id Accession mence: 50	a #: NM_0011	.68			
25							
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	1	1	1	CAGAGGTGGC	1		60
30	CCGCCAGATT	CCTGCCTGGC	AGCCCTTTCT	CARGGACCAC	CGCATCTCTA	CATTCAAGAA	120
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	CCACTGCCCC	ACTGAGAACG	AGCCAGACTT	GGCCCAGTGT	TTCTTCTGCT	TCAAGGAGCT	240 300
	CGCTTTCCTT	TOTOTOANGA	ACCACUCCAT	AGAGGAACAT AGAATTAACC	CTTGGTGAAT	TTTTGAAACT	360
35	GGACAGAGAA	AGAGCCAAGA	ACAAAATTGC	AAAGGAAACC	AACAATAAGA	AGAAAGAATT	420
	TGAGGAAACT	GOGAAGAAAG	TGCGCCGTGC	CATCGAGCAG GGCTGCACCA	CTGGCTGCCA	TGGATTGAGG	480 540
	GTGCCACCAG	CCTTCCTGTG	GGCCCCTTAG	CAATGTCTTA	GGAAAGGAGA	TCAACATTTT	600
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	AAGGCAGTGT	COCTTTTGCT	AGAGCTGACA	GCTTTGTTCG GCTGTCACAG	CGTGGGCAGA	GCCTTCCACA	840
	GTGAATGTGT	CTGGACCTCA	TGTTGTTGAG	GCTGTCACAG TTATCTGTCA	TOCTGAGTGT	GGACTTGGCA	900
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	GTGATGAGAG	ANTOGRGRGRGR	CACTOCOTOC	CTCCTCTACT	GTTTBACBAC	ATGGCTTTCT	1080
	TATTTTTTTT	GAATTGTTAA	TTCACAGAAT	AGCACAAACT GAACTTCAGG	ACAATTAAAA	CTAAGCACAA	1140
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50	AGTGAGCCGC	GGGGCACATG	CTGGCCGCTC	CTCCCTCAGA	AAAAGGCAGT	GGCCTAAATC	1320
	TCTGTCAGCC	CARCUTTORC	ATCTGTCACG	GGGACTGGCT	GGGGGGAGAGA	OGCAGTCOGC	1440
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	Procein Acc	ession #: 1	NP_001159				
60							
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65	FKELEGWEPD	VRRAI BQLAA	SSGCAPLSVK ND	KQFEELTLGE	PLKLDRERAK	NKIAKBINNK	120
0.5							
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	Coding sem	lence: 127-	720	176.1			
70						51 .	
	1	11	21 	31 	41	1 .	
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80	AGACCATCCC	TCAACATCGC	AACTGTGTTG	ACCTCTATTC	AGCTGCTCAT	GTCAGAACCC	480
	AACCCTGATG	ACCCGCTCAT	GGCTGACATA	TOCTCAGAAT	TTAAATATAA	TAMGCCAGCC	540
	GAGGAAGAGA	TGCTTGATA	TCTACCACAG	AAGCATGCAA GCTGGTGACT	CCAGAGTACA	CAACTCAACA	600 660
0.5	CAGAAAAGGA	AGGCCAGTCA	GCTAGTAGGC	ATAGAAAAGA	AATTTCATCC	TGATGTTTAG	720
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	GTACATATGT	ATTTTGAAAT	CTTTTAAACC	TGAAAAATAA	ATAGTCATTT	AATGTTGAAA	900

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-	Prot	ein	Acc	essi	on	#:	NP.	_054895.

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	YPFEPPQIRF						120
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Seq ID NO: 149 DNA sequence Nucleic Acid Accession #: NM_003812 Coding sequence: 224-2722 15

13	Coding sequ	ience: 224-2	2722				
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			AGAAGCATCG				1200
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Seq ID NO: 150 Protein sequence:

	Protein Accession #: NP_003803								
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WO 02/086443
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25
            CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC
                                                                                                                                           900
            COTTOGOGO TEANTGOOR ATCAGORANT ACCTARTAN ANGACTEST STITUTIONS 500 ANGACTANT STITUTIONS TO ANGACTANT ACCTARTAN ANGACTANT STITUTIONS ANGACTANT ACCTARTAN ANGACTANT ACCTARTAN ANGACTAN ACCTARTAN COMMITTED ANGACTAN ANGACTANT ACCTARTAN COMMITTED ACCTARTANCE ACCTARTANT ACCTART
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            Protein Accession #: NP 076404
40
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COCOTACTCC TETTICTAMAT AMGCTOTATC TOTAMICACA GOSTICOTA AGTICTICAG
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WO 02/086443 THTRACARS TROCCAGGS TOSTITIONAL CTCCTGACCT CAASTGACCC ACCTTGGCCT CCCAAGGTTT TOSGATTACA ASTGTGGGCC ACCGGGGCCA GCCTATGATC CATTTTGAT GAATTYTTTA TATOGTGCAA GGTGTCAATC CACCITCACT TITTCTTGGG AATATAGATA TOCAGCIGIT TOACTACCAT TTTTTGAAAG GACTGCCCTT TGCTCTATCA CCTTTGCATT TITGITARAA AGTAGITGIC RAIGIATAIG IGGGITTAIT ICAGGACICI GITTIGITCC ATTGACTGT TITTCTCTC TOMATGCCA TACCATATIT GTATGTAGTG TATGTATTT TCTAATAATT CTTGAAACAG ATAGTATTAA TGTGTCATAT TITTGCTGTT GTTTGTATIT TITGTAGAGA TGGGGTTTCA CCGTGTTGGC CAGGCTGTGT TGAACTCCTG AGCTAAAGCA ATACACTIGC CICGUCCUCC CCATGIGCIG GGATTACAGG CGTGAGCCIT GGTGCTGGCC ARACATRIC CTGFFCTCC CONTRIGUES GANTACHG GRUNGCCT GRECHESC CARGERICAC ANTICITYT GRANITIST THOSGINEN THANGCCT ROTTIFGAT GRUNANTHE GRANCAGGA GGREGERIG GCTTARGCCT GRANICCHE AACTTIGGAS GCCTMARTG GGRGGATCAC TYGAGCTCG GRANITIC CACAGTTACA CGGCAGGCTG AGGTGGGAGG ATCACTTGAA CCCCAGAGGT CAAGACTGCA CACASTRACA GREGARGITA REGITAGRADA RICALTRAGA GOCCARRAGA CARACTERA GREGARGITAGA ATCARCACACA CUTACTOCAGO COTEGGIGAGO, ANAGRAGACA CITATTCTCA ANAGARATTA GGATCARATT GTCAATTTCT ACARCAACAA CAACARARAC COCTOTIGUS CACOCTIGATO CACOCTIGATO ATCARCTATATA TARAACTOTIA CAGGRARITO ACACTIGAT ATCARCACAGO TOTOCTICO TARGITATIA TOTOTICO TARGITATIA TOTOTICO TARGITATIA TOTATTICTO TTAATAATCT TITGTAGTIT TOAGTGTACA GOTOTACCAT GTOAGCATIT CATAGITITG AUGCTAAATG GUATITITAAA ATTICAAATT CUAACCACIT GIIGCIAGUA ARTAGAATA CANTIGATOT TGAACTITGTA TCCTTCAGCC TTGCTAAACT GTGAGTTCTC ATGGTGTTTT TGTAAATTAC ATCAACAGTC ATGTGTTCTA TGAATAAAGA GTTTTACTCC Seq ID NO: 154 Protein sequence: Protein Accession #: BAA11503.1 MFCEXAMELI RELHRAPEGO LPAPHEDGIR QVLEENKALY EQNQSDVNEA KSOGRSDLIP TIKFHRUSLL RURRCTVAYL YDRILBIRDAL RWBYGSVLEM ALKRHMAABE MENEMYKEKS LATYMESIGE DESIDLITOM REPHSLIPEN VICLOSVEREF VDOGTSVLLK XNSQHELPRW KCEOLIROGV LEHILS Seq ID NO: 155 DNA sequence Nucleic Acid Accession #: Eos sequence

Coding sequence: 149-709

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WO 02/086443 TOTGGTGGTG CATGCCTGTA GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGATCACTTG 2880
AACCCCAGAG GTCAAGACTG CAGTGAGGTG AGATCACACC ACTGTACTCC AGCCTGGGTG 2940 ACAAAGTGAG ACTCTATCTC AAAAAGAAAT TAGGATCAAT TIGTCAATTI CTAGAACAAC AACAACAAA ACCCCTGTTG GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAAACTG 3060 TIGGGAGART TGACATCITA ATAATATIGA GTCTTCTGGC CTATAAACAA GGTCTGTCTT 3120 CCTAGGTATT AATGTTTTGT CTTCTATFIC TCTTAATAAT CTTTTGTAGT TTTCAGTGTA 3180 CAGGTCTACC ATGTCAGCAT TTCATAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAAA 3240 TTCTMACCAC TTGTTGCTAG TARATAGARA TACARTGAT GTTGAACTTG TATCCTTCMG CCTTGCTRARA CTGTGAGTTC TCATGGTGTT TTTGTMARTT ACATCRACAG TCATGTGTTC 3360 10 TATGASTAAA GAGTTTTACT CCTTC Seq ID NO: 156 Protein sequence: Protein Accession #: Eos sequence 15 21 31 41 51 MFCEKAMELI RELHRAPEGO LPAPHEDGLE OVLEEMKALY EQNOSOVNEA KSGGRSDLIP TIKFRHOSLL HNRROTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFMNYKRS LATYMRSLGG DEGLDITODM KPPKSLYIEA GCSGAISAOP ATSTSQVHLN CNLHLPGPVS 20 Seg ID NO: 157 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 148-621 25 31 TTCGGCGCCA AAGCGCGGAG CGGAGGCCGA GGCGAGAGCC TGGCGCTGTA GGACTAGAAC GAAAGGAGTG AGGCGCCGAG AGCCCAGATA CCATTTTGGC GTGAGAGCTG GTGGTTGGCA 120 30 AGGCCGCGGG AGTGGGAAGC GTCCGCCATG TTCTGCGAAA AAGCCATGGA ACTGATCCGC 180 GAGCTGCATC GCGCGCCCGA AGGGCAACTG CCTGCCTTCA ACGAGGATGG ACTCAGACAA 240 GTTCTGGAGG AGATGAAAGC TTTGTATGAA CAAAACCAGT CTGATGTGAA TGAAGCAAAG 300 TCAGGTGGAC GAAGTGATTT GATACCAACT ATCAAATTTC GACACTGTTC TCTGTTAAGA AATCGACGCT GCACTGTAGC ATACCTGTAT GACCGCTTGC TTCGGATCAG AGCACTCAGA 35 TGGGAATATG GTAGCGTCTT GCCAAATGCA TTACGATTTC ACATGGCTGC TGAAGAAGTC 480 COGTOTCTAA AAGACTATGG AGAATTTGAA GTTGATGATG GCACTTCAGT CCTATTAAAA 540 ANAANTAGOO AGCACTITIT ACCTOGATOG AAATGTGAGO AGCTGATOAG ACAAGGAGTC CTGGAGCACA TCCTGTCATG ACCATGCGCC GAGGCACTTC CAGGCTTCAC TCAACTCATG 600 CHEGAGRACA TOCHTCARTS ACCARGACT COCTECACT COCTCTTGA TITHAGAAGG
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GCAGTCCCC CACCTINGCT TCTCAAAGTG TGTGAACTCCA GGGGTGAGC CACTGCACCC 840 900 OCCCCCTACT CCTTTTCTA ATANGCTGTA TCTGTAATCA CAGCATTCCT ACAGTTGTTA 1020 45 CASTSTSTTT TTTRAATGAA ASTAAACATS STTACATTTS AATCTCTTAA ATAASCASTC 1080 ACTTGGCTGG ACAGGAAGAA GGTAGATCCT GTGTGTCTTG TTTTCTGGTC ATGTGTATTG 1140 TACANGCTAG AGAGCTGAAT TICTGAGATA CACATTITCA AATCACATGC AAGTGAAGAT 1200 GATGGTCTGT AGAAATTTTC AGTATATATA ATGTTTAATG ACATACTAAT TTATCATCTG GCTATTTGGG AAGGAAGGAC ACACATGGAT TTTGCACATT TCCACCATGG TGGCTGGTGT 1320 50 GGCTTGTGGC TATGGGGTGA TCACCAGTAT CACCACTITG GAAGGGGACA GTGAAATTGG 1380 GOCCHARDAS GARACTICS ACCASIONS CACCASIONS CA 1440 1500 1560 1620 55 1680 TTGTTTTGMG ATGGAGTCTT GTTCTGTCAC CCAGGCTGGG GTGCAGTGGC GTGATCTTGG CTCACTGCAA TCTCTATCCC CTGGGTTCAA GTGATTCTCT TGTCTCAGCC TCCCAAGTAG 1740 1800 CTGGGATTAC AGGCACAGGC CGCCACGCCT GGCTAATTTT TGTATTTTTA GTAGAGACAG AGTITTACCA TGITGGCCAG GCTGGTTTCA AACTCCTGAC CTCAAGTGAC CCACCTTGGC 1920 60 TTTGGGATTA CAAGTGTGGG CCACCGCGGC CAGCCTATGA TCCATTTTGA 1980 ATGANTITIT TATATGGTGC AAGGTGTCAA TCCACCITCA CTTTTTCTTG GGAATATAGA 2040 PROPERTY PROPERTY OF AUTHORITIES A SEASON OF THE COURT CACCETTEES 2100 TITTINTIA AAAGTAGIIG TCAATGIATA TGIGGGIITA TITCAGGACI CIGITIIGII 2160 CCATTGACCT GITTITCTCT CCTGAATGCC AATACCATAT TIGTATGTAG TGTATGTAAT 2220 65 TTTCTAATAA TTCTTGAAAC AGATAGTATT AATGTGTCAT ATTTTTGCTG TIGTTTGTAT 2280 TITTEGTAGA GATGGGTTT CACCOTGTTG GCCAGGCTGT GTTGAACTC TGAGCTAAAG CAATAACACTT GCCTGGTCCT CCCCATGTGC TGGGATTACA GGCGTGAGCC TTGGTGCTCTC CCCATGTCAC ACACTTCTT TTTGAGATTT GTTTTGGCTA TGTTAAGTC TTTGCTTTG 2340 2400 ATGTGAAATT TGGGAACAGG CAGGGTGTGG TGGCTTATGC CTGTAATCCT AGAACTTTGG 2520 70 GAGGCCTAGA TEGGTGEATC ACTTGAGCTC AGGAGTTCCA GACCAGCCCG GGCCTATGGC 2580 ARARCTCCST CTCTACARAR ARTAGRARAR ATTROCCASG TOTGGTGGTG CATGCCTGTA GTCACASTTA CASCAGGGC TERROTEGES GRATICACTIS ARCCCASEG GTCARACTCA CAGTERGCTG ACRICACACC ACTERACTCC ASCCTUGGTG ACMANGTERS ATTCTATCTC 2640 2700 2760 ANAMAGAMIT TAGGATCAAT TIGTCAATIT CTACAACAAC AACAACAAA ACCCCTGTTG GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAAACTG TTGGGAGAAT TGACATCTTA 2880 ATAATATIGA GTCTTCTGGC CTATAAACAA GGTCTGTCTT CCTAGGTATT AATGTTTTGT 2940 CUTCULATURE TETRATARY CUTTUREST THEASTSTA CASSICTACE ATSTCASCAT 3000 TTCATAGTIT TGATGCIAAA TGGIATTITA AAATTICAAA TTCTAACCAC TIGTTGCTAG
TAAATAGAAA TACAATTGAT GTTGAACTIG TATCCTTCAG CCTTGCTAAA CTGTGAGTIC 3060 80 TCATGGTGTT TTTGTAAATT ACATCAACAG TCATGTGTTC TATGAATAAA GAGTTTTACT 3180 Sec ID NO: 158 Protein segmence: Protein Accession #: Eos sequence 85 61

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5	Seq ID NO: Nucleic Ac:	159 DNA ser id Accession sence: 149-2	quence n #: Bos se				
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20		160 Protein					
25		11 AAAAAGCCAT TCAACAATTA		31 CGCGAGCTGC	41 ATCGCGCGCCC	51 CGAAGOGCAA	60
30	Nucleic Ac:	161 DNA sed id Accession sence: 1333-	n #: U10694				
35	ACAGGGAGGC AGGAACCTAA	11 GGATCTCAGG CCTGTGTTCG GGGAGGATCG	ACAGACACAG AGGGTACCTC	TGGTCCCAGG	ATTGGAGAGC	AGTCCAGGTG ATCAAGAGAG	60 120 180
40	CACGTCAGCA CCCACTCAGC	COCTACTGTC GGGATCACTG GAGGGAGGGT AAACACAGAG GATGGACTCC	GTGTCGGGGA CCCAGGCCCT GACCTAGCCC	GGGCTGGCCT GCCAGGAGTC CACCCTGCCC	TGGTCTGAGG CAGGTGCAGA CTTGTGTCAG	CTGAGGGAC CTGAGGGAAG	240 300 360 420 480
45	AGGTCAACAG CTCACCCCAG AACCCTGGGC ATGTGAGCTC CAGGAGAAAG	AGGAGGGTT GACACATGGA AGGTGTGGGC CTGATCTGAG GTCAGGGCCC AGTGTCCAGC	CCAGACCCTG CCCCATTGAA AGATGTTGGT AGACTCTCAG TGAGTGAGCG	CAGGCATCAA TTTAGACATC TGGGGCATGT GCAAGTAGAG CAGAGGGGAC	GATGAGGACC TCTTACTGTA CCTTCTGTTC GAGTAGAGTC CATCCACCCC	AGGCAGTATC CTTCCGAGGA CATATCAGGG CAGTCCCTGC AAAAGTGTGT	540 600 660 720 780 840
50	CAGTCTGCAG CTTGGTCTGA TGAAGGTGAA	CCTAAGGGCC GACAGTGTCC GTGTTCACCC GCACCTGGCC	CCTCGATTCC TCAGGTCGCA TGAATGTGCA	TCTTCCAGGA GAGCAGAGGA CCAAGGGCCC	GCTCCAGGAA GACCCAGGCA CACCTGCCCC	GCAGGCAGGC GTGTCAGCAG AGCACACATG	900 960 1020 1080
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60	GAGACTACCT CCTCCCCAGA AGCCAATTCG CCAGCTCAGC	CCTCCTCTGA GTCCTCAGGG ATGAGGGCTC TGGAGTTCAT	CAGCAAGGAG AGGCGCTTCC CAGCAGTCAA GTTCCAAGAA	GAGGAGGTGT TCCTCCATTT GAAGAGGAAG GCACTGAAAT	CTGCTGCTGG CCGTCTACTA AGCCAAGCTC TGAAGGTGGC	GTCATCAAGT CACTTTATGG CTCGGTCGAC TGAGTTGGTT	1500 1560 1620 1680
65	AGGGTCATCA ATGCAGGTGA CTTGTCACTG AAGGCCGCCC	TOCACAAATA AAAATTACAA TOTTTGGCAC CICTTGGCCT TOCTGATCAT	GCGCTACTTT TGATGTGAAG CTCGTGCGAT TGTCCTGGGT	GAGGTGGACC AGCATGCTGG GTGATCCTAA	TCGGCAAAGC CCGCCGGCCA GTGATGGTCA CCAAAGACAA	CTCCGAGTTC CTCCTACATC TAGCATGCCC CTGCGCCCCT	1740 1800 1860 1920 1980
70	GAAGAGGTTA TTCTACGGGG TACCGGCAGG CACGCTGAAA CCCATCTGCT	TCTGGGAAGC AGCCCAGGAA TGCCCGGCAG CCAGCTATGA ACCCATCCCT	GTTGAGTGTG GCTGCTCACC TGATCCTGCG GAAGGTCATA TTATGAAGAG	ATGGGGGTGT CAAGATTGGG CACTACGAGT AATTATTTGG GTTTTGGGAG	ATGTTGGGAA TGCAGGAAAA TCCTGTGGGG TCATGCTCAA AGGAGCAAGA	GGAGCACATG CTACCTGGAG TTCCAAGGCC TGCAAGAGAG GGGAGTCTGA	2040 2100 2160 2220 2280 2340
75	GCCCCATGTG	CAGCCGGGGC ACATGAGGCC	CATTCTTCGC	TCTGTGTTTG	AAGAGAGCAA	TCAGTGTTCT	2400

CAGREGORET GOGREGARET GACCACACIG TRITUTCATCT CROGGITCCT IGICITATING 2460 GIGATITUGA GATITATCCT INCICCUTT INGAATIGIT CARACTICT ITTATING 2520 AGGITTATION GARTTANCO T GCAGGITANT GANTGACAGT AGGICACAT ATGCGGTT 2560 ATGTTATTTA GGAGTAGGAT TCTGGCTTT GAGTCACATG GGGAAATCCC TGTTATTTTG 2640 TGAATTGGGA CAAGATAACA TAGCAGAGGA ATTAATAATT TFTTTGAAAC TTGAACTTAG 2700

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Seq ID NO: 162 Protein sequence: Protein Accession #: AAA68877.1

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10	PSLYEEVLGE	EQEGV					
10	Nucleic Ac:	163 DNA sec id Accession lence: 30-86	#: AF29210	0			
15	1	11	21	31	41	51	
	Ī	Ī	Ī	1	1	1	60
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	TCGTGAGAAA	GAATATATCT	ACAAATTGCA	CGAAAGTATC	ATARARACAG	TACTCTAGAG	4800

WO 02/086443 CAGCGCTGTC CANTAGAAAT ATAATCTGAG CCACATGTAT AATTTTATTT TCTTCTAGCC 4860 CARACTARAGA AGTARARAGA TACRAGTAGA ACTARITITA ATGITTARI TCAGTATATC CARACTACA TITGACATG TARTRATAT ARAKTERIA ATGIGETAT TRACATICIT 4920 4900 TTGGTAATAC TAGTCTTCAA AATCTGGTAT GTATCTTACA TTGATAGCAC ATCTCACTIT GTACTAGCCA CATTGCAAGT GCTCAGTAGC CACATGTGGC TAGTCGCTAC TGCACTGGAC 5040 5100 AGCACAGTTC TAGGTTCCAC CCTAACACCC AAGTCCTGTG GATTAGAATC CCAGAATCAG 5160 AGCTGGAAGT AAACATAGAG ATCAAACCTC CTTTTAAAAA TGAGGACGCT GAGGCACAGA GTTTAAATGG CTTGCATGAG GTCATACAGC TAAATTCAGC CTCAACAGGG TCTTCTGATT 5280 CCAGGCACTC TTCCCACTCC ACTACATTAC TGTAGTGGTA ATTCTTAGGG TTAAAAAAAA 5340 10 TGTAGAGTAG GCCGGGCCCA GTGGCTCATG CCTGTAATCC CAGCACTTTG GGAGGCCGAA GTGGGCGGAT CACGAGGTCA GGAGATCGAG ACCATCCTGG CCAACATGGT GAAACCCCGT 5400 5460 CTCTACTGAA AATACAAAGC AAAATTAGCC AGGTGTGGTG GCGGGCGCCT GTGGTCCCAG CTGCTCTGGA GGCTGAGGCA GANTGGCGTG AACCCAGGAG GCAGAGATGG CAGTGAGCC 5580 5640 15 AAAAAAAAA AAGAAAGAA AAGAAAAGTC TAGAGAACAT TATATTAAGT GGTTATTATT 5700 GAAGTAGACC AAAGTTTATA CCATRAGGAT ATTTTTCCTT AAATACCATG TTTGAAGAAC AATTATTTAT TGATCCTTGA ATCTGTAAGA TCAAATAACA AGTCTCTATC CATGTTACCA 5760 ANTITRACT TITGAAATA ATAAACITTA AAATATCAGA TETETIATTA CAGGATGATA CITGGAATCA AGTGAAATA ATAAACITTA AAATATCAGA TETETIATTA CAGGATGATA CITGGAATCA AGTGAAATGA GITATATGGI CATCACTAAA TITAGAAATC TATTGTGAAA 5000 5940 20 CAAAGACAAA CAGGAAAGTA CAGAATAGAG ACTITTAGTA AATAAATGGA ATTTAAAAGA 6000 ANGISTITAT TRACACTOTC ACGACAGANA AGGATGTCTT TOTTOTCATA GTCTTTGAGG GATCTCCGTA ALATCTGGGG CALGGTACA AGAATAGCC ATATTTTTGT TCCAGACCA TGTTTAGTA ALATCTGGGT CALGGTACA GTGCAAGAGG TATCTCCCCC TCAGGTGGT 6060 CATCACTGAG CCCTGGAATT GGAGACTCAT ACTTGCCCAG CACAATGTTA CGGGCAGACA 6240 25 OSCCGACATC TATGATTAGC TAGARACCAT AARGARAAGC TECTARATEG CCACTAGGTG 6300
CCACTTITCT GITTTIGTAA TECTTICATT AGCAGATCTT TITTTTCCAA GCICCATGGG 6360 OCCUPATION OF THE PROPERTY OF TOTTTTATGA GARATGOTTT CCAAGGGAGG TOTAGGAAGA TOCIGACACA TAAGAACTTT 6480 GGCTTAGAGA GCTTTCCAGG TGTAGTGCCA ATAAAAACTG ACCTGGAAAG AAAACCTGCC 6540 CAGCACGGAA CATGCTTTCT GAACTCACTT GAGAGTGTAT GGTGTATGTC ACTTCTCATA 30 6600 TATTCTTGAG TTTAGATTTG TCTTTTATAC AATTTTTAGC TCTTTTCCAG TTCACTTGTG
CTCGTCTGTA TATTGGTATT TTTAAATTTT TGTGGTAAAT AATGAAAGA GTGAAATTAT 6660 AUTTIATANT TACTCATTTG TAGTTTITTT TITTAATTTA ATAAACTTCC TCCAAAAAGT OCTOCOTTAN AN 35 Seq ID NO: 166 Protein sequence:

Seq ID NO: 166 Protein sequence Protein Accession #: AAG34652

40 41 MAARREAAAG GKULREENOC IAPVVSSRVS PGTRPTAMGS FSSHWTEFPR KRKGSDSDPS 120 OVEDGENOVK MKAFREAHSO TEKRRRDKNN NLIEELSAMI POCNPMARKL DKLTVLRMAV CHLRSLKGLT NSYVGSNYRP SFLQDNBLRH LILKTANGFL FVVGCERGKI LFVSKSVSKI 100 LNYDQASLTG QSLFDFLHPK DVAKVKEQLS SFDISPREKL IDAKTGLQVH SNLHAGRTRV 240 YSGSRRSFFC RIKSCKISVK BEHGCLPNSK KKEHRKFYTI HCTGYLRSWP PNIVGMEEER 300 ISUSPRISHE CLUAIGRUP YIVPONSGEI NVKPTEFITR FAVNGREVYV DORACALISY
LPORLLGTSC YEVFHODDEN NLITEKHKAUL QSKEKILIDS YKFRAEDGSF VILKSQMFSF 420 INPWIKELEY IVSUNTLVLG HSEPGEASFL PCSSQSSEES SRQSCMSVPG MSTGTVLGAG 480 50 SIGTDIANEI LDLQRLQSSS YLDDSSPTGL MKDTHTVNCR SMSNKELFFP SPSEMGELEA TRONGSTVAV HSHEPLLSDG AQLDFDALCD NDDTAMAAFM NYLEAEGGLG DPGDFSDIQW 540 600

55 Seq ID NO: 167 DNA sequence
Mucleic Acid Accession #: NM_014400
Coding sequence: 86-1126

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60	COTTACTCAT	CCTGGGCTCA	GGTAAGAGGG	CCCGAGCTCG	GAGGCGGCAC	ACCCAGGGGG	60
	GACGCCAAGG	GAGCAGGACG	GAGCCATGGA	CCCCGCCAGG	AAAGCAGGTG	CCCAGGCCAT	120
	GATCTGGACT	GCAGGCTGGC	TGCTGCTGCT	GCTGCTTCGC	GGAGGAGCGC	AGGCCCTGGA	180
	GTGCTACAGC	TGCGTGCAGA	AAGCAGATGA	CGGATGCTCC	CCGAACAAGA	TGAAGACAGT	240
	GAAGTGCGCG	COGGGCGTGG	ACGTCTGCAC	CGAGGCCCTG	GGGGCGGTGG	AGACCATCCA	300
65		TOGCTGGCAG					360
		CTTCACGGGC					420
	CTGCAACGCC	ANGCTCAACC	TCACCTCGCG	GGCGCTCGAC	CCGGCAGGTA	ATGAGAGTGC	480
		AACGGCGTGG					540
	GGGTACATCG	CCGCCGGTCG	TGAGCTGCTA	CAACGCCAGC	GATCATGTCT	ACAAGGGCTG	600
70		AACGTCACCT					660
		GATGAATTCT					720
		TGCCAGGGGT					780
		CCACCCCTTG					840
	CACATCTGTC	ACCACTTCTA	CCTCGGCCCC	AGTGAGACCC	ACATCCACCA	CCAAACCCAT	900
75		ACCAGTCAGA					960
		TTGACTGGAG					1020
		GGGGGGCCCC					1080
		CITCIGITGG					1140
~ ~		CTCACCTACT					1200
80		GACTGGGCTG					1260
		GCTGGTTTGC					1320
	GGGTGTTCTA	GCTTTTTGAG	GACAGCTCCT	GTATCCTTCT	CATCCTTGTC	TCTCCGCTTG	1380
		ATGTTAGGAC					1440
0.5		GCTTCCTACT					1500
85		TGGCTCCCCA					1560
	ATCGGTTCCC	CATATGTCTT	CCTTACTAGA	CTGTGAGCTC	CTCGAGGGCA	GGGACCGTGC	1620
	CTTATGTCTG	TGTGTGATCA	GTTTCTGGCA	CATAAATGCC	TCAATAAAGA	TTTAATTACT	1680

WO 02/086443 TIGTATAGIG AAAAAAA

Seq ID NO: 168 Protein sequence: Protein Accession #: NP 055215

	1	11	21	31	41	51	
	1	1	1	1		1	
		AMINTAGNLL					60
		IHGQFSLAVX					120
10	SRALDPAGNE	SAYPPNGVEC	YSCUGLSREA	COGTSPPVVS	CYNASDHVYK	GCFDGNVTLT	180
	AANVTVSLPV	RGCVODEFCT	RDGVTGPGFT	LSGSCCQGSR	CNSDLRNKTY	FSPRIPPLVR	240
	LPPPEPTTVA	STISVITSIS	APVRPTSTTK	PMPAPTSQTP	ROGVEHEASR	DEEPRLTGGA	300
	AGHODRSNSG	OYPAKGGPQQ	PHNKGCVAPT	AGLAALLLAV	AAGVLL		

Seq ID NO: 169 DNA sequence Nucleic Acid Accession #: NM_006875

	Coding sequ	ence: 186-:	1190				
					41	51	
20	1	11	21	31	11	21	
20	CE STOCOGOS	CONGCO CO	GOGAATCTCA	*OGCTGCGCC	GTCTGCGGGC	GCTTYYYGGGC	60
			ACCCTGGCGC				120
	cccaaccate	CACGCCCTTCC	GGGCTTAGCG	GGTTCMGTGG	GCTCAATCTG	CGCAGCGCCA	180
	CCTCCATGTT	CACCAAGCCT	CTACAGGGGC	CTCCCGCGCGCC	CCCCGGGACC	CCCACGCCGC	240
25	CCCCAGGAGG	CAAGGATCGG	GAAGCGTTCG	AGGCCGAGTA	TOGACTOGGC	CCCCTCCTGG	300
	GTANGGGGGG	CTTTGGCACC	GTCTTCGCAG	GACACCGCCT	CACAGATOGA	CTCCAGGTGG	360
	CCATCAAAGT	GATTCCCCGG	AATCGTGTGC	TGGGCTGGTC	COCCTTGTCA	GACTCAGTCA	420
	CATGCCCACT	CGAAGTCGCA	CTGCTATGGA	AAGTGGGTGC	AGGTGGTGGG	CACCCTGGCG	480
• •			TTTGAGACAC				540
30	CTTTGCCCGC	CCAGGATCTC	TTTGACTATA	TCACAGAGAA	GGGCCCACTG	GGTGAAGGCC	600
			CAAGTAGTGG				660
	TTGTCCATCG	TGACATCAAG	GATGAGAACA	TCCTGATAGA	CCTACCCCCT	GGCTGTGCCA	720
	AACTCATTGA	TTTTGGTTCT	GGTGCCCTGC	TTCATGATGA	ACCCTACACT	GACTTIGATG	780
25	GGACAAGGGT	GTACAGCCCC	CCAGAGTGGA	TCTCTCGACA	CCAGTACCAT	GCACTCCCGG	840
35	CCACTGTCTG	GTCACTGGGC	ATCCTCCTCT	ATGACATGGT	GTGTGGGGAC	ATTCCCTTTG	900
			GAAGCTGAGC				960
	GCTGTGCCCT	AATCCGCCGG	TGCCTGGCCC	CCAAACCTTC	TTCCCGACCC	TCACTGGAAG	1020
			ATGCAAACAC				1140
40	AAAGGAGGCC	CTGCCCCTTT	GGCCTGGTCC AGCCATCCCA	TTGCTACCCT	AAGCCTGGCC	TGGCCTGGCC	1200
40	TGGCCCCCAA	TGGTCAGAAG	CATTACCAGT	TGGCCATGTC	ACAGGGATAG	ATGGMUATIT	1260
	GTTGACTTGG	TTTTACAGGT	AGACATAAAC	CATTANAGIC	CAGTATIACI	AND THACOS	1320
	ATTGAGGATC	AGGGGTTAGA	AACCTGTGGT	CANGILIGOC	CAGTICCCTT	CCCONTCCIA	1380
	CAAAGGAGCC	TTCCTCCCAG	TATTTTGGTG	CCCIGATTI	CATTOTORIC	COCCCCCCCC	1440
45			CCCACATTGG				1500
73			AAGGGTGCTT				1560
	BOTABBOOGS	CCCTTTCCCC	TAGCCTAGGG	TOCCATATES	GGTCAAGCTG	CTTACCTGCC	1620
			TTGGGGGAGG				1680
	TOTOCCOMO	TTTTTTTTTG	GGTGAGGGGA	CCCTACTTTG	TTATCCCAAG	TGCTCTTATT	1740
50	CTGGTGAGAA	GAACCTTAAT	TCCATAATTT	GGGAAGGAAT	GGAAGATGGA	CACCACCGGA	1800
	CACCACCAGA	CANTAGGATG	GGATGGATGG	TTTTTTGGGG	GATGGGCTAG	GGGAAATAAG	1860
	GCTTGCTGTT	TGTTTTCCTG	GGGCGCTCCC	TCCAATTTIG	CAGATTTTTG	CAACCTCCTC	1920
	CTGAGCCGGG	ATTGTCCAAT	TACTAAAATG	TAAATAATCA	CGTATTGTGG	GGAGGGGAGT	1980
	TCCAAGTGTG	CCCTCCTTTT	TTTTCCTGCC	TGGATTATTT	AAAAAGCCAT	GTGTGGAAAC	2040
55	CCACTATTTA	ATAAAAGTAA	TAGAATCAGA	аллааллаал	AAAAAAA		

Seq ID NO: 170 Protein sequence: Protein Accession #: NP_006866

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70 Seq ID NO: 171 DNA sequence Nucleic Acid Accession #: NM_003646 Coding sequence: 89..2875

75	1	11	21	31 l	41	51	
	GCGGCGCGGA	GCGGGCGTGC	TGAGCCCCGG	CCGCCGGCCC	GGCATGGGCG	TCTCCCGCGG	60
			AGGGCCGGAT				120
	GAGCAGCGAC	TOCGAGTOGG	CTTCCGCCTC	GTCCAGCGGC	TCCGAGCGCG	ACGCCGGTCC	180
	CGAGCCGGAC	AAGGCGCCGC	GGCGACTCAA	CAAGCGGCGC	TTCCCGGGGC	TGCGGCTCTT	240
80			CCAAGTCGGG				300
			AGTCAGAGCG				360
			ACATCTGGTT				420
	CGTTGGGGAG	CAGTACTGTG	TAGCCAGGAT	GCTGAAGTCA	GTGTCTCGAA	GAAAGTGCGC	480
0.5	AGCCTGCAAG	ATTGTGGTGC	ACACGCCCTG	CATCGAGCAG	CTGGAGAAGA	TANATTTCCC	540
85			AATCAGGCTC				600
			GACGCCAGGA				660
	CCAGCAGAAG	TTCACCTTCC	ACAGCAAGGA	GATTGTGGCC	ATCAGCTGCT	CGTGGTGCAA	720

	WO 02/	/096443					
	GCAGGCATAC	CACAGCAAGG CACGCAGCCG	TGTCCTGCTT	CATGCTGCAG	CAGATCGAGG	AGCOGTGCTC	780
	GCTGGGGGTC	CACGCAGCCG	TGGTCATCCC	GCCCACCTGG	ATCCTCCGCG	CCCGGAGGCC	840
	CCAGAATACT	CTGAAAGCAA CCTGAGGAGG	GCANGANGAA	GAAGAGGGCA	TCCTTCAAGA	GGAAGTCCAG	900 960
5	GCTCATGAAG	CCCCTGCTGG	TGTTTGTGAA	CCCCAAGAGT	GGGGGCAACC	AGGGTGCAAA	1020
	GATCATCCAG	TCTTTCCTCT	GGTATCTCAA	TCCCCGACAA	GTCTTCGACC	TGAGCCAGGG	1080
	AGGGCCCAAG	GAGGCGCTGG	AGATGTACCG	CAAAGTGCAC	AACCTGCGGA	TCCTGGCGTG	1200
	CGGGGGGGGAC	GGCACOGTGG GTTGCCATCC	GCTGGATCCT	TACTIGGCAAC	GACCAGCTAC	GAACCCTCAA	1260
10	CTGGGGTGGG	OGCTACACAG	ATGAGCCTGT	GTCCAAGATC	CTCTCCCACG	TGGAGGAGGG	1320
	GAACGTGGTA	CAGCTGGACC	GCTGGGACCT	CCACGCTGAG	CCCAACCCCC	AGGCAGGGCC	1380
	TGAGGACCGA	GATGAAGGCG	CCACCGACCG	GTTGCCCCTG	GATGTCTTCA	ACAACTACTT	1500
	AGAGAAATTC	TTTGACGCCC AACAGCCGCT	TTOOGAATAA	GATGTTCTAC	GCCGGGACAG	CTTTCTCTGA	1560
15	CTTCCTGATG	GGCAGCTCCA	AGGACCTGGC	CAAGCACATC	CGAGTGGTGT	GTGATGGAAT	1620
	GGACTTGACT	CCCAAGATCC	AGGACCTGAA	ACCCCAGTGT	GTTGTTTTCC	TGAACATCCC	1680
	CAGGTACTGT	GCGGGCACCA	TGCCCTGGGG	CCACCCTGGG	GAGCACCACG	ACTTTGAGCC	1740 1800
	CONGCIGGAT	GACGACGCT GGCGGACACG	GCGAGCGCCT	CATTGGCTTC	CCCATGACGT	TROTOGCCGC	1860
20	ATCCAAGGCC	ATCCCGGTGC	AGGTGGATGG	CCACCCCTCC	AAGCTTGCAG	CCTCACGCAT	1920
	CCGCATCGCC	CTGCGCAACC	AGGCCACCAT	GGTGCAGAAG	GCCAAGCGGC	GGAGCGCCGC	1980
	CCCCCTGCAC	AGCGACCAGC	AGCCGGTGCC	AGAGCAGTTG	CGCATCCAGG	TGAGTCGCGT	2040
	CAGCATGCAC	GACTATGAGG	TOTOTOGRADA	CRACAAGGAG	CAGCTCAAGG	GTGCCCTGT	2100
25	TGAGAGACTC	ACTGTGGTGG CAGCAGGAGC	CCGATGGTGC	TGGAGCCAAG	TCCCCGACAT	GCCAGAAACT	2220
	GTCCCCCCAAG	TGGTGCTTCC	TGGACGCCAC	CACTGCCAGC	CGCITCTACA	GGATCGACCG	2280
	AGCCCAGGAG	CACCTCAACT	ATGTGACTGA	GATCGCACAG	GATGAGATTT	ATATCCTGGA	2340
	CCCTGAGCTG	CTGGGGGCAT TGCTCACCCA	CGGCCCGGCC	TGACCTCCCA ACTGCA AGGG	GATGCTGCAC	CCCCTCAAGG	2460
30	TGAAGAGCTG	ATTGAGGCTG	CCAAGAGGAA	CGACTTCTGT	AAGCTCCAGG	AGCTGCACCG	2520
	AGCTGGGGGC	GACCTCATGC	ACCGAGACGA	GCAGAGTCGC	ACGCTCCTGC	ACCACGCAGT	2580
	CAGCACTGGC	AGCANGGATG	TGGTCCGCTA	CCTGCTGGAC	CACGCCCCCC	CAGAGATCCT	2640 2700
	TGATGCGGTG	GAGGANAACG CACTACATCG	CCCACACCCTC	TTTGCACCAA	ATCA ACACTAC	A CCA GCAGGG	2760
35	CACCATCIGC	CGGCAGCGGG	CTGAGAAGGC	TCAGGACACC	GAGCTGGCCG	CCTACCTGGA	2820
	GAACCGGCAG	CACTACCAGA	TGATCCAGCG	GGAGGACCAG	GAGACGGCTG	TOTAGOGGGC	2880
	Sea ID NO.	172 Protein	n semience:				
	Protein Ac	cession #: 1	NP 003637				
40			_				
	1	11	21	31	41	51	
	MEDDINGSDEA	RSSDSESASA	Secrembra	DEDDKADERT.	NERREPOLET	POHRKAITKS	60
	CTOUT.ADDDD	TREADCRESS	POTPRTVTWR	REATVORREW	PETNYSGDEC	YVGROVCVAR	120
45	MLKSVSRRKC	AACKIVVHTP	CIECTEKINE	RCKPSFRESG	SRNVREPTFV	RHHWVHRRRQ	180
	DGKCRHCGKG	FOOKFTFHSK PONTLKASKK	BIVAISCSWC	KQAYHSKVSC	PMLQQIEEPC	SEGVHAAVVI	240 300
	NEKROGNOGA	KIIQSFLWYL	NPROVEDLSO	GGPKRALEMY	REVHILRILA	CGGDGTVGWI	360
							420
50	LHAEPNPEAG	PEDRDEGATD DFLMGSSKDL	RLPLDVFNNY	FSLGFDAHVT	LEPHESREAN	PEKFNSRFRN	480
	KNFYAGTAFS	DFLMGSSKDL	AKHIRVVCDG	MDLTPKIQDL	KPQCVVFLN1	PRYCAGIMPW	540 600
	GEPCKLAASP	PQRHDDGYLE IRIALRNQAT	MADKAKESSY	APLHSDOOPV	PROLETOVSE	VSMHDYEALH	660
							720
55	TTASRFYRID	RAQEHLNYVT	EIAQDEIYIL	DPELLGASAR	PDLPTPTSPL	PTSPCSPTPR	780
	SLQGDAAPPQ	GEELIEAAKR LDAVEENGET	NDFCKLQELH	RAGGDLMHRD	EGSRTLLHHA	VSTGSKDVVR	900
	AODTELANI.	ENROHYOMIO	PEDORTAV	KIICHIIVEM	OWSTRAKTING	GDIFRGROADK	300
	-		-				
60	Seq ID NO:	173 DNA sec	quence				
	Nucleic Ac:	id Accession	n #: AF23277	/2			
	Course sed	Tence, 1-10	02				
CE	1	11	21	31	41	51	
65	!				1	managamaga	60
	ATGCCGGTGC	AGCTGACGAC GCATCCTGGC	AGCCCTGCGT	ACCCCCTACC	AGTTCATCA	CACCCCTGGCA	120
	CACTACCTGT	CCTTCGGCCT	GTACGGCGCC	ATCCTGGGCC	TOCACCTGCT	CATTCAGAGC	180
70	CTTTTTGCCT	TCCTGGAGCA	CCGGCGCATG	CGACGTGCCG	GCCAGGCCCT	GAAGCTGCCC	240
70	TCCCCGCGGC	GCCTGCGCTC	GGCACTGTGC	ATTGCCGCAT	ACCAGGAGGA	CCCTGACTAC	300 360
	TTGCGCAAGT	GCAACOGCCA	GGCCCAGCGC	TACATOCTICC	ACATOTTOCA	CONGRETATO	420
	GGCGGCACCG	AGCAGGCCGG	CTTCTTTGTG	TOGCOCAGCA	ACTTCCATGA	GGCAGGCGAG	480
	COTTORGROUND	AGGCCAGCCT	GCAGGAGGGC	ATGGACCGTG	TGCGGGGATGT	GGTGGGGGCC	540
75	AGCACCTTCT	CGTGCATCAT TCGGCGATTC	GCAGAAGTGG	GGAGGCAAGC	GCGAGGTCAT	GTACACGGCC	600 660
	TTCAAGGCCC	GCACCATCGA	GATGGACTAC	ATCCAGGTGT	ACCAMCOCCA	ACTROCCCA	720
	GTCGGGGGAG	ATGTCCAGAT	CCTCAACAAG	TACGACTCAT	CCATTTCCTT	CCTGAGCAGC	780
00	GTGCGGTACT	GGATGGCCTT	CAACGTGGAG	CGGGCCTGCC	AGTOCTACTT	TGGCTGTGTG	840
80	CAGTGTATTA	GTGGGCCCTT	GGGCATGTAC	CGCAACAGCC	TOCTCCAGCA	GTTCCTGGAG	900
	GACTGGTACC	ATCAGAAGTT TCCTGAGCCT	TOCCTACCOCA	AAGTGCAGCT	TUGGGGATGA	CANGRACCTC	960 1020
				UCTIVIDATIVE.	COCOCIC	CHARLOCCTC	1020
	ACAGAGACCC	CCACTAAGTA	CCTCCGGJYGG	CTCAACCAGC			
0.5	ACAGAGACCC TACTTCCGGG	CCACTAAGTA AGTGGCTCTA	CAACTCTCTG	TGGTTCCATA	AGCACCACCT	CTGGATGACC	1140
85	ACAGAGACCC TACTTCCGGG TACGAGTCAG	AGTGGCTCTA TYGGTCACTGG	CAACTCTCTG	TGGTTCCATA TTCTTCCTCA	AGCACCACCT	CTGGATGACC	1140
85	ACAGAGACCC TACTTCCGGG TACGAGTCAG TTCTACCGGG	AGTGGCTCTA TGGTCACGGG GCCGCATCTG	CAACTCTCTG TTTCTTCCCC GAACATTCTC	TGGTTCCTCA TTCTTCCTCA CTCTTCCTGC	AGCACCACCT TTGCCACGGT TGACGGTGCA	CTGGATGACC TATACAGCTT GCTGGTGGGC	1140
85	ACAGAGACCC TACTTCCGGG TACGAGTCAG TTCTACCGGG	AGTGGCTCTA TYGGTCACTGG	CAACTCTCTG TTTCTTCCCC GAACATTCTC	TGGTTCCTCA TTCTTCCTCA CTCTTCCTGC	AGCACCACCT TTGCCACGGT TGACGGTGCA	CTGGATGACC TATACAGCTT GCTGGTGGGC	1140 1200 1260

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	CTCTACTCCC	TOCTCTATAT	GTCCAGCCTT	CTGCCGGGCCA	AGATCTTTGC	CATTGCTACC	1380
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5	GGCTGCTACT	GGGTGGCCCCT	CCTCATGCTA	TATCTGGCCA	TCATCGCCCG	GCGATGTGGG .	1620
	AAGAAGCCGG	AGCAGTACAG	CTTGGCTTTT AGGGAGGGAA	GCTGAGGTGT	GACATGGCCC	CCAAGCAGAG	1680
	GGGAGGAGGG	AGTGCTGTGT	TTTAGTCTCT	TAATGGTCCA	AAGGACAAAT	CTANANTGCA	1800
	AAGAACGGTG	ATGTAGTATG	GCCTGACAGC	TCTGTTTAGA	GGAGGCAACA	CTGATCCCCC	1860
10	AGATGCAGGG	CTGCAGGGGA	TTCTGTGTTT	TCAGACTGCC	TGTCTGCTTG	CATCTGCACA	1920
	TAGGCAGTAG	CCTCCTCCTG	TGTGATAGGT	GGCACTCAGA ACCTGAGTGA	COCCAACCTG	COGRAGGAGG	2040
	TTCTCCCAGC	CCATCTGAAC	ACAACCAGAG	GTGGCAGGAG	AATTTCTACT	GAGCGAGGTG	2100
	GGCCGGTTAG	TOTATGTCAC	CCCCACCCCA	CCCATAAGTA	GTCATCAATG	CANTARGATT	2160
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	CAGGGGGTTA	GCACTGAGATA	GCTTTTAAAA	GTGCACATTA	AAAAGGAAAG	TTTGCCAGGA	2340
	GGAACAAAGA	GATTGTGGTG	GTGCTAAAGG	AGGCCATAAG	CTACACAGAG	GCCTTGGGTG	2400
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20	GGGGAGATAA	AAAGATTAAG	CCCCAACATG TCCTCTCAAA	TTCAGAAAAG	ARGIGRAGIC	PAGACACACT	2520
	CCCCACTTCA	CTTTCTTCAA	AGCCACATTT	TTTGAGGTAT	CACTGCAGTC	ACCTCTTCTA	2640
	CCCTCATCAT	CATAGGTAAG	GTTTTCAAGG	TGGCAATTGG	GGCGGAGCCC	CGGCTTCTTA	2700
25	TAGAAGCTTC	AGCAGGAGGC	AAGCGTGTTC TTGGAGCTGC	TCAGCACATA	TOOGRACIAT	CAGGAGCCTC	2760
23	ATOTOTOROT	TTCAGGCTAC	TRITCTTGAC	AATCATCTCC	AATGGAAAGC	TTTTCAGTGT	2880
	TCCCRAAGTG	AACTCTCAAA	TCCAAAATGG	TTATCTTTGA	GACCATCCAT	TCTCCTCAGT	2940
	GGCTTCTCCA	GGGAATTCTT	ACAGCCAAGT	TGTGACAGTC	ACTGCATTTG	CCTGCTTCTT	3000
30	TOCAGANACC	AAACTAGGAG	ATGAAACTG3 TTTTGGCTGT	TTCCTACATC	CTARGGITCT	GGRATGAGGG	3120
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	TGGGATCCTG	ACTAAGCCTT	TGACTTAAGG	GTTGCTTGCT	TGCCCTCCAA	ATGTCCTTTC	3240
	TCAAAGGGGC	CAACTAACCC	GTGCAGAACC GCTTCCTACA	AGCACTAAGG	TGGACAGCAG	ACARGROGGC	3360
35	GGGCAAACCC	TGGTGCTTTC	CTTCATCTCC	CACGAACTCA	AGGGTTTTCC	AAGTGTAGCT	3420
	AACAGTTGCC	ACATCACACA	GACCTCCAGT	TTCTGGTAAG	ACTOCTOGTT	GACATCAGAC	3480
	CCAACCCATT	GAAGGCTGGA	AGGCAGCAGG AAACTATTTT	CATTTGCTAA	GGCAGCTGAT	CCAGGCAATC	3540
	CARGINGCAGA	CURAGARGIT	CGCTAAGGGC	TTGTTTTTCT	TCAGCATTTA	CTTGAAGATT	3660
40	ABTOTACOAT	CACAGGCTCT	CCTGGCTGTC	CTACCATCAG	CTCTGCCTTG	CACTGTOGTC	3720
		CTCAAATCAA	AAACAGGCAG	GTACAGGTAG	TGGGCTCACA	ACGTTTGACC	378Q 3840
	TCGACTGGTT	TTTCTAAGTT	ATTTTGTACA GCAAGGGAAG	ACCOTTONA	CRATTGGACG	CATTTTTGGTT	3900
	THEY STORES	CACCATTCAL	ATCCTCTTTT	GTATTGTTTC	TACAATAATT	TGTAAACATA	3960
45	TTTATTTTTA	GAGAATTCAA CCTGCTTTTT	ATCCTCTTTT	GTATTGTTTC	TACAATAATT	TGTAAACATA	3960 4020
45	TTTATTTTTA	CACCATTCAL	ATCCTCTTTT	GTATTGTTTC	TACAATAATT	TGTAAACATA	
45	TTTCCTCATT TTTATTTTTA CTTATTTGTC Seg ID NO:	GAGAATTCAA CCTGCTTTTT AAAATAAAGA 174 Protei:	ATCCTCTTT TTTTTTTTT TTCTCACAT	GTATTGTTTC	TACAATAATT	TGTAAACATA	
	TTTCCTCATT TTTATTTTTA CTTATTTGTC Seg ID NO:	GAGAATTCAA CCTGCTTTTT	ATCCTCTTT TTTTTTTTT TTCTCACAT	GTATTGTTTC	TACAATAATT	TGTAAACATA	
45 50	TTTCCTCATT TTTATTTTTA CTTATTTGTC Seq ID NO: Protein Acc	GAGAATTCAA CCTGCTTTTT AAAATAAAGA 174 Protein mession #:	ATCCTCTTT TTTTTTTTT TTCTCACAT n sequence: AAF36984	GTATTGTTTC TAATTTTCAG	TACAATAATT GTCAAGTTTT	TGTAAACATA	
	TTTCCTCATT TTTATTTTTA CTTATTTGTC Seq ID NO: Protein Acc	GAGAATTCAA CCTGCTTTTT AAAATAAAGA 174 Protein mession #: 1	ATCCTCTTT TTTTTTTTTT TTCTCACAT n sequence: AAF36984	GTATTGTTTC TAATTTTCAG	TACAATAATT GTCAAGTTTT	TGTAACATA TTATACTGCA 51	4020
	TTTCCTCATT TTTATTTTTA CTTATTTGTC Seq ID NO: Protein Acc	GAGAATTCAA CCTGCTTTTT AAAATAAAGA 174 Protein mession #: 1 11 1 VVGTSLFALA	ATCCTCTTT TTTTTTTTT TTCTCACAT n sequence: AAF36984 21 VLGGILAAYV	GTATTGTTTC TAATTTTCAG 31 1	TACAATAATT GTCAAGTTTT 41 HYLSPGLYGA	TGTARACATA TTATACTGCA 51 ILGLELLIQS	4020
50	TTTCCTCATT TTTATTTTTA CTTATTTGTC Seq ID NO: Protein Acc	GAGAATTCAA CCTGCTTTTT AAAATAAAGA 174 Protei: :ession #: ; 11 VVGTSLFALA BEACOALKLP	ATCCTCTITT TTTTTTTTTT TTCTCACAT n sequence: AAF36984 21 VLGGILAAYV SPERGSUALC	GTATTGTTTC TAATTTTCAG 31 TGYOFIHTEK TAAYOEDPDY	TACAATAATT GTCAAGTTTT 41 HYLSPGLYGA LEKCLESAOR	TSTARACATA TTATACTGCA 51 ILGLHLLIQS ISFPDLKVVM	4020 60 120
	TTTCCTCATT TTTATTTTTA CTTATTTGTC Seq ID NO: Protein Acc 1 NPVQLTTALR LFAFLEHRRM VVDGNRQEDA STESCIMONN	GAGAATTCAA CCTGCTTTTT AAAATAAAGA 174 Protei: cession #: i 11 vvgTsLFALA RRAGQALKLP YMLDIFHEVL GGKRUNYTA	ATCCTCTTT TTTTTTTTT TTCTCACAT n sequence: AAF36984 21 VLGGILAAYV SPRRGSVALC GGTEQAGFFV FRALGDSVDY	GTATTGTTTC TAATTTCAG 31 TGYOFIHTEK IAAYQEDPDY WESHFHEAGE IOVCOSDTVL	TACAATAATT GTCAAGTTTT 41	TGTAJACATA TTATAGTGCA 51 ILGLHLLIQS ISPPDLKVVM MDRVEDVVRA VLBEDPOVGS	60 120 180 240
50	TTTCCTCATT TTTATTTTA CTTATTTTTC Seq ID NO: Protein Acc 1 MPVQLTTALR LFARLERRRM VVDGRVQEDA STFSCIMQKM VGGDVQLINK	GAGAATTCAA CCTGCTTTT AAAATAAGA 174 Protei: cession #: i VGTSLFALA RRAGQALKLP YMLDIFHEVL GGKREVMYTA YDSNISFLSS	ATCCTCTTT TTTTTTTTT TTCTCACAT n Bequence: AAF36984 21 vLGGILAAYV SPRRGSVALC GGTBQAGFFV FKALGDSVDY WYYWARMVB	GTATTGTTC TAATTTCAG 31 TGYOFIHTEK IAAYQEDPDY WRSHFHBAGE IQVCDSDTVL RACQSYFGCV	TACAATTT GTCAAGTTTT 41	TGTARACATA TTATACTGCA 51 ILGLHLLIQS ISFPDLKVVM MDRVRDVVRA VLEEDPQVGA RNSLLQQFLE	60 120 180 240 300
50	TTTCCTCATT TTTATTTTTA CTTATTTTTA Seq ID NO: Protein Acc	GAGAATTCAA CCTGCTTTTT AAAATAAAGA 174 Protei: eession #:: 11 VVGTSLFALA RRAGQALKLP YMLDIFHEVL GGKREVMYTA YDSWISFLSS KCSFGDDRHL KCSFGDDRHL	ATCCICITIT TITITITIT TTCTCACAT n Bequence: AAF36984 21 VLGGILAAYV SPRRGSVALC GGTBQAGFFV FKALGDSVDV VRYWAFENUE TNRVLSLGYR	GTATTGTTC TAATTTCAG 31 TGYQEIHTEK IAAYQEDDDY WRSIFHBAGE IQVCDSDTVL RACQSYFGCV KYTARSKCL	41 	TOTANCATA TTATACTGCA 51 ILGLHLLIOS ISFPDLKVVM MDRVRDVVRA VLEEDPOVGG RNSLLQGFLE LNQQTRNSKS	60 120 180 240 300 360
50	TTTCCTCATT TTTATTTTA CTTATTTTTA Seq ID NO: Protein Acc 1 MPVQLTTALR LFAFLEKRN VVDGNRQEDA STFSCIMGN VGGDVQLIMGN DWYHQKPLGS	GAGAATTCAA CCTGCTTTTT ARAATAAAGA 174 Protei: ccssion #: i 11 VVGTSLFALA RRACQALKLP YMLDIFHEVL GGKREVNYTA YDENISFLS KCSFGDDRHL	ATCCCTTTT TTTTTTTTTTT TTCTCACAT n sequence: AAF36984 21 VLGGILAAYV SPRRSSVALC GGTEQAGFFV FKALGDSVDY VRYWHAFNVE TNRVLSLGYR	31 TGYOPIHTEK IAA YQEDDDY WRSHPHBAGE IQVCDSDTYLC TRACTSPTOCU TKYTARSKGL	41 HYLSPGLYGA LEKCLESAQE GETEASLOBO DPACTIENLE GCISCPLONY TETPTKYLEN PROPERIOR	TOTALACATA TTATACTGCA 51 ILGLHLLIQS ISFPDLKVVM MDRVADVVRA VLEEDQVGG ENSLLQQFLE LNQQTENSKS	60 120 180 240 300 360 420
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50	TTTCCTCATT TTTATTTTA CTTATTTTTA Seq ID NO: Protein Acc 1 MPVQLTTALR LFAFLEKRN VVDGNRQEDA STFSCIMGN VGGDVQLIMGN DWYHQKPLGS	GAGRATTCAA CCTGCTTTTT ARAATAAACA 174 Protesi eession #: ; 11 VWCTSLFALA RRAOQALKLP YMLDIFHEVL GGKREVNYTA YDENISFLSS KCSFGDDRSL WFHXHELDHT RGNABMIFMS LBGLAYTAY	ATCCICITIT TITITITIT TTCTCACAT n Bequence: AAF36984 21 VLGGILAAYV SPRRGSVALC GGTBQAGFFV FKALGDSVDV VRYWAFENUE TNRVLSLGYR	31 TGYOPIHTEK IAA YQEDDDY WRSHPHBAGE IQVCDSDTVL EACQSYPGCV TKYTARSKGL	41 HYLSPGLYGA LEKCLESAQE GETEASLOBO DPACTIENLE GCISCPLONY TETPTKYLEN PROPERTY	TGTAACATA TTATACTGCA 51 ILGLHLLIQS ISFPDLKVVM MDRVADVVRA VLEEDQVGG RNSLLQQFLE LNQQTRNSKS	60 120 180 240 360 420 480
50	TITICTICATT TTAATITITAA CTTATITIGTC Seq ID NO: Protein Acc 1 NPVQLTTALR LFAFLERRN VVCONROEDA STFSCIMCKN VGCDVQLINK DWYROKPLGS VFRENLYNSL IIKATYACFL LIPVSIWVK KKPEQYSLAF	GAGRATTCAA CCTGCTTTTT ARAATAAAGA 174 Protesi cession #: i VCGTSLFALA RRAGQALKLP YMLDIFHEVL GGKREVNYTA YDSNISFLSS KCSFGDDRHL WFEKHELHNT RGNAEMIFMS LLBGLAYTAY AEV	ATCCCTTT TTTTTTTTTT TTCTCACAT n sequence: AAF36984 21 VLGGILAAYV SPRRSVALC GGTEQAGFFV FKALGOSVDY VRYWAFENUE TNRVLSLGYR YESVVTGFFP LYSLLYMSSLL CQDLFSETEL	31 TGYOPIHTEK IAA YQEDDDY WRSHPHBAGE IQVCDSDTVL EACQSYPGCV TKYTARSKGL	41 HYLSPGLYGA LEKCLESAQE GETEASLOBO DPACTIENLE GCISCPLONY TETPTKYLEN PROPERTY	TGTAACATA TTATACTGCA 51 ILGLHLLIQS ISFPDLKVVM MDRVADVVRA VLEEDQVGG RNSLLQQFLE LNQQTRNSKS	60 120 180 240 360 420 480
50	TTTCTCATT TTTATTTTTA CTTATTTTTA Seq ID NO: Protein Acc	GAGRATTCHA CCTGCTTTTT ARAATARACA 174 Protei: cession #: ; 11 VVGTSLFALA RRACQALKLP YMDDIFHEVL GGKREVMYTA VDSWISFLS KCSFGDDRHL WFEXHELMIFMS LUBGLAYTAY AEV 175 DNA se-	ATCCCCTTT TTTTTTTTTTT TTCTCACAT n sequence: RAF36984 21 VLGGILAAYV SPRRSVALC GGTBQAGFFV FKALGDSVDY VRYWHAFBVE TNRVLSLGYR YESVVTGPP LYSLLYMSSL CQDLFSETEL Quence	31 TAXTTTCAG 31 I TGYOFIHTEK IAAVQEDPDY WRSIFHBAGE IQVCDSDTVL RACQSYPGCV TKYTARSKCI FPLIATY (IQL LPAKIFAIAT APLVSCAILY	41 HYLSPGLYGA LEKCLESAQE GETEASLOBO DPACTIENLE GCISCPLONY TETPTKYLEN PROPERTY	TGTAACATA TTATACTGCA 51 ILGLHLLIQS ISFPDLKVVM MDRVADVVRA VLEEDQVGG RNSLLQQFLE LNQQTRNSKS	60 120 180 240 360 420 480
50 55 60	TITICITICATE TITRATITITA Seq ID NO: Protein Acc I MPVQLITALR LFAFLERRM VUCDINGEDA SIFSCIMEN VUCDIVOLINK DWHOKPLUS LIKATYACFL LIFVSIMVA KKPRQYSLAF Seq ID MO: Nucleic Ac:	GAGRATTCHA CCTGCTTTTT ARAATARACA 174 Protei: cession #: ; 11 VVGTSLFALA RRACQALKLP YMDDIFHEVL GGKREVMYTA VDSWISFLS KCSFGDDRHL WFEXHELMENTA KFEXHELMENTA AEV 175 DNA se-	ATCCCCTTT TTTTTTTTTTTTTTTCTCACAT n sequence: AAF36984 21 ULGGILAAYV SPRRSSVALC GGTEGASFFV YKALGBSVDY VRYWAFAVE TNRVLSION YESVVTGFFP LYSLIMMSSL CQDLFSETEL QUENCE n #: NM_0000	31 TAXTTTCAG 31 I TGYOFIHTEK IAAVQEDPDY WRSIFHBAGE IQVCDSDTVL RACQSYPGCV TKYTARSKCI FPLIATY (IQL LPAKIFAIAT APLVSCAILY	41 HYLSPGLYGA LEKCLESAQE GETEASLOBO DPACTIENLE GCISCPLONY TETPTKYLEN PROPERTY	TGTAACATA TTATACTGCA 51 ILGLHLLIQS ISFPDLKVVM MDRVADVVRA VLEEDQVGG RNSLLQQFLE LNQQTRNSKS	60 120 180 240 360 420 480
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50 55 60 65	TITCOTCANT TITATITIA CTTATITIC Seq ID NO: Protein Acc 1 NPYOLITALR LFALBERA STRSCHOOK VOSDVOLIAN V	GGGAATCAA COTGCTTTT AAAATAAAGA 174 Protein #: i 11 VUGTSLFALA RRACQALKLP VUGTSLFALA RRACQALKP VUGTSLFALA LUGGLAVTAY ABV 175 DNA Ged dd Accession 11 11 11	ANCCICITY TITTITITY TITTITY TITTITY TOTCHCAT a sequence: AAR736984 21 VILIGIILAAYV SPRESSVLOS GOTISOASPY FKALGOSVDY VERWHANDEN VERWHANDEN LYSLLYNSSL CQOLPSETEL QUENCE QUENCE QUENCE 1404 21 GRANASCOTT	GTATIGITIC TAAITITCAG 31 TOTO THE TOTO THE TAIL TO THE TAIL TO THE TAIL TO THE TAIL THE TA	41 HILB FOLYGA EFFECTION 41 HILB FOLYGA EFFECTION EFFECTION COLSOPLOW TETPIXLEN	TOTALICATA TTATACTICA TATACTICA	60 120 180 240 300 420 480 540
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50 55 60 65 70	TITOCICOATE TITATITIAT CTTANTITIAT CTTANTITIAT CTTANTITIAT Seq ID NO. Protein Acc 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GRIGATTONA COTSCITTITA ANAATAACA 174 Protein cession #: . 11	ANCOLOTITE TITITITITIT TITITITITITITITITITITIT	31 GYOPINTEK I DAYOPINTEK I D	41	51 ILGUILLIOS ISPELIAVIM ROVENDAM INCLUMENTA	60 120 120 240 300 480 540
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50 55 60 65 70	TITOCICONT TITATITIS Seq ID NO. Probein Acc 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GRIGATICAA COTGCITTITA NAAATAACA 174 Protein cession #:: 11 11 12 13 14 Protein 174 Protein 174 Protein 174 Protein 175 Protei	ANCOCITITY TTOTICHANA a Sequence ansequence ansequence place ansequence ansequence proper prop	31	41	TOTAMACHTA TTATACTOCA	60 120 180 240 360 420 480 540
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	AGCCTGGAGG	AGGCCATCCA	GTTCATCAAC	CAGCGTGAGA	AGCCCCTGGC	CCTCTACATG	1140
							1200
~	GCGGCCAACG	ATGTCATCGT	CCACATCACC	TTGCACTCTC	TGCCCTTCGG	GGGGGTGGGG	1260
5	AACAGCGGCA	TOOGATCCTA	CCATGGCAAG	AAGAGCTTCG	AGACTTTCTC	TCACCGCCGC	1320
	TCTTGCCTGG	TGAGGCCTCT	GATGAATGAT	GAAGGCCTGA	AGGTCAGATA	CCCCCCGAGC	1380
	CCGGCCAAGA	TGACCCAGCA	CTGAGGAGGG	GITGCTCCCC	CTGGCCTGGC	CATACTGTGT	1440
	CCCATCGGAG	TGCGGACCAC	CCTCACTGGC	TCTCCTGGCC	CTGGAGAATC	GCTCCTGCAG	1500
10							1560
10	GGGCCCAGGC	CTCACCATTC	CAAGTCTCCA	CCCCTTTCTA	GACCAATAAA	GAGACAMATA	1620
	CAATTTTCTA	ACTOGG					
	0 TD 170	176 Protein					
	Bed ID NO:	ession #: 1	D 000682				
15	PIOCEIN ACC	ennion w. I					
10	1	11	21	31	41	51	
	ī	Ī	Ī	1	1	1	
	MSKISEAVKR	ARAAFSSGRT	RPLOFRFOOL	EALORLIOEO	EQELVGALAA	DLHKNEWNAY	60
	VERWOVER	TRYMTOKLDE	WAADEPVEKT	POTOODELYI	HSEPLGVVLV	IGTHNYPFNL	120
20	TIOPMVGAIA	AGNAVVLKPS	ELSENMASLL	ATTIPQYLDK	DLYPVINGGV	PETTELLKER	180
	PDHILVT387	GUGKTIMTAA	AKHLTPVTLE	LOGKSPCYVD	KNCDLDVACR	RIANGKFMNS	240
	GOTCVAPDYI	LCDPSIQNQI	VEKLKKSLKE	FYGEDAKKSR	DYGRIISARH	FORVMGLIEG	300
	OKVAYGGIGD	AATRYIAPTI	LTDVDPQSPV	MQEBIFGPVL	PIVCVRSLEE	AIQFINQREK	360
~ ~					PEGGACINGGM	GSYHCKKSFE	420
25	TESHRRSCLV	RPLMNDEGLK	VRYPPSPAKM	TOH			
	Seq ID NO:	177 DNA sec	ruence				
	Nucleic Aci	d Accession	1 #: NM_001	.067.1			
30	Coding sequ	ence: 108-	1703				
50	_		21	31	41	51	
	1	11	1.	1*	7*	ĭ*	
		OCCUPATION NAMED IN	Channecooc	TTGGTCGGGG	GTGGTCTCGT	degarcerec	60
	CIMACCOACO	COCCITCION	THETTERES	CCTTCACCAC	CGTCACCATG	GAAGTGTCAC	120
35	Character	TOTALLTON	BATATOCAAC	TCAACAAAA	AAAGAAAAAT	GAAGATGCTA	180
55	AGRARAGACT	OTOTOTO CAA	ACAATCTATC	264422446	ACAATTGGAA	CATATTTTGC	240
	TOTOCCCACA	CACCTACATT	GOTTOTOTO	AATTAGTGAC	CCAGCAAATG	TGGGTTTACG	300
	ATCRACATOR	TOTOTATE	TATACCCAAC	TCACTTTTGT	TOCTGGTTTG	TACARAGTCT	360
	TTGATGAGAT	TCTACTTAAT	GCTGCGGACA	ACAAACAAAG	GGACCCAAAA	ATGTCTTGTA	420
40	TTAGAGTCAC	AATTGATCCG	GAAAACAATT	TAATTAGTAT	GGACCCAAAA ATGGAATAAT	GGAAAAGGTA	480
	TECCEGERA	TGAACACAAA	GTTGAAAAAGA	TGTATGTCCC	AGCTCTCATA	TTTGGACAGC	540
	TOTALOTTO	TACTAACTAT	GATGATGATG	AAAAGAAAGT	GACAGGTGGT	CGAAATGGCT	600
	ATGGAGCCAA	ATTGTGTAAC	ATATTCAGTA	CCAAATTTAC	TGTGGAAACA	GCCAGTAGAG	660
	AATACAAGAA	AATGTTCAAA	CAGACATGGA	TGGATAATAT	GGGAAGAGCT	GGTGAGATGG	720
45	NA COUCH ACCC	CTTCBBTGGB	GARGATTATA	CATCTATCAC	CTTTCAGCCT	GATTTGTCTA	780
	AGTTTAAAAT	GCAAAGCCTG	GACAAAGATA	TTGTTGCACT	AATGGTCAGA	AGAGCATATG	840
	ATATTGCTGG	ATCCACCAAA	GATGTCAAAG	TCTTTCTTAA	TGGAAATAAA	CTGCCAGTAA	900
	AAGGATTTCG	TAGTTATGTG	GACATGTATT	TGAAGGACAA	GTTGGATGAA AGTGTGTTTA	ACTGGTAACT	960
50	CCTTGAAAGT	AATACATGAA	CAAGTAAACC	ACAGGTGGGA	AGTGTGTTTA	ACTATGAGTG	1020
50	AAAAAGGCTT	TCAGCAAATT	AGCTTTGTCA	ACAGCATTGC	TACATCCAAG	GGTGGCAGAC	1140
	ATGTTGATTA	TGTAGCTGAT	CAGATTGTGA	CTAAACTTGT	TGATGTTGTG TCACATGTGG	AAGAAGAAGA	1200
	ACAAGGGTGG	TGTTGCAGTA	AAAGCACATC	AGGTGAAAAA	TCACATGIGG	ATTITIONAL DATA	1260
	ATGCCTTAAT	TGAAAACCCA	ACCTPIGACT	CTCAGACAAA	AGAAAACATG TATCAAAGCT	COCKETTACARC	1320
55	CCAAGAGCTT	TOGATCAACA	TOCCAATTOA	TOTAL CONTENTS	GGCCCAAGTC	CACTTADACA	1380
55	GTGGTWTTGT	AGMANGUATA	CIMARCIOGO	TORROCCART	TCCCAAACTC	GATGATGCCA	1440
							1500
	CCSTTTCHOO.	CCCCCCCAAC	GGCCTTGCTG	TGGTTGGGAG	AGACAAATAT	GGGGTTTTCC	1560
							1620
60	CTCACATTAA	CARTATCATC	AAGATTGTGG	GTCTTCAGTA	CAAGAAAAAC	TATGAAGATG	1680
	AAGATTCATT	GAAGACGCTT	CGTTATGGGA	AGATAATGAT	TATGACAGAT	CAGGACCAAG	1740
							1800
	TGCGACATCG	TTTTCTGGAG	GAATTTATCA	CTCCCATTGT	AAAGGTATCT GAAGAGTTCT	AAAAACAAGC	1860
	AAGAAATGGC	ATTTTACAGC	CTTCCTGAAT	TTGAAGAGTG	GAAGAGTTCT	ACTCCAAATC	1920
65	ATARARATG	GAAAGTCAAA	TATTACAAAG	GTTTGGGGCAC	CAGCACATCA	AAGGAAGCTA	1980
	DECEMBER OF T	TOTACATATO	AAAAGACATC	GTATCCAGTT	CAAATATTCT	GGTCCTGAAG	2040
	ATGATGCTGC	TATCAGCCTG	GCCTTTAGCA	AAAAACAGAT	AGATGATCGA	AAGGAATGGT	2100
		CATTOGAGGAT	AGAAGACAAC	GAAAGTTACT	TGGGCTTCCT	GAGGATTACT	2160
	TARCTARTIT						
70	manufacture.	NA CONTROCTOR	TATCTGACAT	ATAATGACTT	CATCAACAAG	GAACTIATET	
70	TGTATGGACA	AACTACCACA	GAGAGATCTA	TOCCTTCTAT	GGTGGATGGT	TTGAAACCAG	2280
70	TGTATGGACA TGTTCTCAAA GTCAGAGAAA	AACTACCACA TTCTGATAAC GGTTTTGTTT	GAGAGATCTA	TOCCTTCTAT	CAAGCGAGAA	TTGAAACCAG GTAAAGGTTG	2280 2340
70	TGTATGGACA TGTTCTGAAA GTCAGAGAAA CCCAATTAGC	AACTACCACA TTCTGATAAC GGTTTTGTTT	GAGAGATOTA ACTTGCTTCA GCTGAAATGT	AACGGAATGA CPTCTTATCA	CAAGCGAGAA TCATGGTGAG	TTGAAACCAG GTAAAGGTTG ATGTCACTAA	2280 2340 2400
70	TGTATGGACA TGTTCTCAAA GTCAGAGAAA CCCAATTAGC TGATGACCAT	AACTACCACA TTCTGATAAC GGTTTTGTTT TGGATCAGTG TATCAATTTG	GAGAGATCTA ACTTGCTTCA GCTGAAATGT GCTCAGAATT	AACGGAATGA CTTCTTATCA TTGTGGGTAG	CAAGCGAGAA TCATGGTGAG CAATAATCTA	TTGAAACCAG GTAAAGGTTG ATGTCACTAA AACCTCTTGC	2280 2340
70 75	TGTATGGACA TGTTCTCAAA GTCAGAGAAA CCCAATTAGC TGATGACCAT AGCCCATTAG	AACTACCACA TTCTGATAAC GGTTTTGTTT TGGATCAGTG TATCAATTTG TCAGTTTGGT	GAGAGATCTA ACTTGCTTCA GCTGAAATGT GCTCAGAATT ACCAGGCTAG	TCCCTTCTAT AACGGAATGA CTTCTTATCA TTCTGCGTAG ATGGTGGCAA	CAAGCGATGGA TCATGGTGAG CAATAATCTA GGATTCTGCT	TTGAAACCAG GTAAAGGTTG ATGTCACTAA AACCTCTTGC AGTCCACGAT	2280 2340 2400 2460 2520
70 75	TGTATGGACA TGTTCTCAAA GTCAGAGAAA CCCAATTAGC TGATGACCAT AGCCCATTAG	AACTACCACA TTCTGATAAC GGTTTTGTTT TGGATCAGTG TATCAATTTG TCAGTTTGGT	GAGAGATCTA ACTTGCTTCA GCTGAAATGT GCTCAGAATT ACCAGGCTAC	TCCCTTCTAT AACGGAATGA CTTCTTATCA TTCTCCGTAG ATCCTCGTAT GATTCTTATT	GGTGGATGGT CAAGCGAGAA TCATGGTGAG CAATAATCTA GGATTCTGCT TCCACCAAAA	TTGAAACCAG GTAAAGGTTG ATGTCACTAA AACCTCTTGC AGTCCACGAT GATGATCACA	2280 2340 2400 2460
	TOTATOGACA TOTTCTCAAA GTCAGAGAAA CCCAATTAGC TGATGACCAT AGCCCAITAG ACATCTITAC CGTTGAAGTT	AACTACCACA TTCTGATAAC GGTTTTGTTT TGGATCAGTG TATCAATTTG TCAGTTTGGT AA TGCTCAGC TTTATATGAT	GAGAGATCTA ACTTGCTTCA GCTGAAATGT GCTCAGAATT ACCAGGCTAC TCTTTGGCTC GACAACCAGC	TCCCTTCTAT AACGGAATGA CTTCTTATCA TTGTGGGTAG ATGGTGGCAA GATTGTTATT GTGTTGAGCC	GGTGGATGGT CAAGCGAGAA TCATGGTGAG CAATAATCTA GGATTCTGCT TCCACCAAAA TGAATGGTAC	TTGRAACCAG GTARAGGTTG ATGTCACTAA AACCTCTTGC AGTCCACGAT GATGATCACA ATTCCTATTA	2280 2340 2400 2460 2520 2580
	TGTATGGACA TGTTCTCAAA GTCAGAGAAA CCCAATTAGC CGAATGACCAT AGCCCATTGG ACATCTITAC CGTTGAAGTT TTCCCATGGT	AACTACCACA TTCTGATAAC GGTTTTGTTT TGGATCAGTG TATCAATTTG TCAGTTTGGT AATGCTCAGC TTTATATGAT GCTGATAATAA	GAGAGATCTA ACTTGCTTCA GCTGAAATGT GCTCAGAGTTA ACCAGGCTAC TCTTTGGCTC GACAACCAGC GGTGCTGAAG	TOCCTTCTAT ARCGGAATGA CTTCTTATCA TTGTCGGTAG ATGGTGGCAA GATTGTTATT GTGTTGAGCC GAATCGGTAC ACATCAGCAC	GGTGGATGGT CAAGCGAGAA TCATGGTGAG CAATAATCTA GGATCAGCAAAA TGAATGGTAC TGGTGGTCC TTTGGTGGTCC	TTGRAACCAG GTARAGGTTG ATGTCACTAA AACCTCTTGC AGTCCACGAT GATGATCACA ATTCCTATTA TGCAAAATCC GGAGGAAGGAC	2280 2340 2400 2460 2520 2580 2640 2700
75	TGTATGGACA TGTTCTCAAA GTCAGAGAAA CCCAATTAGC CGAATGACCAT AGCCCATTGG ACATCTITAC CGTTGAAGTT TTCCCATGGT	AACTACCACA TTCTGATAAC GGTTTTGTTT TGGATCAGTG TATCAATTTG TCAGTTTGGT AATGCTCAGC TTTATATGAT GCTGATAATAA	GAGAGATCTA ACTTGCTTCA GCTGAAATGT GCTCAGAGTTA ACCAGGCTAC TCTTTGGCTC GACAACCAGC GGTGCTGAAG	TOCCTTCTAT ARCGGAATGA CTTCTTATCA TTGTCGGTAG ATGGTGGCAA GATTGTTATT GTGTTGAGCC GAATCGGTAC ACATCAGCAC	GGTGGATGGT CAAGCGAGAA TCATGGTGAG CAATAATCTA GGATCAGCAAAA TGAATGGTAC TGGTGGTCC TTTGGTGGTCC	TTGRAACCAG GTARAGGTTG ATGTCACTAA AACCTCTTGC AGTCCACGAT GATGATCACA ATTCCTATTA TGCAAAATCC GGAGGAAGGAC	2280 2340 2400 2460 2520 2580 2640
75	TOTATOGACA TOTTCTCAAA GTCAGAGAAA CCCAATTAGC TGATGACCAT AGCCCATTAG CGTTGAAGTT TTCCCATGGT CCAACTITGG CGTTGAAGTT TTCCCATGGT CCAACTITGGCTAACTT	AACTACCACA TTCTGATAAC GGTTTTGTTT TGGATCAGTG TATCAATTTG TCAGTTTGGT AATGCTCAGC TTTATATGAT GCTGATAAAA GCTTCCAAGG	GAGAGATCTA ACTTGCTCA GCTGRAATGT GCTCRGAATTT ACCAGGCTAC TCTTTGGCTC GACAACCAGC GGTGCTGAAG ATTGTAAATA TACAAGAACTT	TOCCTTCTAT AACGGAATGA CTTCTTATCA TTGTGGGTAG ATGGTGGCAA GATTGTTATT GTGTTGAGGC GAAT CGGTAC ACATCAGGCG TCAAGGGTAC	GGTGGATGGT CAAGGGAGAA TCATGGTGAG CAATAATCTA GGATCTGCT TCCACCAAAA TGAATGGTAC TGGGTGGTCC TTTGATGGAT TATGAAGAA	TTGAAACCAG GTAAAGGTTG ATGTCACTAA AACGTCTTGC AGTCCACGAT GATGATCACA ATTCCTATTA TGCAAAATCC GGAGAAGAAC CTGGCTCCAA	2280 2340 2400 2460 2520 2580 2640 2700 2760
	TOTATOGACA TOTTOTCAGA GCCAGAGAA CCCAATTAGC TGATGACCAT AGCCCATTGA ACACCTITAC CGTGAAGTT TCCCATGGT CCAACTITGA CTTTGCCAT	AACTACCACA TTCTGATAAC GGTTTGGTT TGGATCAGTG TATCAATTTG TCAGTTTGGT AATGCTCAGC TTTATATGAT TGTGGGTGAA GCTTCCAAGT GATTAGTGGT	GAGAGATCTA ACTITICATORA GCTGARATGT GCTCAGACTAC TCTTTGGCTC GACAACCAGC GGTGCTGAAG ATTGTARATA TACAAGAACT GAAGTAGCTA	TCCCTTCTAT AACGGAATGA ACTCCTTATCA TTGTCGGTAG ATGGTGGCAA GATTGTTTATT GTGTTTGAGC GAAT CGGTAC ACATCAGGCTAC TCAAGGGTAC ACAAGGATAC ACAAAGGAACA ACAAAGGAACA ACAAAGGAACA ACAAAGGAACA ACAAAGGAACA ACAAAGGAACA ACAAAGGAACA ACAAAGGAACA	GGTGGATGGT CAAGGGAGAA TCATGGTGAG CAATACTCTA GGATTCTGCT TCACCAAAA TGAATGGTAC TTTGATGGAT TATTGAAGAA TACAACCATT AGTTCTAGAA	TTGAAACCAG GTMAAGGTTG ATGTCACTAA AACCTCTTGC AGTCCACGAT GATGATCACA ATTCCTATTA TGCAAAATCC GGAGAAGAAC CTGGCTCCAA GAAATCTCAG CCCATGTTGA	2280 2340 2400 2460 2520 2580 2640 2700 2760 2820 2880 2940
75	TOTATOGACA TOTTOTCAAA TOTTOTCAAA GCCAATTAGC TGATGACCAT AGCCCATTGG ACATCTITAC CGTTGAAGTT TTCCCATGGT CCAACTITGA ACTACTATGCAAT ATCAATATGT AGCTTCCCAT ATCAATATGT AGGTTCCCGT ATCAATATGT AGGTTCCCGT	AACTACCACA TTTGATTAC TGGATCACTG TGGATCACTG TATCAATTG TCAGTTTGGT TCAGTTTGGT TCAGTTGGT TTTATATGAT GCTGATAAAT TGTGGGTGAA GCTTCCAGGT GATTAGTGGT CAGAACATGG	GAGAGATCTA ACTITOCTICA GCTGARATGT GCTCAGAGTTA CCAGGCTAC TCTTTGGCTC GACAACCAGC GGTGCTGAAG ATTGTAAATA TACAAGAACT GAAGTAGCTA ACCCAGACAT CCTCTCATAA	TOCTTOTAT AACGGAATGA CTTCTTATCA TTGTGGGTAG ATGGTGGGTAG GAAT GGGTAC GAAT CAGGGTAC TCAAGGGTAC TCAAGGATA ACAACGAAC ACAGCGTAC CAGACGATAAGACAAC CAGACTATAG	GGTGGATGGT CAAGGGAGAA TCATGGTGAG CAATAATCTA GGATTCTGCT TCCACCAAAA TGAATGGTAC TGTGGTGGTC TTTGATGGAT TATTGAAGGA TACAACCATT AGTTCTAGAA GGAATACCAT	TTGNAACCAG GTAAAGGTTG ATGTCACTA AACCTCTTGC AGTCACCA ATTCCTATTA TGCAAAATCC GGAGAAGAAC CTGGCTCCAA GAAATCTCAG AAACTCTCAA AAACTCTCAA AAACTCTCAA AAACTCTCAA AAACTCTCAA AAACTCTCAA AAACTCTCAA AAACCAAACCAA	2280 2340 2400 2460 2520 2580 2640 2700 2760 2820 2880 2940 3000
75	TOTATOCACA TOTTCTCAAA GTCAGAGAAA CCCAATTAGC TGATGACCAT AGCCCATTGAACTT TTCCCATGGT CCAACTTTGACTT TTCCCATGGT CCAACTTTGACATT ACCATTTGACATAT ACCATTTGACAATT ACCATTTGACAATT ACCATTTGACAATT ACCATTTGACACTAA ATGACACTACAATT AGCTTCCGGT ATGGCACCGAA CTTTGGAAATT CTTTCGAAATT CTTTCAAAATT	AACTACACA TTOTGATAAC GSTTTTGTT TGGATCAGTG TATCAATTG TCAGTTTGGAT AATGCCAGC TTATATATAT TGCTGAGAT TGTGGTGAA GCTTCCAGGT GATTAGTGGT CAGAACACCT TGTTGGAAG	GAGAGATCTA ACTITACTICA GCTGRAATGT GCTCRGAATT ACCAGGCTAC TCTTTGGCTC GACARCCAGC GGTGCTGAAG ATTGTAATA TACAAGAACT GAAGTAGCTA ACCCAGACAT ACCCAGACAT ACCCAGACAT ACTOCATAA ATGACTGAAG	TOCOTTCIAT AACGGARIGA CTTCTTATCA TTGTGGGTAG ATGGTGGCAA GATTGTTATCT GTGTTTAGGCC GAATCGGGTAC TCCTAGATCA CAGACCTAC CAGACCTACA AMAAACTGGC AMAACTGGCAA AMAAACTGGC	GGTGGATGGT CAAGGAGAA TCATGGTTGAG CAATRATCTA GGATTCTGCT TCCACCAAAA TGAATGGTAC TGGGTGGTCC TTTGATGGAT TATTGAAGAA TACAACCATT AGTTCTAGAA GGAATACCAT AGGGCAGAG	TTGNAACCAG GTANAGGTTG ATGTCACTAA AACCTCTTGC AGTCACCAT GATGATCACA ATTCCTATTA TGCAAAATCC GGAGAAGAAC CTGGCTCCAA GAAATCTCAG CCCATGTTGA ACAGATACCA AGAGTTGGAC AGAGTTGGAC AGAGTTGGAC	2280 2340 2400 2460 2520 2580 2640 2700 2820 2880 2940 3000 3060
75 80	TOTATOGACA TOTATOCACA TOTATOCACA TOTATAGC TGATGACCAT GACCATTAGC COSTIGAAGT TTOCCATGGT CCAACTITGA CTTTGCCAAT ATCAACTITGA AGCTTCCCAT ATCAACTAGT AGCTTCCCGT ATGGCAACT ATG	AACTACCACA TACTACTACACA GSTTTGTTT TGGATCACT TATCAATTG TATCAATTG TATCAATTG TTAATATGAT GCTGATAAAT TGTGGGTGAA GCTTCCAAGT GATTAGTGGT CAGAACATGG GAAGACACT TGTTGTGAAGA TGTTGTGAAGA TGTTGTGAAGA TGTGGAACACTC TGTTGTGAAGA TGTTGTGAAGA	GAGAGATCHA ACTTGCTTCA GCTGRAATGT GCTCRGRATT ACCAGGCTRA TCTTTGGGTC GACAACCAGC GGTGCTGRAG ATTGTRAATA TACAAGRACT GAGGTAGCTRA ACCCAGACAT CCTCTCATRA ATGACTGRAG	TOCOTTCIAT AACGGARIGA TOTTCITATCA TTOTGOGIAG ATGGTGGCA GAITGTTATT GTGTTGAGCC GAATGGGGA TCAAGGGGTAC TTCTTAATTC CAGAGGAAAAACTGGG AAAAAACTGGG AAAAAACTGGGA AAAAAACTGGCA AAAAAACTGGCA AAAAAACTGGCA AAAAAACTGGCA AAAAAACTGGCA AAAAACTGGCA AAAAACTGCAAAACTGGCAAAACCTGGCAAAACCTGCAAAACCTGCAAAACCTGCAAAACCTGCAAAACCTGCAAAACCTGCAAAACCTGCAAAACCTGCAAAACCTGCAAAACCTGCAAAACCTGCAAAACCTGCAAAAACCTGCAAAAACCTGCAAAAACCTGCAAAAACCTGCAAAAACCTGCAAAAACCTGCAAAAAAACTGCAAAAAAAA	GSTGGATGGT CAAGGAGAA TCATGSTGAG CAATAATCTA GGATTCTGCT TCCACCAAAA TGAATGGTAC TSTGTGAGAT TATTGAAGAA TATTGAAGAA TACAACCATT AGTTCTAGAA GGAATACCAT AGAGCACGAG	TTGRACCAG GTARAGGTTG ATGTCACTRA AACCTCTTGC AGTCCACGAT GATGACACA ATTCCTATTA TGCARAATCC GGGGAGAGGAC GAGATCTCAG GAAATCTCAG GAAATCTCAG GAAATCTCAG GAAATCTCAG GAATCTCAG CCCATGTTGA ACGGTTGAC ACGGTTGAC ACGGTTGAC ACGGTTTGAC ACGGTTTGAC ACGGTTTGAC ACGGTTTGAC ACGGTTTGAC ACGTTTGAC ACGTTTGAC ACGTTTGAC ACGTTTGAC ACGTTTGAC ACGTTTGAC ACGTTTTGAC ACGTTTTGAC ACGTTTTGAC ACGTTTTGAC ACGTTTTTGAC ACGTTTTTGAC ACGTTTTTGAC ACGTTTTTGAC ACGTTTTTTGAC ACGTTTTTTGAC ACGTTTTTTGAC ACGTTTTTTGAC ACGTTTTTTGAC ACGTTTTTTGAC ACGTTTTTTGAC ACGTTTTTTTTGAC ACGTTTTTTTTTGAC ACGTTTTTTTTTGAC ACGTTTTTTTTTGAC ACGTTTTTTTTTT	2280 2340 2400 2460 2520 2580 2700 2760 2820 2880 2940 3000 3120
75	TOTATOGACA TOTTCTCAAA GTCAGAGAAA GTCAGAGAAA GCCATTAGC TGATGACCAT AGCCATTAGC ACATCTITAC COTTGAACT TCCACTGTT TCCACTGTT ACCATCTTAGCAAT ATCAATATAT ACCATAGAT ATCAATATAT ACCATCGTT ACCACAAAAT TACCACAAAAT ACCACAAAAT ACCACACAAAT ACCACAAAAT ACCACAAAT ACCACAAAAT ACCACAAAAT ACCACAAAAT ACCACAAAT ACCACAAAAT ACCACAAAT ACCACAA	AACTACACA TOTTACTATAC TOTTACTATAC TOTTACTATTOT TOGATCACT TATCAATTOT TATCAATTOT TATCAATTOT TATCAATTOT GCTGATAAAT GCTGCAAG GATTACGAT GATTAGGT CAGAACATOG GAAGACACC TOTTGTGAAG CTTCAAACAC TTTAAAGAA TTTAAAGAA	GAGAGATCTA ACTTGCTTCA GCTCBGAATT GCTCBGAATT ACCAGGCTAC TCTTTGGCTC GACAACCAGC GSTGCTGGAG ATTGTAAATA TACAAGAACT TCCAGGACAT ACCAGGACAT ACCAGGACAT ACTGAGGAA ATGACTGAAG ATGACTGAAG TATGACTGAAG TATGACTGAAG	TOCETTETAT AACGGARTGA CTTCTTATCA TTOTCOSTING ATTOTTGACCA GATTGTTATT GTGTTTGACCC TCAACGGCT TCATCAGCGT TCATCAGTATC ACATCAGACT ACATCAGACT ACAACTACAG AMAACTGCC TCACATGCAA AMAACTGCC TCACATGCAA TCTTCATTATC AMAACTGCC TCACATGCAA TCTTCACATTCAC TCTTCACTCAC	GSTGGATGGT CAAGCAGAA TCATGGTGAG GAATAATCTA GGATTCTGGT TCCACCAAAA TGAATGGTAC TGGGTGGTC TTTGATGGAT TATTGAAGAA TACAACCATT AGTTCTAGAG GGAATACCAT AGAGCACT AGAGGAC TCTATGGTG TCTATGT TCTATGT TCTATGT TCTATGT TCTATGT TCTATGT TCTATG TCTATGT TCTATGT TCTATGT TCTATGT TCTATGT TCTATGT TCTATGT TCTATGT	TTGRACCAG GTARAGGTTG ATGTCACTAA AACCTCTTGC AGTCACCGAT GATGATCACA ATTCCTATTA TGCAAAATCC GGAGAAGGAC CTGGCTCCAA AGAATCTCAG CCATGTTGA ACAGATACCA AGAGTTGAG CCTTTTTGAC TTTTTTGAC TTTTTTGAC	2280 2340 2400 2460 2520 2580 2760 2820 2880 2940 3000 3120 3180
75 80	TOTATOGACA TOTTCT CAAA GTCAGAGAAA GTCAGATTAGC TGATGACCATTAGC AGCCCATTAGC ACATTATC GTTGAAGTT TTCCCATGGT CCAACTITAA CTTTGCCAAT ATCAATATATA AGCTTCCCGT ATGAGATT ATGAGACACA AGGTCAGAAAAT AGTAGACAAAAT AGTAGACAAAT AGTAGACATA	AACTACACA TOTGATAAC GSTTTGTT TGGATCATT TGGATCATT TGASTCTGGT TATCATTTGGT TCASTTTGGT AATGCTCAGT GCTGATAAAT TGTCGAGT GATTAGTGT CAGACATGG GAAGACACCT TGTTGTGAGT GTTCAAGT GTTCAAGT GTTCAAGT GTTCAAGAAAC TTTAAAGAAAC TTTAAAGAAA	GAGAGATCTA ACTTGCTTCA GCTGAGATTA GCTCAGGATTA ACCAGGCTAC GTGTTGGGTC GACAACCAGC GGTGCTGAAG ATTGTAGATA TACAAGAACTA CCTCCATAA ATGACTGAAG CAACTAGTC TATGACAGGAG CAACTAGTC TATGACAGGAG TAGACTAGTC TATGACAGGAG TAGACTAGTC TATGACAGGAG	TOCOTTOTAT ANOGGANTGA ANOGGANTGA ATTOTOGOTAG ANOGTOGOTAG GANTOGGTAG ACATCAGGCG TCAAGGGTAC ACAAGGAAC ACAAGGAAC ACAAGGAAC ACAAGGACA ACAAGGACA ACAAGGACA ACAAGGACA ACAAGGACA ACAAGGACA ACAAGGACA ACAAGGACA AAAAACTGGG TCACATGCAA	GSTGGATGOT CAAGGGAGAA TCATGSTGAG CAATAATCTA GGATTATCTAT TCACCAAAA TGAATGGTAC TGTGTGGAT TATTGAGGAA TACAACCATT AGTCTAGAA GGAATACCAT AGTCTAGAA GGAATACCAT TGATGAGAA GGAATACCAT TGATGAGAA GGAATACCAT AGGCCAGAG CTCTATGGTG TCTAAGAGAC TCTATGGTG	TTGRACCAG GTARAGGTTG ATGTCACTAA AACCTCTTGC AGTCACCGAT GATGATCACA ATTCCTATTA TGCAAAATCC GGAGAAGGAC CTGGCTCCAA AGAATCTCAG CCATGTTGA ACAGATACCA AGAGTTGAG CCTTTTTGAC TTTTTTGAC TTTTTTGAC	2280 2340 2400 2460 2520 2580 2700 2760 2820 2880 2940 3000 3120

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TTGAAAATAA GCCTAAGAAA GAATTAATTA AAGTTCTGAT TCAGAGGGGA TATGATTCGG 3360 ATCCTGTGAA GGCCTGGAAA GAAGCCCAGC AAAAGGTTCC AGATGAAGAA GAAAATGAAG 3420 AGAGTGACAA OSAAAAGGAA ACTGAAAAGA GTGACTCCGT AACAGATTCT GGACCAACCT 3480 TOTAL CHARGE TOTAL CONTENTS ATTENDED A COMPANIES A CARGO CALCAR CONTENTS 3540 GCAGGCTAAG AAATGAAAAA GAACAAGAGC TGGACACATT AAAAAGAAAG AGTCCATCAG 3600 ATTIVITOGAA AGAAGACTTG GCTACATTTA TTGAAGAATT GGAGGCTGTT GAAGCCAAGG 3660 AAAAAGAAGA TGAAGAAGTC GGACTTCCTG GGAAAGGGGG GAAGGCCAAG GGGAAAAAAA CACAAATGGC TGAAGTTTTG CCTTCTCCGC GTGGTCAAAG AGTCATTCCA CGAATAACCA 3780 TAGAAATGAA AGCAGAGGCA GAAAAGAAAA ATAAAAAGAA AATTAAGAAT GAAAATACTG 3840 10 ARGUARGOTO TORRGRAGAT GOTOTOGRAG TROCRAGGOTT ARRECARAGA TTAGRARAGA 3900 AACAGAAAAG AGAACCAGGT ACAAAGACAA AGAAACAAAC TACATTOGCA TTTAAGCCAA 3960 TCAAAAAAGG AAAGAAGAGA AATCCCTGGC CTGATTCAGA ATCAGATAGG AGCAGTGACG ARAGTARTIT TGRIGICCCI CCRCGAGARA CAGAGCCACG GAGAGCAGCA ACARARACAA 4080 AATTCACAAT GGATTTGGAT TCAGATGAAG ATTTCTCAGA TTTTGATGAA AAAACTGATG 4140 15 ATGAAGATTI TGTCCCATCA GATGCTAGGC CACCTAAGAC CAAAACTTC CCAAAACTTA GTAACAAAGA ACTGAAACCA CAGAAAGTG TCGTGTCAGA CCTTGAAGCT GATGATGTTA 4200 4260 AGGGCAGTGT ACCACTGTCT TCAAGCCCTC CTGCTACACA TTTCCCAGAT GAAACTGAAA 4320 TTACAAACCC AGTTCCTAAA AAGAATGTGA CAGTGAAGAA GACAGCAGCA AAAAGTCAGT 4390 4440 4500 4560 CAGTCACAAG CAAGAAATCC AAGGGGGAGA GTGATGACTT CCATATGGAC TTTGACTCAG CTOTOGCTCC TCGGGCALAA TCTGTACGGG CRAAGRAACC TATRAAGTAC CTGGAAGAGT CAGATGAAGA TGATCTGTTT TAAAATGTGA GGCGATTATT TTAAGTAATT ATCTTACCAA 4740 25 GCCCAAGACT GGTTTTAAAG TTACCTGAAG CTCTTAACTT CCTCCCCTCT GAATTTAGTT 4800 TGGGGAAGGT GTTTTTAGTA CAAGACATCA AAGTGAAGTA AAGCCCAAGT GTTCTTTAGC 4860 TTTTTATAAT ACTGTCTAAA TAGTGACCAT CICATGGGCA TTGTTTTCIT CICTGCTTTG TOTGTGTTIT GAGTOTGCTT TOTTTTGTGT TTAAAACCTG ATTTTTAAGT TOTTCTGAAC 4980 E040 30 5100 5160 TITITETTIA AGCARTGAGA ARTIGCTCAT GITCITCATC TICTCAARTC ATCAGAGGCC 5280
AAAGARAAAC ACITIGGCTG TGTCTATARC TTGACACAGT CAATAGAATG AAGARAATTA 5340 35 GAGTAGTTAT GTGATTATTT CAGCTCTTGA CCTGTCCCCT CTGGCTGCCT CTGAGTCTGA 5400 ATCTCCCARA GAGAGARACC AATTTCTAAG AGGACTGGAT TGCAGAAGAC TCGGGGGACAA 5460 CATTEGATO: AAGATOTTAA ATGTTATATT GATAACCATG CICAGCAATG AGCTATTAGA TTCATTTTOG GAAATCTCCA TAATTTCAAT TIGTAAACTT TGTTAAGACC TGTCTACATT 5640 GTTATATOTG TOTGACTTGA GTAATGTTAT CAACGTTTTT GTAAATATTT ACTATGTTTT TOTATTAGOT ASSUTCOMO SATURDISTA TUTAGESAS TOTTOTAMO ATTIC

Sec ID NO: 178 Protein sequence: Protein Accession #: NP 001058.1

45 31 41 MEVSPLOPVN ENMOVNKIKK NEDAKKRLSV ERIYOKKTOL EHILLRPDTY IGSVELVTOO MWVYDEDVGI NYREVTFVPG LYKIFDEILV NAADNKQRDP KMSCIRVTID PENNLISIWN 120 NGKGIPVVEK KVEKMYVPAL IFGQLLTSSN YDDDEKKVTG GRNCYGAKLC NIFSTKFTVE 100 TASREYKKMF KOTWIDNINGR AGENELKPFN GEDYTCITFQ PDLSKFKMQS LDKDIVALMV RRAYDIAGST KDVKVFLNON KLPVKGFRSY VDMYLKDKLD ETGNSLKVIH BOVNHRWEVC 240 300 LYMSEKGFOO ISFVNSIATS KOGRHVDYVA DOIVTKLVDV VKKKNKGGVA VKAHOVIGHM 360 WIFVNALIEN PTFDSQTKEN HTLQPKSFGS TCQLSEKFIK AAIGCGIVES ILMWVKFKAQ 420 VQLNKKCSAV KHNRIKGIPK LDDANDAGGR NSTECTLILT BGDSAKTLAV SGLGVVGRDK 480 YGVFPLRGKI LNVREASHKQ IMENABINNI IKIVGLQYKK NYEDEDSLKT LRYGKINIMT 540 DODODOSHIY GLIINETHEN MESLIRHEEL PERITETUKU SKNKORMARY SLERFERMKS 600 STPNHKKWKV KYYKGLGTST SKEAKEYFAD MKRHRIOFKY SGPEDDAAIS LAFSKKQIDD RKEWLINFME DRRORKLIGL PEDYLYGOTT TYLTYMDFIN KELILFSNSD NERSIPSMVD 720 GLEPGORKVL FTCFKRNDKR EVKVAQLAGS VAEMSSYHHG EMSLAMTIIN LAQNFVGSNN LNLLOPIGGF GTRHGGKNS ASPRYIFTHL SSLARLLEFF KODHTLEFLY DDKQRVEEEN VIFIIPNVLI NGABGIGFG SCKIPHFOVR EIVNNIRRLM DGEBPLOMLF SYKHYKSTIE 700 60 840 900 ELAPNOYVIS GEVAILNETT IEISELPVRT WTOTYKEQVL EPMLNGTEKT PPLITDYREY HTDTTVKFVV KMTEEKLAEA ERVOLHKVFK LQTSLTCNSM VLFDHVGCLK KYDTVLDILR 1020 DPFELRLKYY GLRKEWLLGM LGAESAKLNN QARFILEKID GKIIIENKPK KELIKVLIQR GYDRDPVKAM KEAOOKVPDE EENEESDNEK STEKSDSVTD SGFTFNYLLD MPLWYLTKEK 1080 65 1140 KURLCRURNE KEOELDTLKR KSPSDLWKED LATFIEBLEA VEAKEKODEO VGLPGKGCKA 1200 KOKKTONAEV LPSPRGORVI PRITIEMKAE AEKKNKKKIK NEWTEGSPOE DGVELEGLKO RLEKKOKREP GTKTKKOTTL AFKPIKKGKK RNPWPDSESD RSSDESNEDV PPRETEPRRA 1320 ATKTKFINDL DSDEDFSDFD EKTEDEDFVP SDASPPKTKT SPKLSNKELK POKSVVSDLE 1380 70 ADDVKGSVPL SSSPPATHEP DETEITNEVP KKNYTVKKTA AKSOSSTSTT GAKKRAAPKG TKKDPALNSG VSOKPDPAKT KNRKRKPST SDDSDSNFEK IVSKAVTSKK SKGESDDFHM 1440 1500 DEDSAVAPRA KSVRAKKPIK YLBESDEDDL F

75 Seg ID NO: 179 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 148-7095

11 31 80 CACACATACG CACGCACGAT CTCACTTCGA TCTATACACT GGAGGATTAA AACAAACAAA CARABARAR ATTTCCTTCG CTCCCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120 COOCCAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCCT CGCTTGCATT CACCTCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240 85 CTTGTTGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAAG AAAATATCAA CATGTAATAG CCCAMAACAA TCTCCTATCA ATATTGATGA AGATCTTACA CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTGGGGOT GGATAAAAC ATCATGGAA 300 360

51

AACACHTCA TICKTAACA TOGGANANCA GIGGANATTA ATCTCACTA TGACTACCGT GICACCGGAG GAGITTCAGA ARGENGITI MAMGCAMGCA AGATACHTI TACCTCGGA TACCCAGA TGCATCGGA TGGATCAGAG CATAGTTIAG AAGGACAAAA ATTICCACT 600 GAGATSCALA TOTACTGOTT TGATGOGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA 660 GCAAAAGGGA AGTTAAGAGC TITATCCATT TIGTTTGAGG TIGGGACAGA AGAAAATTIG 720 GATTTCAAAG CGATTATIGA TEGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT TRACATOCAT TOATACTOTT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTTTGTG AAGTTCTTAC AATGCAACAA 960 10 TOTOGITATS TOATGOTGAT GGACTACITA CAAAACAATT TICGAGAGCA ACAGTACAAG
TICTOTAGAC AGGTGITITC CICATACACI GGAAAGGAAG AGATTCATGA AGCAGITIGI 1020 1080 AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTTACA TOGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCAGT TTTGTACCAG 1200 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTTGA CAGATGGCTA TCAAGACTTG 1260 15 GGTGCTATTC TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1220 TGCACTAATG GCITATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT AATCCTCAAC TTGATCTTTT CCCTGAATTA ATTGGAACTG AAGAAATAAT CAAGGAGGAG GAAGAGGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA 1500 ARCCARTCE GGARARAGGA ACCCAGATT TCTECCACA CRESCTACA TCCCATAGGA ACGARATACA ATRAGACCANA GARTALCCATA CACCACACA CACCATAGA ACGARATGA ATTCTCTGGA ARCGARATGA TCCCCARCA CARCAGACACA CACCATAGA ATTCTCTGGA ARCGATACA TCCCARTACA TCCCATACACA CACCATACA CACATAGACA TACATTAGAC 1560 20 1620 1686 ACAGAAAAAG ATATTTCCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAAACTG TTCTTAGATC TCCACATATG AACTTOTOGG GGACTGCAGA ATCCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860 25 AGTITATIGA CCAGITICAA GCTIGATACT GGAGCIGAAG ATTCTTCAGG CTCCAGICCC 1920 GCARCTTCTG CTATCCCATT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCCTCC 1980 GARANCCCAG AGRCANTARC ATATGATGTC CITATACCAG AATCTGCTAG AAATGCTTCC GAAGATTCAA CTTCATCAGG TTCAGAAGAA TCACTAGAGG ATCCTTCTAT GGAGGGAAAT GTOTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 30 AGCTTTCTCC AGACTAATTA CACTGAGATA COTGTTGATG AATCTGAGAA GACAACCAAG 2220 TOOTTTTOTO CAGGOCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAAATGCCA 2280 CATTATTOTA COTTTGCCTA CTTCCCAACT GAGGTAACAC CTCATGCTTT TACCCCATCC TCCAGACAAC AGGATTTGGT CTCCACGGTC AACGTGGTAT ACTCGCAGAC AACCCAACCG 2400 GTATACAATG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460 35 ACCCCTTTGT TGCTTGACAA TCAGATCCTC AACACTACCC CTGCTGCTTC AAGTAGTGAT 2520 TOGGCTTOC ATGCTACCC TOTALTICC ACTOCOACT TOTCATTOA ATCCATCOTT CTTCCTATC ATGCTACCC TTTCTTCCAT TITCCTTCC TTCCTTCC TAGTCATCAT TTCCCCATC TCCATCAGT TTCCTCAATC CTTCCACACA TTACTTCAGC TACCAGAGAT 2580 GATAAGGTGC CCTTGCATGC TTCTCTGCCA GTGGCTGGGG GTGATTTGCT ATTAGAGCCC 2760 40 AGCCTTGCTC AGTATTCTGA TGTGCTGTCC ACTACTCATG CTGCTTCAGA GACGCTGGAA
TTTGGTAGTG AATCTGGTGT TCTTTATAAA ACGCTTATGT TTTCTCAAGT TGAACCACCC 2820 2880 AGCAGTGATG CCATGATGCA TGCACGTTCT TCAGGGCCTG AACCTTCTTA TGCCTTGTCT 3000 GATAATGAGG GCTCCCAACA CATCTTCACT GTTTCTTACA GTTCTGCAAT ACCTGTGCAT GATTCTGTGG GTGTAACTTA TCAGGGTTCC TTATTTAGCG GCCCTAGCCA TATACCAATA 3060 45 CCTAAGTOTT COTTAATAAC COCAACTGCA TCATTACTGC AGCCTACTCA TGCCCTCTCT
GGTGATGGGG AATGGTCTGG AGCCTCTTCT GATAGTGAAT TTCTTTTACC TCACACAGAT 3120 3180 GGGCTGACAG CCCTTAACAT TTCTTCACCT GTTTCTGTAG CTGAATTTAC ATATACAACA TCTGTGTTTG GTGATGATAA TAAGGCGCTT TCTAAAAGTG AAATAATATA TOGAAATGAG 3300 ACTGAACTGC AAATTCCTTC TTTCAATGAG ATGGTTTACC CTTCTGAAAG CACAGTCATG 3360 50 CCCAACATGT ATGATAATGT AAATAAGTTG AATGCGTCTT TACAAGAAAC CTCTGTTTCC 3420 ATTTCTAGCA CCAAGGGCAT GTTTCCAGGG TCCCTTGCTC ATACCACCAC TAAGGTTTTT 3480 GATCATGAGA TINGTCANGT TOCAGAAAAT AACTITICAG TICAAGCTAC AGATACTGTC
TCTCAAGCAT CTGGTGACAC TTCGCTTAAA CCTGTGCTTA GTGCAAACTC AGAGCCAGCA 3 60 0 TOCTOTGACC CIGCITCIAG IGAAATGITA TOTCOTICAA CICAGOTOTI ATTITATGAG 3660 55 ACCTCAGCTT CTTTTAGTAC TGAAGTATTG CTACAACCTT CCTTTCAGGC TTCTGATGTT 3720 CACACCTICC TIANACTOT TOTTCCAGCT GIGCCCAGIG ATCCAATATT GGTTGAAACC 3780 CCCARACTTO ATAGASTRA TECTACASTS TIGCATCICA TECTATCASA TECTGCTICA AGTGAAAACA TGCTGCACTC TACATCTGTA CCAGTTTTTG ATGTGTCGCC TACTTCTCAT ATGCACTCTG CTTCACTTCA AGGTTTGACC ATTTCCTATG CAAGTGAGAA ATATGAACC 3960 60 4020 CITTICITAA AAAGIGAAAG TICCCACCAA GIGGTACCIT CITIGTACAG TAATGATGAG TTGTTCCAAA CGGCCAATTT GGAGATTAAC CAGGCCCATC CCCCAAAAGG AAGGCATGTA 4080 TTTGCTACAC CTGTTTTATC AATTGATGAA CCATTAAATA CACTAATAAA TAAGCTTATA CATTCCGATG AAATTTTAAC CYCCACCAAA AGTTCTGTTA CYGGTAAGGT ATTTGCYGGT ATTCCAACAG TIGCTICIGA TACATITIGTA TCTACTGATC ATTCTGTTCC TATAGGAAAT 4260 65 OGGCATGITG CCATTACAGC TGTTTCTCCC CACAGAGATG GTTCTGTAAC CTCAACAAAG 4320 TYGCTGTTTC CITCTAAGGC AACITCTGAG CYGAGTCATA GYGCCAAATC TGATGCCGGT 4380 TRACTOGOTO GROUTOAROA TOGTGACACT GATGATGATG GRGATGATGA TGATGATGAC AGAGGTAGTG ATGGCTTATC CATTCATAG TGTATGTCAT GCTCATCCTA TAGAGAATCA 4500 CAGGARAAGG TAATGAATGA TICAGACACC CAGGARAACA GICITATGGA TCAGAATAAT 4560 70 CCAATCTCAT ACTCACTATC TGAGAATTCT GAAGAAGATA ATAGAGTCAC AAGTGTATCC 4620 TORGROAGTO ARROTOSTAT GGACAGARGT CONGGUARANT CACCATORGO ARATGOGOTA 4680 TOTALBARC ACRATGRING BARRINGER BATCHETT AGAINSTIN TOTALGET 4740 CCTCTCAGCC CTGAATCTAA AGCATGGGCA GTTCTGACAA GTGATGAAGA AAGTGGATCA 4800 COGCAAGGTA CCTCAGATAG CCTTAATGAG AATGAGACTT CCACAGATTT CAGTTTTGCA 4860 75 GACACTAATG AARAAGATGC TGATGGGATC CTGGCAGCAG GTGACTCAGA AATAACTCCT 4920 GGATTCCCAC AGTCCCCAAC ATCATCTUTT ACTAGCGAGA ACTCAGAAGT GTTCCACGTT TCAGAGGCAG AGGCCAGTAA TAGTAGCCAT GAGTCTCGTA TTGGTCTAGC TGAGGGGTTG 4980 5040 GAATCCGAGA AGAAGGCAGT TATACCCCTT GIGATCGTGT CAGCCCTGAC TTTTATCTGT 5100 CTAGTGGTTC TTGTGGGTAT TCTCACTGT GTGTGGGGGAAT GCTCCAGGG TGCACCTGT TACTTAGAGG ACAGTACATC CCCTAGAGTT ATATCCACAC CTCCAACACC TATCTTTCCA 5160 80 5220 ATTTCAGATG ATGTCGGAGC AATTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA 5280 CATGCARGIA GIGGGITTAC TGARGARITI GAGACACTGA ARGRGITITA CCAGGRAGIG CAGGCIGIA CIGGITGACIT AGGIATITACA GCAGACACCI CCARCCACCA AGACACAACAA 5340 CACAAGAATC GATACATAAA TATCOTTGCC TATGATCATA GCAGGGTTAA GCTAGCACAG 5460 85 CTTGCTGARA AGGATGGCAR ACTGACTGAT TATATCRATG CCRATTATGT TGATGGCTAC 5520 AACAGACCAA AAGCTTATAT TOCTGCCCAA GGCCCACTGA AATCCACAGC TGAAGATTTC 5586 TGGAGAATGA TATGGGAACA TAATGTGGAA GTTATTGTCA TGATAACAAA CCTCGTGGAG

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PCT/US02/12476

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ARAGORAGGA GARARTOTA TCAGTACTGG CCTGCCGATG GGAGTGAGGA GTACGGGAAC 5700
TITCTGGTCA CTGGGAAGG TGTGCAAGTG CTGCCTATT ATACTSTGAG GAATTTTACT 5700
TAMGANACA CARARATRAA ARAGOGGTCC CAGRAAGGAG GACCCATGG ACGTGTGGTC 5820 ACACAGTATC ACTACACGCA GTGGCCTGAC ATGGGAGTAC CAGAGTACTC CCTGCCAGTG 5880 CIGACCTITG TGAGAAAGGC AGCCTATGCC AAGCGCCATG CAGTGGGGCC TGTTGTCGTC 5940 CACTOCAGTG CTGGAGTTGG AAGAACAGGC ACATATATTG TGCTAGACAG TATGTTGCAG 6000 6060 CACAMPCARC ACCIACCIAC METCARCATA STRUCCUTTOT TARRACACAT CONTICACAA AGAAATTATT TGGTACAAAC TGAGGAGCAA TATGTCTTCA TTCATGATAC ACTGGTTGAG 6120 OCCATACTTA GYARAGARAC TGAGGTGCTG GACAGTCATA TYCATGCCTA TGTTAATGCA 6180 CTCCTCATTC CTGGACCAGC AGGCAAAACA AAGCTAGAGA AACAATTCCA GCTCCTGAGC 6240 CAGTCAAATA TACAGCAGAG TGACTATTCT GCAGCCCTAA AGCAATGCAA CAGGGAAAAG 6300 AATOGAACTT CTTCTATCAT CCCTGTGGAA MGATCAAGGG TTGGCATTTC ATCOCTGACT GGGAAGGCA CAGACTACAT CAATGCCTCC TATATCATGG GCTATTACCA GAGCAATGAA 6360 6420 TICATCATTA CCCAGCACCC TCTCCTTCAT ACCATCAAGG ATTTCTGGAG GATGATATGG 6480 GACCATAATG CCCAACTGGT GGTTATGATT CCTGATGGCC AAAACATGGC AGAAGATGAA 6540 GACCATARTO CCCMACTORT GETTATRATH CHICAGAIGAC ARABCATGGA ABRUGATIGHA TITTOTTITAC GOCCAMATAA AGACGGCCT ATRAATATGA GACGACTETAA GGTCATCATA ATGACTGAAG AACACAAATG TCTATCATAT GAGGAAAAAC TTATAATTCA GGACTITATC TTAGAAGCTA, CACAGGAGA TTATGTATT GAAGTGAGGC ACTITCAGTS TCCTATAATGA 6600 6660 6720 CCAAATCCAG ATAGCCCCAT TAGTANAACT TITGAACTTA TAAGTGTTAT AAAAGAAGAA 6780 GCTGCCAATA GOGATGGGCC TATGATTGTT CATGATGAGC ATGGAGGAGT GACGGCAGGA 6840 ACTITICIONE CICIGACAC CCTIATGCAC CACTRAGAA AGGAGATIC CGIGGATGIT TACCAGGITAG CCAMANGAT CAATCIGATG AGGCAGGAG TCTTTGCTGA CATTGAGCAG 6900 6960 TATCAGTITC TCTACAAAGT GATCCTCAGC CTTGTGAGCA CAAGGCAGGA AGAGAATCCA TCCACCTCTC TGGACAGTAA TGGTGCAGCA TTGCCTGATG GAAATATAGC TGAGAGCTTA 7080 CAGTOTITAG TITAACACAG AAAGGGGTGG GGGGACTCAC ATCTGAGCAT TGTTTTCCTC 7140 TTCCTAMANT TAGGCAGGAA ANTONGTOTA GTTCTGTTAT CTGTTGATTT CCCATCACCT 7200 GACASTAACT ITCATGACAT AGGATTCTGC CGCCAAATTT ATATCATTAA CAATGTGTGC 7260 CHTTTTGCAA GACTTGTAAT TTACTTATTA TGITTGAACT AAATGATG AATTTTACAG TATTTCTAAG AATGGAATTG TGGTATTTT TTCTGTATTG ATTTTAACAG AAMATTTCAA 7380 TTTATAGAGG TTAGGAATTC CAAACTACAG AAAATGTTTG TTTTTAGTGT CAAATTTTTA 7440 TTTATAGAGG TTAGGAGATT CAMACIACAG MAMATUTTG TTTTAMGAG GAGATITTA GCGGGATTG AGCAGATTG LAGGTTGGT AGRANATHAG CITTTAMTAC AGTAGCAGAT MAMTAMAGCA CCCTCCCATA TGATATTCAA CATTITACAA CTGCGGTATT CACCHAAGAT AGRACHAGT COTTACTTAT TGHAMAGCT GCCCTAGGGT CTCCATGGGC CAMATITATA TTTATAGTG TAGATTITA TATTITACTA CTGAGTCAAG TITTCTAGTI CTGGGTAAT 7600 7560 7620

GTTTAGTTTA ATGACGTAGT TCATTAGCTG GTCTTACTCT ACCAGTTTTC TGACATTGTA

TTGTGTTACC TAAGTCATTA ACTITGTTTC AGCATGTAAT TTTAACTTTT GTGGAAATA

GAAATACCTT CATTITGAAA GAAGIITITTA TGAGAATAAC ACCITACCAA ACATIGIICA AATGGIITIT ATCCAAGGAA ITGCAAAAAT AAATATAAAT ATTGCCATTA AAAAAAAAA AAAA AAAAAAAA AAAAAAAAA

Seg ID NO: 180 Protein sequence: Protein Accession #: Bos sequence

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	ILFEVGTEEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
50	TOTVOWIVEK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LONNFREQOY	KFSRQVFSSY	300
	TGKEEIHEAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLIDGYQD	LGAILMNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPPE	420
	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNBAKTN	480
		GKGDVPNTSL					540
55		MNLSGTAESL					600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLOTNYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPHAFTP	SSROQDLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVEPL	VTPLLLDNQI	780
~	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSE	LFRHLHTVSQ	840
60	ILPQVTSATE	SDKVPLHASL	PVAGGDLLLE	PSLAQYSDVL	STTHAASETL	RPGSESGVLY	900
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	SLFSGPSHIP	IPKSSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
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10	LNASLQETSV	SISSTKOMPP	GSLAHTTTKV	FOHEISQVPE	NNPSVQPTHT	VEGASGETSL	1140
65	KPVLSANSEP	ASSDPASSEM	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	ADALTECTATA	1200
	AVPSDPILVE	TPKVDKISST	MLHLIVSNSA	SSEMMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
	TISYASEKYE	PVLLKSESSH	QVVPSLYSND	ELFQTANLEI	NOAHPPKORH	VFATPVLSID	1320
	EPLNTLINKL	INSDEILTST	KSSVTGKVFA	GIPTVASDTF	VSTDESVPIG	NGHVAITAVS	1440
70	PHRDGSVTST	KLLFPSKATS	ELSHSAKSDA	GLVGGGEDGD	TDDDGDDDDDD	DRGSDGLSIN	1500
/0	KCMSCSSYRE	SQEKVMNDSD	THENSLMDON	NPISYSLSEN	SEEDNRVISV	SSDSQTGMDR	1560
	SPGKSPSANG	LSQKHNDGKE	ENDIQTGSAL	LPLSPESKAW	AVLITSDEESG	SGQGTSDSLN	1620
	ENETSTOFSF	ADTNEKDADG	ILANGDSEIT	PGFPQSPTSS	VISENSEVER	VSEARASNSS	1680
	HESRIGLARG	LESEKKAVIP PISDDVGAIP	LVIVSALTFI	CEVATAGLET	TWRKCPUTAH	PILEDSISPR	1740
75		KHKNRYINIV					1800
13	TADSSNHPDN	FWRMINEHNV	AIDHSKVKLA	OPWENDOWN	MADGORRAG	NET PROVENO	1860
	QGPLKSTAED	TLRNTKIKKG	BAIAMIINDA	ENGREKCEQI	MINE CORRECT D	MLTAIGEOAN	1920
	VLATTIVENE	VHCSAGVGRT	SQAGRESORV	OCTORNOMIN	TROPI WILLIAM	ADILANGULE	1980
	AKKHAVGPVV	EAILSKETEV	CTITYLDSOID	DOLUMEGI AN	TEGEDINATES	COUNTOCON	2040
80	OTAL MOCKED	KNRTSSIIPV	PDSETHWIAN	CORCERN THA	CALMMAN	PUTTYOUPI.I.	2100
00	SAALIQUIKE	WDHNAOLVVM	TRECOMMAND	SORGIDITION	DINCPOPULT	I MADDINGT OF	2160
	NEDERICAL TOOLS	ILEATODDYV	TANDRESCHER	MDNDDSDISK	TERLISVIKE	RAAMRINGPMT	2220
	THE PROPERTY	GTFCALTTLM	HOTEKENSAD	VYOVAKNINI	MRPGVFADIR	OYOFLYKYII	2280
	CINCEPOPEN	PSTSLDSNGA	* LDDCNTARS	LESIA		4-4	
0.5	ODVOLKUDBN	* OT DEPOSITOR	WW POWAMPO	2000			

Seq ID NO: 181 DNA sequence Nucleic Acid Accession #: Bos sequence 7680

7740

7800

WO 02/086443 Coding sequence: 148-4518

	Courng sequ	ience: 140-4	1218				
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5	1	1	1	I	1	1	
3	CACACATACG	CACGCACGAT	CTCACTTOGA	TCTATACACT	GGAGGATTAA	AACAAACAAA AGGAGCCGCA	60 120
	CCCCCCACCCC	COSCAGACCG	TCTGGGAAATG	CHARTCCTAR	AGCGTTTCCT	CCCTTCCATT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
10	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAA	TTGGGGAAAG	300
10	AAATATCCAA	CATGTAATAG	CCCAAAACAA GAAACTTAAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360 420
	ADDRADAGA AA	THYPATACAC	TYCKS A A A C A	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
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1.5	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGITTAG	AAGGACAAAA	ATTTCCACTT	600
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	GATTTCAAAC	CGATTATTGA	TEGRACTOGRA	AGTGTTAGTC	CTTTTGGGAA	GCAGGCTGCT	780
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20							960 1020
	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	ACATTOTATO	ACAGTACAAG AGCAGTTTGT TCTTGTTACA	1080
	ACTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
0.5	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC AACCAAGCAT GCTACCCAAT	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
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	GGTGCTATTC	TCAATAATTT	AAAATACAGC	CACCAACTOCA	TTCTTCAGAT	AGTAGCCATA CCCTACTCAT	1320 1380
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35							1860
	AGTITATIGA	CCAGTTTCAA	GCTTGATACT CATCTCTGAG	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920 1980
	CHARACTTCIG	BORCASTARC	ATATCATCE	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
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	AAGAATOGAA	GCACAGACTA	CATCCCTGTG	TOCTATATOA	TOGGCTATTA	CCAGAGCAAT	3840
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WO 02/086443

WV 02/08/CH3 CT PATERDAM ACTOCOMA DISTORMO GACCHARTH SALE
ADDIALIZAR ACCURATE TATERDAM ACTOCOMA DISTORMO GACCHARTH SALE
ADDIALIZAR ACCURATE TATERDAM ACTOCOMA DISTORMO SALE
STRUTTAR ACCURATE TATERDAM ACTOCOMO TATERDAM TITORISMA SALE
ADDIALIZAR CONTROLLA SALE
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10 Seq ID NO: 182 Protein sequence: Protein Accession #: Bos sequence

	raccern no	ession #.	son nequence				
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25			VLI PESARNA				660
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			EFETLKEFYQ				900
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			EPINCESFKV				1320
			KTFELISVIK				1380
	MEQLEKENSV	DVYQVAKMIN	LMRPGVFADI	EQYQFLYKVI	LSLVSTRQEE	NPSTSLDSNG	1440
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40							

Seq ID NO: 183 DNA sequence Nucleic Acid Accession #: EOS sequence Coding sequence: 148-4494

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	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
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	GAGATGCAAA	TCTACTGCTT	TGATGCAGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
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	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
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65			TCAGGCTGAC				1140
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	TCCMGACAAC	AGGATTTGGT	TAGTAGCCAT	CACCOCCCC	PROCESOR	ance construction	2460
	GINTACAATG	MUUUCCAGTAA	TMGTMGCCAT	ONOTCICCIN	* TOOLCIMOC	TONOGGETTG	**00

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Seq ID NO: 185 DNA sequence Nucleic Acid Accession #: BOS sequence Coding sequence: 501-4514

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	TTATAATTG	AGATTTTTA	T ATTTTACTA	G TOTTACTOT	A CCAGTTTT	T GACATTGTAT	5160
	TTAGTTA	- LUNCOTAGT					

5

PCT/US02/12476

Seq ID NO: 186 Protein sequence: Protein Accession #: EOS sequence

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	LSILFEVGTE	ENLDFKAIID	GVBSVSRFGK	QAALDPFILL	NLLPNSTDKY	YIYNGSLTSP	120
		FKDTVSISES					180
	SYTGKEEIHE	AVCSSEPENV	OADPENYTSL	LVTWERPRVV	YDTMIEKFAV	LYQQLDGEDQ	240
15	TKHBFLTDGY	ODLGAILNNL	LPNMSYVLQI	VAICTMGLYG	KYSDQLIVDM	PTDNPBLDLF	300
	PELIGTEEII	KEEEEGKDIE	EGAIVNFCRD	SATNQIRKKE	POISTTTHYN	RIGTKYNEAK	360
	TNRSPTRGSE	FSGKGDVPNT	SLNSTSQPVT	KLATEKDISL	TSQTVTBLPP	HTVEGTSASL	420
	NDGSKTVLRS	PHMNLSGTAE	SLNTVSITBY	ERESLLTSPK	LIDTGAEDSSG	SSPATSAIPF	480
	ISENISOCYI	PSSENPETIT	YDVLIPESAR	NASEDSTSSG	SEESLKDPSM	EGNVWFPSST	540
20	DITAOPDVGS	GRESFLOTNY	TEIRVDESEK	TTKSFSAGPV	MSQGPSVTDL	EMPHYSTPAY	600
	FPTEVTPHAF	TPSSROODLY	STUNUVYSOT	TOPVYNEASN	SSHESRIGLA	EGLESEKKAV	660
	IPLVIVSALT	FICLVVLVGI	LIYWRKCFOT	AHPYLEDSTS	PRVISTPPTP	IFPISDDVGA	720
	IPIKHFPKHV	ADLHASSGFT	REFETLKERY	QEVQSCTVDL	GITADSSNHP	DMKHKNRYIN	780
	IVAYDHSRVK	LAOLAEKDGK	LTDYINANYV	DGYNRPKAYI	AAQGPLKSTA	EDFWRM I WEH	840
25	NVEVIVMITN	LVEKGRRKCD	OYWPADGSEE	YGNFLVTOKS	VOVLAYYTVR	NFTLRNTKIK	900
	KGSOKGRPSG	RVVTQYHYTO	WPDMGVPEYS	LPVLTFVRKA	AYAKRHAVGP	VVVHCSAGVG	960
	RTGTYTVLDS	MLQQIQHEGT	VNIFGFLKHI	RSORNYLVOT	EBOYVFIHDT	LVEAILSKET	1020
	EVLDSHIHAY	VNALLI PGPA	GKTKLEKOFO	LLSOSNICOS	DYSAALKQCN	REKNRTSSII	1080
	PVERSEVGIS	SLSGEGTDYI	NASYINGYYO	SHEFIITOHP	LINTIKOPWR	MINDHNAQLV	1140
30	VMIPDGONMA	EDEFVYWPNK	DEPINCESFK	VTLMABEHKC	LSNEEKLIIQ	DFILEATODD	1200
	YVLEVRHFOC	PKWPNPDSPI	SKTFELISVI	KEEAANRDGP	MIVHDEHGGV	TAGTFCALTT	1260
		VDVYQVAKMI					1320
	GAALPDGNIA						

35 Seq ID NO: 187 DNA sequence Nucleic Acid Accession #: BOS sequence Coding sequence: 148-4632

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40	Ť	11	i ·	ĭ	ī	ĭ	
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	CARRADARC	ATTTOCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCOGCA	120
	CGGCGAGGGG	CCGCAGACCG	TOTGGARATG	CGAATCCTAA	AACGTTTCCT	CGCTTGCATT	180
	CACCECCECE	GTGTTTGCCG	CCTGGATTGG	CCTAATCCAT	ACTACAGACA	ACAGAGAAAA	240
45	CTTCTTGAAG	AGATTGGCTG	GTCCTATACA	GCAGCACTGA	ATCARARAR	TTGGGGGAAAG	300
10	ABATATOCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CARCULARTO	TGAATCTTAA	GARACTTARA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGBAATTA	ATCTCACTAA	TGACTACOGT	480
	GTCAGCTGAG	GAGTTTCAGA	ARTGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
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• •	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTCAGGA	AGCAGT CAAA	660
	GGRAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CCATTATTCA	TOGAGTOGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
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55	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
		TCTCTGAAAG					960
	TOTGOTTATG	TCATGCTGAT	GCACTACTTA	CARARCARTT	TTCGAGAGCA	ACAGTACAAG	1020
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	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
60	TOGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	CCTTATATOG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	ARTCCTGRAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG	1440
65	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
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	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
70		CAGCCTCTTT					1800
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75	CARGATTCAA	CTTCATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
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	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTTCTG	CAGGCCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATICTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
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	GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
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0.5	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	2640
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	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	2760
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15	CHCHCACCCA	COCTGGAGTG	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCCTCTCCCT	3720
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25	GANGCTACAC	AGGATGATTA GCCCCATTAG	TOTACTTORM	CAACTTATAA	CTCTTATAGA	AGAAGAAGCT	4320
23	COCALTAGGG	ATGGGCCTAT	GATTGTTCAT	GATGAGCATG	GAGGAGTGAC	GGCAGGAACT	4380
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30	CAGTTTCTCT	ACAGAGTGAT ACAGTAATGG	CCTCAGCCTT	GTGGGCACAA	OGCAGGAAGA	CACCETACAG	4620
30	ACCTETETEG	AACACAGAAA	COCCMOCATIO	COLCULATION	TOLOGRAPHOT	TTTCCTCTTC	4680
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	TACTTTAATC	ACGTAGTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTTCTGA	CATTGTATTG	5340
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	CCTTTTTATC	CAAGGAATTG	CAAAAATAAA	TATAAATATT	GCCATTAAAA	AAAAAAAAA	5460
45	AAAAAAAAA	AAAAAAAAA	A				
	Seq ID NO:	188 Protein cession #: 1	n sequence:				
	Procern wo	cession #1	nos nequenc	•			
50	1	11	21	31	41	51	
	1	1	1	1	1		60
	MRILKRFLAC	IQLLCVCRLD TQVNVNLKKL	WANGYYRQQR	KLVEBIGWSY	TGALNQKNWG	RKYPTCNSPK	120
	OSPINIDEDL	GKCNMSSDGS	KLOGMUKISP	LEMOTYCEDA	DRESSPERAV	KGKGKLRALS	180
55	TT DDUCTOOM	T.DEVATIDAY	BSASBECKUY	ALDEPTIANI.	LPNSTDKYYI	YMGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL CSSEPENVQA	AVECEVLINQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSSY	300
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00	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
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							720
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33							900
							960
	RUTUMITALV	RKGRRKCDOY	WPADGSEEYG	NFLVTQKSVQ	VLAYYTVRNF	TLENTKIKKO	1020
70	SOKGRPSGRV	VTOYHYTOWP	DMGVPEYSLP	VLTFVRKAAY	AKRHAVGPVV	VHCSAGVGRT	1080
70	GTYIVLDSML	QQIQHEGTVN	IFGFLKHIRS	TLEBRI BCBC	TI SAHOW DI	PGLTDPPTSA	1200
	COUNCETTI-C	OWNTOOSDAS	AVPROCABER	NRTSSITPVE	RSRVGISSLS	GEGTDYINAS	1260
	YIMCYYOSNE	PILITOHPLLH	TIKEFWRMIW	DHNAOLVVMI	PDGONMARDE	FVYWPNKDEP	1320
	INCRSEKVIL	MARRHKCLSN	REKLIIODFI	LEATODDYVL	EVRHPQCPKW	PNPDSPISKT	1380
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Seq ID NO: 189 DNA sequence Nucleic Acid Accession #: NM 002820 80 Coding sequence: 304..831

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PELISVIKEE AANROOPHIV HOSHGOVTAG TFCALITIME CLEKENSVOV YQVARMINIM 1440 RPGVFADIEQ YQFLYKVILS LVGTRQEENP STSLDSNGAA LPDCNIAESL ESLV

	WO 02/						
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5		GCGGGGGGTC					420
5	CTTCACCATC	TCCTCCATGA TGATCGCAGA	AATOCACACA	CCTGAAATCA	GAGCTACCTC	GGAGGTGTCC	480 540
	CCTAACTCCA	AGCCCTCTCC	CAACACAAAG	AACCACCCCG	TCCGATTTGG	CTCTGATGAT	600
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		TTTTTCATTT					1260
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	CCTOGCATGC GCTATCGTGG GCGGCCACGG GCCAACCTGT GGCCCGGAAG GTGGATTTGC	GCCTGGTGGT AGGCCTTTCT AGAGCGCGGC CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG	CACCOCGGAC GGCCGGGGCT GGAGCTGGCC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC	GACTTTGGTT GTGACCAGCG CGCAGGCACA CCGGCCCGCC GGATTCCGGG GAGGCCCAAC	ACTGCCCGCG TGTCCCTGCT GCATCCCCAC GTGGCCCCTC AGGCCGCTGCT TAAGCTGCTT	ACCICGATGAG GGTCAACGGT GGGCCTCCAC ATCICCTCCCC GGCCGGAGAC CCGGGAGCTG	120 180 240 300 360 420
45 50	CCTCGCATGC GCTATCGTGG GCGGCCACGG GCCAACCTGT GGCCCGGAAG GTGGATTTGC CTGGGCAGGG	GCCTGGTGGT AGGCCTTTCT AGAGCGCGGC CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG CCCCCACGCA	CACCOCGGAC GGCCGGGGCT GGAGCTGGCC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC CGCGGACGGC	GACTTTGGTT GTGACCAGCG CGCAGGCACA CCGGCCCGCC GGATTCCGGG GAGGCCCCAAC CACCAGCACC	ACTGCCCGCC TGTCCCTGCT GCATCCCCAC GTGGCGCCTC AGGCGGTGGC TAAGCTGCTT TGCACGTGCT	ACOCGATGAG GGTCAACGGT GGGCCTCCAC ATCGCTGCTC GGCCGGAGAC CCGGGAGCTG CCCAGGCCTG	120 180 240 300 360 420 480
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	CCTCGCATGC GCTATCGTGG GCGGCCACGG GCCAACCTGT GGCCCGGAAG GTGGATTTCC CTGGGCAGGG TGCCAGGTGT CACCGCGGTC GTGGAGCCCG	GCCTGGTGGT AGGCCTTTCT AGAGGGCGG CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG CCCCACGCA TCGCCGAGGC TGGGTGGCTG ACGCCGGGGC	CACCOCGGAC GGCCGGGGCT GGAGCTGGC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC CGCGGACGGG GCTGCAGGCC CACTTGGCTG CACCTGGGCC	GACTTTGGTT GTGACCAGGG CSCAGGCAGC COGCCCGGG GAGTCCCGGG GAGGCCCAAC CACCAGCAGG TATGGGGTGC GAGGCCCCG GAGGCCCCG CCCTTGTCCC	ACTGOCCGOC TGTCCCTGCT GCATCCCAC GTGCCGCCTC AGGCGGTGGC TAAGCTGCTT TGCACGTGCT GCCTTTACCG GCCACGCCTT GCCACGCCTT	ACCOGATGAG GGTCAACGGT GGGCTCCAC ATCGCTGCTC GGCCGGAGAC CCGGGAGAC CCGGGAGCTG ACTGCCGCTG CGCCTGCGCCC GGCGTGGACA GGGGTGGACA	120 180 240 300 360 420 480 540 600 660
50	CCTCGCATGC GCTATCCTGG GCGGCCACCGG GCCACCTGT GGCCCGGAAG GTGGATTTCC CTGGGCAGGG TGCCAGGTGT GAGCGCGTGT GAGCGCGGGGG GAGGCCTTCG	GCCTGGTGGT AGGCCTTTCT AGAGCGCGGC CCGAGGGGCC GCTTCTTCCT CTCAGGTGCG CCCCACGCA TCGCCGAGGC TCGCCGGGC TGGGCCTGAG TCGCCCGGGC	CACCOCGGAC GGCCGGGGCT GGAGCTGGC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC CGCGGACGGG GCTGCAGGCC CACTTGCGGG CGCCTGGGGC CACTTGCGGGC CACTTGCGGCC CACTTGCGGGC CACTTGCGGGC CACTTGCGGCC CACTTGCGGGC CACTTGCGGCC CACTTGCGCGC CACTTGCGCGC CACTTGCGCGC CACTTGCGCGC CACTTGCCGCC CACTTGCCGCC CACTTGCCCC CACTTCCCC CACTTCCCC CACTTCCCC CACTTCCCC CACTTCCCCC CACTTCCCCC CACTTCCCCCC CACTTCCCCCC CACTTCCCCCC CACTTCCCCCCC CACTTCCCCCCC CACTTCCCCCCCC	GACTTTGGTT GTGACCAGGC GCCGGCCGGC GGATTCCGGG GAGGCCCAAC CACCAGCAGG TATGGGGTGC GAGGCCCCG CCCTTCTCCC CCGCACATGT	ACTGOCCGOC TGTCOCTGCT GCATOCCAC GTGGOGCCTC AGGCGGTGGC TAAGCTGCTT TGCACGTGCT GCGTTGCCTT GCCACGGCCT CCGCTCACCG	ACCOGATGAG GGTCAACGGT GGGCTCCAC ATCGCTGCTC GGCCGGAGAC CCGGGAGAC CCGGGAGCCTG ACTGCCGCTG ACTGCCGCTC GGGGTGGACA CGTGTCCGGG	120 180 240 300 360 420 480 540 600 660 720
	CCTCGCATGC GCTATCCTCG GCGCCACGG GCCAACCTGT GGCCGGGAGG GTGGATTTCC CTGGGCAGGG TGCCAGGGTGT GACCGCGGTG GACGCCTTCG GCCCTGGCGC GGCGACCCCG	GCCTGGTGGT AGGCCTTTCT AGAGGGGGC CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG CCCCACGCA TCGCCGAGGC TCGCCGGCGC TCGGCCGGGC TCGGCCTGGA GGCTCGGG GCTACCCAGG GCTACCCAGG	CACCOCGGAC GGCCCGGGGCT GGAGCTGGGC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC CGCGGACGGG GCTGCAGGCC CACTTGCGGG CACCTGGCGG CACCTGCGGC CACCTGCGGC CACCTGCGGC CACCTGCGGC CACCTGCGGC CACCTGCGGC CACCTGCGGC CACCTGCCCC	GACTITOSTE GTGACCAGG CGCCGGCCCA CCGGCCCGACCAG GAGTCCCGAGCAGG CACCAGCAGG CACCAGCAGG CAGGCCCCG CCTTCTCCC CGGGACATGT CCGGGCCACA ACCGGCGCACA	ACTGCCCCCC TGTCCCTAC TGTCCCCAC GTGCCCCTC AGGCGGTGGC TAAGCTGCTT TGCACGTGCT GCTTTACGCG CCCTGCCTT GCCACGCCT CCCCTCACCG GCGGTGACAC GCGGTGACAG GCGGTGACAG	ACOGATGAS GOTCAACGOT GOGCTOCAC ATOCCTGCTC GOCCGAGAGAC CCCAGGCCTG ACTGCCGCTG ACTGCCGCTG GCCGGTGGACA COTGTCCGCG GCGGTGGACA COTGTCCGGCG CCAGGCTGATG CCCAGGCTGATG CCCCGCGCGCGCTGATG CCCCGCGCGCGCTGATG CCCCGACGCT	120 180 240 300 360 420 480 540 600 660 720 780 840
50	CCTCGCATGC CCTATCCTCG CCTATCCTCG CCCAACCTGT GGCCGGAAG GCCAACCTGT GGCCGGAAG TGCCAGCTGT AACCCGGTG GACGCCTCG GCCTGCCCCC GCCTGCCCCCC TTCTCTTGCT	GCCTGGTGGT AGGCCTTTCT AGNACGCGGC CCCAAGGGCCG CCTCACGTCCG CCCCACGCA TCGCCGACGCC TCGCCGGCC TCGCCTCGCGGC TCGCCTCGAC GCTCCTCGAC GCTCCTCGAC GCTCCTCGAC CTTCGCAAGC CTTCGCAAGC CTTCGCAAGC CTTCGCAAGC CTTCGCAAGC CTTCGCAAGC CTTCGCAAGC	CACCOCGGAC GGCCGGGGGGGGGGGGGGGGGGGGGGGGG	GACTITOSTE GTGACCACCE GGCAGGCACA CCGGCCCAC GGATITCCGG GAGGCCCAA TATGGGTIGC GAGGCCCCAC CCTTCTCCC CGGCACATGT CCGGCCACA ACCGCCCCC CTGCCCGTCC	ACTGCCGCC TGTCCCTCCT TGTCCCTCCT GTGCCCCCC GTGCCCCCT AGGCCGTGCCT TGCACGTGCCT GCCATGCCTT GCCACGGCCT CCCCTCACAG CCCGCTCACAG TCACCGCT CCGCTCACAG TCACCGCCC TACCGCT TACCGCCC TCCCCT TACCGCCC TCCCCCCCC TCCCCCC TCCCCCC TCCCCCC TCCCCCC	ACOCGATICAG GOTTCAACGOT GOGOCTCCAC ATCOCTCCTC GOCCGAGACT CCCAGGACT CCCAGGACT CCCCTCCCCC GCCTCCCCC GCCTCCCCC CCGCTCAGCC CCCAGGACAC CCCCAGCACC CCCCAGCCC CCCCAGCCC CCCCCCCC	120 180 240 300 360 420 480 540 600 720 780 840 900
50	CCTCGCATGC GCTATCCTCG GCTATCCTCG GCCCGGAAG GCCAACCTGT GCCCGGAAG TGCCAGCTCC GAGCGCTCG GCCCTCG GCCCTCG GCCCCCC TTCTCTTGCT GCCCACCTCT	GCCTGGTGT AGGCCTTTCT AGGACGGC CCTAGGGCCG CCTCTCTCCT CCCCACCA TCGCCGACGC ACCCCACCCA TCGCCGACGC TCGCCCGCGC TCGCCCTGGA GCTCCTGGA GCTACCCCAC CCTGGGACGC TCGGGACGC TCGGGACGC TCGGGACGC TCGGGACGC TCGGGACGC TCGGGACGC TCGGGACGC TCCGGACGC TCGGGACGG	CACCOCGGAC GGCCGGGCC GGCGGGGCC GGCGAGAGATG GGAGGAGCAC GGCGGACGGG CCCGTGGGG CCCGCGGACGGG CCCCTGGGGC CACTTGGCGG CACTTGCGGC CACTTGCGCT TGTGCCTCCC GCTGCATCAG CCTGCACCAC CCTCCACC CCTGCACCAC CCTGCACCAC CCTCCACC CCTCCCC CCTCCACC CCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCC	GACTITOGIT GTGACCAGCE GGCAGGCACA COGGCCGCC GGATTCCGGG GAGGCCCAAC TATGGGSTGC GAGGCCCCG CCCTTCCCC CGCGACATGT CGGGGCCACA ACCGCGCCCC CTGCGCGTCC	ACTICOCICCI TGTCOCTCCT TGTCOCTCCT GCATCCCAC GTCCOCCTC AGCCOGCTC AGCCOGTCGC TCAACTCCTT TGCACGTCT TGCACGTCCT GCCACGCCT CCCCTCACCG CCCTCACCG CCCTGACAG CCCGGTGAAG CCGGTGAAG CCGCTGAAG ACGACTGGA	ACOCGATCAG GOTCAACGOT GOGCCTCCAC AT COCTGCTC GGCCGGAGAC CCCGGAGACTC CCCAGGCCTG ACTGCCGCTG GCCTGCGCC GCGCTGGACA CTGCCGCTG GAGCTGACA CTGCCGCTC CCCGAGCCTC CCCGAGCCTC CCCGAGCCTC CCCGAGCCT CCCAGCCTCAGAC CCCGAGCCT CAGCCTCGAGC	120 180 240 300 360 420 480 540 600 660 720 780 840
50	CCTCGCATAC CCTCACATG CCGCCACG CCCACCTG CCCCACG CCCCACG CCCCACCTG CCCCACG CCCCCACG CCCCCACG CCCCCCACG CCCCCCCC	GCTGGTGGT AGAGGGGG CGAAGGGGGG CGAAGGGCGG GCTCTTCCT CTCAGGTGCG CCCCACGCA TGGCTGGCT TGGCTGGCT TGGCTGGCT TGGCTGGAGG CTGGCTGGAGG CTGGGCTGAG GCTCCTGGA GCTCCTGGA GCTCCTGGA GCTCCTGGA AGGCCCCTGC CCCAGGATGG AGGTCCCCTG AGGCCCCTGC CCCAGGATGG AGGTCCCCTG CGAGAAACCA	CACCOCGGAC GGCGGGGCT GGAGGTGGCC CCCCGTGGGT TGGCAAGATC CGCGGACGAGCCC CACTTGGCTC CGCGGCCCCACTTGGCTC CGCGCTGGGC CACTTGGCTC CACTTGGCTC CACTTGCGCC CACTTGCGCC CACTTGCGCC CACTTGCACCTA TGTGCCTCCC CTGCATCGACCTT TGACCCCACT AGCACTATA	GACTITOGIT GTGACCAGCG GGCAGGCACA COGGCCCGC GGATTCCOGG GAGGCCCAAC CACCAGCAGG CAGGCCCCCG COGTAGCAGG CGGCACAGG CGGCACAGG CGGCACAGG CGGCACAGG CGGCACAGG CGGCACAGG CGGCACCC CTGCACCGC CTGCACCGC CCCTTAGTACCC	ACTIOCOCICE TOTICOCTICT TOTICOCTICT GCATCCCAC GTGGCGCCT AAGCTGCT TGCACGTGCT TGCACGTGCT GCCACGCCT GCCACGCCT CCCTGACAGC CCCTGACAGC CCCTGACAGC CCCTGACAGC CCAGACCTGGA TCACCGGGCC ACGACCTGGA TCCTGGAAAGG	ACOCGATCAG GOTCAACGOT GOGCCTCCAC ATCOCTCGTC GOCCOGGAGCT CCCAGGCOTG CCCAGGCOTG CCCAGGCOTG CGCTCCGCC CGCTCCGCC CGCTCCGCC CGCTCCGCC CGCTCCGCC CGCTCCAGCC CCCCAGCCT CCCCAGCCT CCCCACAGCC CTCCAACAGC CTCCAACAGC CTCCAACAGC CTCCAACAGG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50	CCTOGONTOC COTATOCTOS CCGACCOS CCCAACCTOT GGCCGGGAAG GTGGATTTOC CTGGCCAGGTOT CACCCTGCGGC GACCCTTCC GCCTGCGGC GCCCTGCGGC TTTCCTTGCT GCCAGGCTTC CCCAGGCTTC CCCAGGCAGCTTC CCCAGGCAGCTTC CCCAGGCAGCTTC CCCAGGCAGCTTC CCCAGGCAGCTTC CCCAGGCAGCTTC CCCAGGCAGCTTC CCAGGCAGCTTC CCCAGGCAGCTTC CCCAGGCAGCTTC CCAGGCAGCTTC	GCTGGTGGT AGGGCGGC AGGGCGGC CGAAGGCCGG CCCAAGGGCGGC TGGCTGGCTGAG AGGCCGGGC TGGCCTAAG GCTACCCAAG AGGCCCAAG CCCACGAAG CCCACGAAG CCCACGAAG CCCACGAAG CCCACGAAG CCCACGAAG CCCACGAAG AGGTCCCCTG AGGCCCACG AGGTCCCCCACG CCCACGAAG AGGTCCCCTG CCACGAAGAACC CCCACGAAGAACC CCCACGAAGAACC CCCACGAAGAACC CCCACGACC CCCACGCCCAC CCCACCCCCAC CCCACCCCCAC CCCACCCCCAC CCCACCCCCC	CACCOCGGAC GGCCGGGCCT GGACCTGGCC CCCCGTGGGT TGGCAAGATO GGAGGACCTC GCCCTGGGC CACTTGGCCC CACTTGGCCC CACTTGGCCC CACTTGGCCC CTGCACGAC CTGCACGAC CTGCACGAC CTGCACCAC AGCACTACC AGCACT	GACTITOGTE GTGACCAGG GTGACCAGG GGATCCGG GAGCCCAAC CACCAGCAGG GAGGCCCAAC CACCAGCAGG GAGGCCCCAG CACCAGGAGG CACCAGGAGG CACCAGGAGG CACCAGGAGGCCACA ACCGGCGCCACA TGCGCCGCGG CTGCACCAGG CTGCACCAGG CTGCACCAGG CTGGACCCCG CTGGAACCCT CTGGAACCCT CTGGAACCCT TGGAGCACAG	ACTIOCOCOC TOTOCOCOC TOTOCOCCC TOTOCOCCC TOTOCOCCC TAGCCOTTOC TAGCCOTTOC TOCOCCC CCCTTACOC CCCTTACOC CCCTTACOC CCCTTACOC CCCTTACOC CCCTTACOC CCCTTACOC TCCCCCC TCCCCC CCCTTACOC CCCTTACOC TCCCCCC CCCTTACOC TCCCTGAAO TCCCTGAAO TCCCTGAAO TCCCTGAAO TCCTTGAAC TCCTTGAAC TCCTTGAAC	ACOCGATCAG GOTCAACGOT GOGCCTCCAC AT COCTGCTC GOCCGAGACAC CCCAGGCCTA ACTCCCCCAC ACTCCCCCC CCCAGGCCTA ACTCCCCCC CCCAGGCCTA ACTCCCCCC CCCAGGCCTAC CCCCAGCCTAC CCCCAGCCTAC CCCCACACAC CTCCCACACAC CTCCCACACACA	120 180 240 300 360 420 600 660 720 780 840 900 960 1020 1080
50	CCTOGOATME COTATOCISIS GCGCACCAC GCGAACCTGT GCCCGGAAG GTGGATTTOC GCCCTGCGCC GAGGCCTTCG GCCCTGCGCC TTCTCTTGCT GCCCAGCTTC GCCCAGCTTC GCCCAGCTTC GCCCAGCTTC GCCCAGCTTC GCCCAGCTTC GCCCAGCTTC GCCAGCTTC GCAGCAGCTC GCAGCAGCTC GCAGCTCC GCAGCTTC GCAGCTCC GCAGCTTC GCAGCTCC GCAGCTTC GCAGCTCC GCAGCTTC GCAGCTCC GCACCTCC GCACCTCC GCACCTCC GCACCTCC GCACCTCC GCACCTCC GCCCCC GCCCCCC	GCTGGTGGT AGGGCTGGT AGGGCGG CGAAGGGCGG GCTTCTTCCT CTCAGGTGCG CCCCACACAC TCGCCGAGGC TGGGTGGTGG GGGCTGAG GGTTCTGG GGGCTGAG GCTACCCAG CTTGGGAGGC CCCAGGATG AGGTCCCCAG AGGCCCAG AGGCCCAG AGGCCCAG AGGCCCAG AGGCCCAG AGGCCCAG AGGCCCAG AGGCCCAG AGCTCTGGGC CCAGGACCCAG ACCTCTGGGC CCCAGGACCCAG ACCTCTGGGC CCTGGGGCCAG ACCTCTGGGC CCTGCAGGCA	CACODOGAC GGCCTGGCC GGACTGGCC CCCOTGGGT TGGCAAGATO GGAGGACCC CCCOTGGGC CACTTGGCCA CGCCTGCGCC CACTTGGCCA TGTGCCCCC CCTGCATCAG CCTGCACCAC TGAGCCCCC TGAGCCCC TGAGCCCCC TGAGCCCCC TGAGCCCCC TGAGCCCCC TCAGCTGCCCC CCGCTGGGCC CCGCTGGGCCCCC TGAGCCCCCC CCGCTGGGCCCCC CCGCTGGGCCCCCCCCCC	GACTITIOGTE GTGACCACCA GTGACCACCA GCGACCACCA GCGATTCOGG GAGGCCCAC CACCACCACCA CACCACCACCA CACCACCACC	ACTIOCOCOC TOTICCOCOC TOTICCOCC TOTICCOCC TOTICCOCC TOTICCOCC TOTICCOCC TOCOCOCC TOCOCOCC COCCTACOS COCCACA COCCACA TOCOCOCC TOCOCCC TOCCC T	ACCCARTAGA GGCCCARTAGA GGCCCTCCAC AT COCTOCTC GGCCCGAGGCTC GCCCAGGCCTC ACTCCCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCC GCCTCCCAGGC GCCCCCAGGC GCCCCAGGCC GCCCCAGGC GCCCCCAGGC GCCCCCAGGC GCCCCCCCC	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200
50	CCTCGCATEC CCTCGCATEC CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	GCTGGTGGT AGGGCTGT AGGGCTGT AGGGCTGC CCGAGGGCCG GCTCTTCCT CCAGGTCCG CCCCACCA TCGCCGAGGC TCGCCGAGGC TGGCCCAGGC TGGCCCTGGA GCTCCTGGA GCTACCCGAG CTAGGAGCC CCAGGATGG AGGCCCAG AGGCCCAG AGGCCCAG AGGCCCAG AGGCCCAG AGGCCCAG CCCAGGATGG AGCCCCAGGCCCAG CCCAGGATGG AGCCCCAGGATGG AGCCCCAGGCCCAG CCCAGGATGGAGCC CCAGGATGGAGCC CCAGGATGGAGCC CCAGGATGGAGCC CCAGGATGGA	CACCOGGGC GGCCGGGCT GGCAGGGCT GGCAGGAGTG GGCGAGGGG GCCCGGGGCC GCCCTGGCC CACTTGGGC CACTTGGGC CACTTGGGC CACTTGGGC CACTTGGGC CACTTGGGC CACTGCACCT TGGCCCCC TGGACCTA AGCACCT AGCACCT AGCACCT TGGGCCCC TGGGTGGCC TGGGTGGCC TGGGTGGCC TGGGTGGCC TGGGCCCT TGGGCCCCT TGGGCCCT TGGCCCT TGGCCCT TGGCCCT TGGCCCT TGGCCCT TGGCCCT TGGCCCT TGGCCCT TGGCCCT TGGCCCT TGCCCT TGCCCT TGCCCT TGCCCT TGCCCT TGCCCT TGCCCT TGCCCT TGCCCT TGCCCT TGCCT	GACTITIOGTE GTGACCACCA GTGACCACCA GCGACCACCA GCGATTCOGG GAGGCCCAC CACCACCACCA CACCACCACCA CACCACCACC	ACTIOCOCOC TOTICCOCOC TOTICCOCC TOTICCOCC TOTICCOCC TOTICCOCC TOTICCOCC TOCOCOCC TOCOCOCC COCCTACOS COCCACA COCCACA TOCOCOCC TOCOCCC TOCCC T	ACCCARTAGA GGCCCARTAGA GGCCCTCCAC AT COCTOCTC GGCCCGAGGCTC GCCCAGGCCTC ACTCCCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCC GCCTCCCAGGC GCCCCCAGGC GCCCCAGGCC GCCCCAGGC GCCCCCAGGC GCCCCCAGGC GCCCCCCCC	120 180 240 300 360 420 480 600 660 720 780 840 900 1020 1080 1140
50	CCTOGCATME COTATOCTISE COGACCACE COCACACT COCACAC COCACACT COCACAC COCACAC COCACAC COCACAC COCACAC COCACAC COCACAC COCACAC COCACA	GCTGGTGGT AGAGCGCGG GCTTGTTCT AGAGCGCGG GCTTGTTCT CCTCAGGTGGCG GCCCACDCA TGGCCTAGAG TGGCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG AGATCCCCAG AGACAACCA CCAGGATGG AGATCCCTGAG CCAGGATGG AGATCCCCAG CCAGGATGG AGATCCCCAG CCAGGATGG AGATCCCCAG CCAGGATGG AGATCCCCAG CCAGGATGG AGATCCCCAG CCAGGCCAG CCAGGATGG AGATAACGT CCATGTTGCA AAATAACGT	CACOOGGGAC GGCOGGGCT GGCACAGCT GGCAAGAT GGCAAGAT GGCAAGAT GGCAAGAT GGCAAGAT GGCATCAGGCC GCCGCTGGCC GCCGCTGGCC GCTGCATCAGCC GCTGCATCAGC GCTGCATCAG GCTGCATCAG GCTGCATCAG GCTGCATCAG GCTGCATCAG GCTGCATCAG GCTGCATCAG GCTGCATCAG GCTGCATCAG GCTGCATCAC GCTGCATCAC GCTGCATCAC GCTGCATCAC GCTGCATCAC GCTGCATCAC GCTGCATCAC GCTGCATCAC GCTGCATCAC GCTGCCTACCCT GCCTAGCCT GCCTAGCCT GCCTAGCCT GCCTAGCCT GTCCTTCC	GACTITIOGTE GTGACCACCA GTGACCACCA GCGACCACCA GCGATTCOGG GAGGCCCAC CACCACCACCA CACCACCACCA CACCACCACC	ACTIOCOCOC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOCACAC TOCACACAC TOCACACAC TOCACACAC TOCACACAC TOCACACACAC TOCACACACAC TOCACACACACACACACACACACACACACACACACACACA	ACCCARTAGA GGCCCARTAGA GGCCCTCCAC AT COCTOCTC GGCCCGAGGCTC GCCCAGGCCTC ACTCCCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCC GCCTCCCAGGC GCCCCCAGGC GCCCCAGGCC GCCCCAGGC GCCCCCAGGC GCCCCCAGGC GCCCCCCCC	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200
50	CCTOSCATUSE COTATICOTORIO COTATICOTORIO COCACO GOCCACO	GCTGGTGGT AGACGTGGT AGACGTGGT AGACGTGGT CTGAGTTCGT CTGAGTTCGT CTGAGTTCGT TGGTCGAAGCT TGGCCGAAGCT TGGCCGAAGCT TGGCCTGAA CGTCACCAGAACCT CCCAGACAACA CTGGCAACACA CTGGCAACAC CCCAGACATGA AGGTCCCTGA AGGTCCCTGA AGGTCCCTGA AGGTCCCTGAACCA CCAGACATGA CCTGTGAGCC CAGACATGA CCTGTGAGC CCAGCCTTGAA	CACCOGGAC GACCOGGAC GACCOGGAC GACCOGGAC GACCOGGAC CACCOGGAC GACCOCCAGAC CACCOGGAC CACCAC CACCAC CACCAC CACCAC CACCAC CACCAC	GACTITIOGTE GTGACCACCG GTGACCACCA CCGCCCCCC GGATTCCGG GAGGCCCAC TATGGGTGC CACCACCACCACCACCACCACCACCACCACCACCACCA	ACTIOCOCOC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOCACAC TOCACACAC TOCACACAC TOCACACAC TOCACACAC TOCACACACAC TOCACACACAC TOCACACACACACACACACACACACACACACACACACACA	ACCCARTAGA GGCCCARTAGA GGCCCTCCAC AT COCTOCTC GGCCCGAGGCTC GCCCAGGCCTC ACTCCCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCC GCCTCCCAGGC GCCCCCAGGC GCCCCAGGCC GCCCCAGGC GCCCCCAGGC GCCCCCAGGC GCCCCCCCC	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200
50 55 60 65	CCTOSCATUSE COTATICOTORIO COTATICOTORIO COCACO GOCCACO	GCTGGTGGT AGAGCGCGG GCTTGTTCT AGAGCGCGG GCTTGTTCT CCTCAGGTGGCG GCCCACDCA TGGCCTAGAG TGGCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG GCTCCTGAG AGATCCCCAG AGACAACCA CCAGGATGG AGATCCCTGAG CCAGGATGG AGATCCCCAG CCAGGATGG AGATCCCCAG CCAGGATGG AGATCCCCAG CCAGGATGG AGATCCCCAG CCAGGATGG AGATCCCCAG CCAGGCCAG CCAGGATGG AGATAACGT CCATGTTGCA AAATAACGT	CACCOGGAC GACCOGGAC GACCOGGAC GACCOGGAC GACCOGGAC CACCOGGAC GACCOCCAGAC CACCOGGAC CACCAC CACCAC CACCAC CACCAC CACCAC CACCAC	GACTITIOGTE GTGACCACCG GTGACCACCA CCGCCCCCC GGATTCCGG GAGGCCCAC TATGGGTGC CACCACCACCACCACCACCACCACCACCACCACCACCA	ACTIOCOCOC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOTICCOCCAC TOCACAC TOCACACAC TOCACACAC TOCACACAC TOCACACAC TOCACACACAC TOCACACACAC TOCACACACACACACACACACACACACACACACACACACA	ACCCARTAGA GGCCCARTAGA GGCCCTCCAC AT COCTOCTC GGCCCGAGGCTC GCCCAGGCCTC ACTCCCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCCC GCCTGCCC GCCTCCCAGGC GCCCCCAGGC GCCCCAGGCC GCCCCAGGC GCCCCCAGGC GCCCCCAGGC GCCCCCCCC	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200
50	CCTCGATAC GCTATCATCA GCCGCACCA GCCACCACCA GCCACCACCA GCCCGGAAG GTGGATTCC GGCCGGAAG GTGGATTCC GGCCCGGAGG GACGCCTTCG GCCCCGGCCACCA GCCCTCGCCC GCCCACCCCC GCCCCCC GCCCCC GCCCC GCCC GCC GCCC GCCC GCC GCCC GCC	GCTGGTGOT AGNGGGTGC AGNGGGTGC CGTAGGGTGC GCTCGTTCCT CTCAGGTGCC CCCCAGCA TGGCGTGCC TGGCGTGCC TGGCGTGCC TGGCGTGCC TGGCGAGCA CCCAGCA TGGCGAGCA CCAGCA TGGCGAGCA CCAGCA TGGCGAGCA CCAGCA TGGGCAGCA CCAGCA CCAGCAGCA CCAGCA CCAGCAGCA CCAGCAGCA CCAGCAGCA CCAGCTGCGA AAATTACGT 192 Probein	CACCOTGGAC GACCAGGAC GACCAGCAGCAC GACCAGCAGCAC GACCAGCAGCAC GACCAGCAC GACCAC GACCAGCAC GACCAGCAC GACCAGCAC GACCAGCAC GACCAGCC GACCACC GACC	GACTITOPTE GRIGACEMO GRIGACEMO GRIGACEMO GRIGACEMO GRIGACEMO TATORIGA GRIGACEMO TATORIGA GRIGACEMO TATORIGA GRIGACEMO TATORIGA GRIGACEMO TATORIGA GRIGACEMO TATORIGA GRIGACEMO TATORICA GRIGACEMO TATORICA GRIGACEMO TATORICA TORICA TORI	ACTIGOCGOO TOTOCOCCE GOATOCCEAC TOTOCOCCE GOATOCCEAC TAMOCTOCT TOTOCOCCE GOATOCC TAMOCTOCT TOCACOTTOC COCTACACO CCCTTACACO CCCTTACACO CCCTTACACO CCCTTACACO CCCTTACACO CCCTTACACO CCCTTACACO TCCCTTACACO TCCCTTACACO TCCCTTACACO TCCTTACACO TCCTTA	ACCOCATORA GOSTICALOGO GOSTICA	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200
50 55 60 65	CCTGGATGC GCTATGCTGG GCGGGATGC GCGACCTGG GCCGGGATG GCCGGGATG GCCCGGGATG GCCGGGATG GCCGGATG	GCCTGGTGOT ASAGCGTCC ASAGCGTGC ASAGCGTGC ASAGCGGGG GCTCTTCCT CTCAGGTGCC CCCCAGCA TGGCTGGCC TGGCGTGGCT TGGCGAGGC TGGGTGCTGG GCTCAGGAGC TGGGTGCTGG GCTCAGGA GCTACCCGA GCTAGGAACCA CCTTGGGAACCA CCTTGGGAACCA CCCAGCAACCA TGGGTGCTGGAACCA CCAGCTTGGGAACCA CCAGCTTGGGAACCA CCAGCTTGGGAACCA CCAGCTTGGAACCA CCAGCTTGAACCA CCA	CACCIOGGAC GGCCIGGAC GGCCIGGAC GCCCCCTGGGC GCCCCCCTGGGC GCCCCCCGTGGCC CACCTGGCC CACCTGGCC CACCTGGCCC CACCTGGCCC CACCTGGCCC CACCTGGCCC CACCTGGCCC CACCTGGCCC CACCTGGCCC CACCTGGCCC CACCTGCCCC CACCTGCCC CACCTGCCCC CACCTGCCC CACCTGCC CACCTCC CACCTGCC CACCTGCC CACCTGCC CACCTGCC CACCTGCC CACCTCC CACCTGCC CACCTGCC CACCTGCC CACCTGCC CACCTGCC CACCTGCC CACCTGCC CACCTGCC	GACTITOTIT GEGACCIAC GEGACCIAC GEGACCIAC GATTCOSG GASTCOSG GASTCOSG GASTCOSG GASCOCIAC GAGCOCIC	ACTGCCGCC TOTOCCTGCT TOTCCTGCT TOTCCTGCT TOTCCTGCT AGGCGTTGC TAAGCTGCT TOCACGTGC CCCTGCACG CCCTGCACG CCCTGCACG CCCTGCACG TCCCTGCACG CCCTGCACG CCCTCCTCCC CCCTCCCCC CCCTCCCCC CCCTCCCCC CCCTCCCCC CCCTCCCCCC	ACCOCATORA GOSTICALOGO GOSTICA	120 180 240 300 420 480 540 660 720 780 840 960 1020 1080 1140 1200 1320
50 55 60 65	CCTGGATGE GCTATGCTGGATG GCGGGATG GCGGGATG GCGGGATG GGCCGGGATG GCCGGGATG GCCGGGATG GCCGGGATG GCCGGGATG GCCGGGATG GCCGGATG GCCGGATG GCCGGATG TTCTGTGCC GCGGATG TTCTGTGCC GCCGGCTT TTATTTCCTGC AGCCTTTTTCC GCAGCGCTC TTATTTATT Seq ID No TTCGTCCCCC TATATTTAT Seq ID No TCGTCCCCC TATATTTAT L	GCCTGGTGGT AGACGGGGG GCTCTTACT CCCAGGAGGGGG GCTCTTACCT CCCAGGAGGGGG CCCCCAGCA TOGCTGGCGGGG GCTCCTTACCT TOGCCGAGGG GCTCCTTACCT CCCAGGATGCA TOGCTGCAGGA GGTCCCTGGA AGGTCCCTGGA AGGTCCCTGGA AGGTCCCCTG AGACGACCA CCCAGGATGCA CCCAGGATAC CCCCAGGATAC CCCCAGGATAC CCCCAGGATAC CCCCAGATAC CCCCAGGATAC CCCAGGATAC CCCCAGGATAC C	CACCOGGGAC GGCCGGGAC GGCCGGGGAC GGCCGGGGAC GGCCGGGGAC GCCGGGGAC GCCGGGGAC GCCGGGAC GCCGGAC GCCGGAC GCCGGAC GCCGAC GCCCAC	GACTITOTIT GRIGACOMO GRAGOCIACA COGGCCOCC GRATICOMO GRAGOCIACA CACCACA CACCACA CACCACA CACCACACA CACCAC	ACTGCCGCC TOTTCCTGCT COATCCCAA GCCGCCAC AGGCGGTGCC AGGCGGTGC COCTTACAGC CCCTTACAGC CCCTGCAC CCCTCCAC CCCTGCAC CCCTCCAC CCCCCCCAC CCCCCCCC	ACOCCATTORS OSTITATORS OSTITATORS ATTORNSOR OSCIOSARION CONSISTATOR OCCASION OCCASIO	120 180 240 300 420 480 540 600 660 720 780 840 900 900 1020 1120 1220 1240 1320
50 55 60 65	CCTGGATGC GCTATGCTGG GCGGCAGGG GCGACCTGG GCCGGGAAG GTGGATTGG GCCCGGAAG GTGGATTGG GCCGGAAG GCGGCGG GCGGACGG GCGGACGG GCGACCGG GCCGACCTG CCCGACTTG CCCGACTTG CCCACGTTG C	GCTGGTGOT AGGCTGTGC AGGCTGTGC AGGCTGTGC AGGCTGTGC AGGCTGGGGGGC AGGCTGGGGGGGGGG	CACCOGGGAC GGCCGGGGCG GGCAGGGCG GGCAGGGCG GGCAGGGCG GGCAGGGCGC GGCAGGGCG GGCAGGGCG GGCGGGCG	GACTITOSTI GEGACCIO GEGACCIC GRATICOSG GRACCIC GRATICOSG GRACCIC GRATICOSG GRACCIC GRATICOSG GRACCIC COSG CONTO COST COST COST COST COST COST COST CO	ACTOCCOCO TOTOCOTOC TOTOCOTOC TOTOCOTOC AGRICANTOC AGRICANTOC TARACTICAT AGRICANTOC CONTINUE COCOTOCCO COCOTOCO COCOTOCCO COCOTOCCO COCOTOCO COCOTOCCO COCOTOCCO COCOTOCCO COCOTOCCO COCOCO COCOTOCO	ACOCCATORA GOSTICACOS	120 180 240 300 420 480 540 660 720 780 840 960 1020 1080 1140 1200 1320
50 55 60 65 70	CCTOCANGE COTATIONS COUNTRICATE COUNTRICAT	GCCTGGTGOT AGNGCGGGG GCCCAGGAGGGGG GCTCTTTCCT CCCAGGAGGGGG GCCCCAGGAGGAGGGG GCCCCAGGAGGAGGGGG GCCCCAGGAGGAGGGGGGGG	CACCOGGIAC GGCCGGGCC GGACAGAGA GGACAGAGA GGACAGAGA GGACAGAGA GGACAGAGAGA GGACAGAGAGA GGACAGAGAGA GGACAGAGAGA GGACAGAGAGA GGACAGAGAGAG	GACTITOTIT GRIGACCHICO GRAPICO GRAPI	ACTOCCOCO TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCO TOTOCO	ACCOCATORS GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT GOTT GOTT GOTT GOTT GOTT GOTT GOTT	120 180 240 300 420 480 540 600 720 780 840 900 900 910 1020 1140 1200 1320
50 55 60 65 70	CCTCGATGC CTTATCTTCG CCGGATGC GCCGCCGGGATG GCCACCGGGATG GCCCGGGTG GCCCGGTG GCCCGGTG GCCCGGTG GCCCGTGGCG GCCCGTGGCG GCCCGCGGGGT TTGTGCTTGCC CCCTGGGGGGGG	GCCTGGTGGT AGNGCGTGC AGNGCGTGC GCTTGTTTGCT AGNGCGTGGC GCTTGTTGCT AGNGCGTGGC CCCAAGAC TGGCCAAGAC TGGCCAAGAC AGGCCTTGA AGGCCTGGA AGGCCTGA	CACCOGGIAC GGCCGGGGC GGCCGGGCG GGCGGGGCG GGCGGGGCG GGCGGGGCG GGCGGGGGC GGCGGGGGC GGCGGGGGC GGCGGGGGC GGCGGGGGG	GACTITOTIT GRIGACCHICO GRAPICO GRAPI	ACTOCCOCO TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCO TOTOCO	ACCOCATORS GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT GOTT GOTT GOTT GOTT GOTT GOTT GOTT	120 180 240 300 420 480 540 660 720 960 1020 1140 1200 1250 1320
50 55 60 65 70	CCTCOANTEC COTATIONTO COTATIONTO COCANCER COCANC	GCCTGGTGGT AGAGGGTGGT AGAGGGTGGT AGAGGGTGGT CCCCAGGGGGG CCCCAGGGGG AGGGGGGGGGG	CACCOTOGRAC GRACOTRIGOT GRACOT GRACOTRIGOT GRACOT GR	GACTITOTIT GRIGACCHICO GRAPICO GRAPI	ACTOCCOCO TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCO TOTOCO	ACCOCATORS GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT GOTT GOTT GOTT GOTT GOTT GOTT GOTT	120 180 240 300 420 480 540 600 720 780 840 900 900 910 1020 1140 1200 1320
50 55 60 65 70	CCTCIACNACE COTTATIONACE GOOGLAGE GOOGL	GCCTGGTGGT AGNGCGTGC AGNGCGTGC GCTGGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	CACCOGGRAC GGCCGGGGGC GGAGCTGGGCC GGAGCTGGGCC GGAGCTGGGCC GGCGGCGGGCC AGGTACCGGCC AGGTACCGGCC AGGTACCGGCC GGCGGCGGCC AGGTACCGGCC GGCGGCGGCC GGCGGCGGCC GGCGGCCC GGCGGC	GACTITOTT GTGACCAGG GTGACCAGG GTGACCAGG GTGACCAGG GAGG G	ACTOCCOCO TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCO TOTOCO	ACCOCATORS GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT GOTT GOTT GOTT GOTT GOTT GOTT GOTT	120 180 240 300 420 480 540 600 720 780 840 900 900 910 1020 1140 1200 1320
50 55 60 65 70	CCTOCANTEC COTTACCTACE GOOGLOAGE GOO	GCCTGGTGGT AGAGGGTGGT AGAGGGTGGT AGAGGGTGGT CCCCAGGGGGG CCCCAGGGGG AGGGGGGGGGG	CACCOGGRAC GRACOTGGRAC TOTGGRAC TOTG	GACTITOTT GTGACCAGG GTGACCAGG GTGACCAGG GTGACCAGG GAGG G	ACTOCCOCO TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCOC TOTOCOCO TOTOCO	ACCOCATORS GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT ACTIVICACIÓN GOTTALOGOT GOTT GOTT GOTT GOTT GOTT GOTT GOTT	120 180 240 300 420 480 540 600 720 780 840 900 900 910 1020 1140 1200 1320
50 55 60 65 70	CCTOCANTEC COTTACCTACE GOOGLOAGE GOO	GCTGGTGGT AGNGCGGGG AGGCTGTTGCT CTCAGGTGCG CCCCACGCA TCGCCGAGGC TCGCCGAGGC TCGCCGAGGC TCGCCGAGGC TGGCCTGAG CTGGCCGAGGC TGGCCTGAG CCCAGGATGC CCC	CACCOTOGRAC GRACATOGOT	GACTITOTIT GRIGACOMO GRIGACOMO GRIGACOMO GASTICCOMO GASTICCOM	ACTGCCGOOT TOTOCOTOC TOTOCOTOC TOTOCOTOC TOTOCOTOC	ACOCCATOR ODOCTORO OD	120 180 240 300 420 480 540 600 720 780 840 900 900 910 1020 1140 1200 1320
50 55 60 65 70	CCTOCIANTEC COTTACIONATE COTTACIONATE COCCAACTOR COCCAA	GCCTGGTGGT AGNGCGTGGT AGNGCGTGGT AGNGCGTGGT CCCAGGTGGT CCCAGGTGGT CCCAGGTGGT AGNGCGTGGT AGNGCGTGGT AGNGCGTGGT AGNGCGTGGT AGNGCGTGGGT AGNGCCTGAG AGTGCCCTGA AGGTCCCCGA CCCAGCCCAG	CACCOTOGRAC GRACOTAGOT GRACOT	GACTITOTIS GEGACOMO GEGACOMO GEGACOMO GEGACOMO GASTICOMO	ACTGCCGOOT TOTOCOTECT CONTOCCONC CONTOCCONC TOTOCCONC TANGETOCOTECT TANGETOCOTECT TOTOCCONC COCTTANGETOCOTECT COCTTANGETOCOTECT COCTTANGET COCCONC COCCONG COCCONG TOTOCCONC TOT	ACCOCATGAR ACCOCATGAR ACCOCATGAR ACCOCATGAR ACCOCATGAR COSSIGNATION ACCOCATGAR ACCO	120 240 360 480 660 720 860 900 1140 1200 1200 1200 1200 1200 1200 12
50 55 60 65 70 75 80	CCTOCIANTEC COTTANCIANO CONTACTORIO CONTAC	GCTGGTGGT AGNGCGGGG AGGCTGTTGCT CTCAGGTGCG CCCCACGCA TCGCCGAGGC TCGCCGAGGC TCGCCGAGGC TCGCCGAGGC TGGCCTGAG CTGGCCGAGGC TGGCCTGAG CCCAGGATGC CCC	CACCOTOGRAC GRACITAGOCT GRACIT	GACTITOSTI GRIGACOMO GONATION GRIGACOMO GASTICOMO GASTIC	ACTIGOCOGO TOTOCOTOC TOTOCOTOC TOTOCOTOC TOTOCOTOC	ACCOCATIONS OTTORACOTY AT DICTORY AT DICTORY AT DICTORY OTTORY OTTORY AT DICTORY OTTORY OTTORY AT DICTORY OTTORY O	120 180 240 300 420 480 540 600 720 780 840 900 900 910 1020 1140 1200 1320

	WO 02/						
	AGAAGATGAA	GGATATCGAC	ATACCAAAAC	ACTATATCAT	CCCCAGTCCT	OGGTATAGAA	180
	GTGTGAGGGA	GAGAACCAGC	ACTTCTGGGA	CGCACAGAGA	CCCTGAAGAT	TCCAAGTTCA	240 300
	GGAGAACTCG	ACCUTTGGAA TGCCTCCATG	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA CCATCACCAC	CATCYCAAGG	360
5	GARAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	ARACACCAGG	420
-	ACCCAGTGGA	CARTGCTGGG	CTTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCCTCTCCC	CCACAAGAAG	COCCACCTCT	CARTGGAAGA	CCTCTCCTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	CTOCCARGAA	GAGCTGAATG	600
10	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
10	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720 780
	TCATGGTGAA	GCTGGGCCTC	GAGTATACCC	AGGCAACAGA	CTCTAACCTG	CRETACACTOR	840
	CTTGGGGCATT	GAATTACCGA	ACCCCTGTCC	CCTTGCGGGG	CCCCATCCTA	ACCATGGCAT	900
	TTAAGAAGAT		AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATGAACA	960
15	TTTGCTCCAA	CGATGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG		1080
	GCTTCCTGGG	ATCAGCTGTT	TTTATCCTCT	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1200
	TCACAGCATA ATGAAGTTCT	TTTCAGGAGA TACTTACATT	AAATGCGTGG	COGCUACGGA	CTGGGTCAAA	CAGAUGATGA	1260
20	ATGARGTTCT	AAAAATCCGC	CACCACCACC	CTCCCATATT	GGAAAAAGCC	GGGTACTTCC	1320
20	AGGGTATCAC	TOTGGGTGTG	GCTCCCATTG	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTCTTCATAT	GACCCTGGGC	TTCGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCTTCAATTC	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
25	AAGCCTCAGT	GGCTGTTGAC	AGATTTAAGA	CTTTCTTTCT	AATGGAAGAG	GTTCACATGA	1560
25		ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GARARATGCC	ACCTTGGCAT	1620 1680
	GGGACTCCTC ACAAGAGGGC	TTCCAGGGGC	ATCCAGAACT	NOCTON COCT	COTOCAGG	ATGAMOUNG	1740
	AGGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCCTCCTGGA	CAGTGACGAG	CGGCCCAGTC	1800
	CCGAAGAGGA	AGAAGGCAAG	CACATCCACC	TOGGCCACCT	GCCCTTACAG	AGGACACTGC	1860
30		TCTGGAGATC	CAAGAGGGTA	AACTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCCTGTTT	GGGAAGGAAT	ATGATGAAGA	CAGCGACCTG	TCTGTGCTGA	2100
35	ACAGCTGCTG GAGAGCGAGG	CCTGAGGCCT	AGCGGGGGG	TTCTTCCCAG	CAUCCACCTE	COCCGGGCCT	2220
55	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACCACCCCT	CAGTGCCTTA	GATGCCCATG	2280
		CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG		2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA		ATGAAAGAGG	2400
40		GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
40	CCATTTTTAA		CTGGGAGAGA		TGAGATCAAT		2520
	AGGAAAAAGC	TTCACAGAAG AGTAAAGCCA	AAGTCACAAG	ACAAGGGTCC	GCTGGAAGAG	TCAGTAAAGA	2580 2640
	GTTCAGTGCC	CTGGTCAGTA	TATGGTGTGT	ACATOCAGO	TOCTGGGGGC	CCCTTGGCAT	2700
	TOCTGGTTAT	TATGGCCCTT	TTCATGCTGA		CACCGCCTTC		2760
45	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	CCAACACCAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCATG	CTGATCCTGA	AAGCCATTCG	AGGAGTTGTC	TTTGTCAAGG	2940 3000
		AGCTTCCTCC TTTTGACACG	CGGCTGCATG	ACGAGCTTTT	COGRAGGATC	CTTCGAAGCC	3060
50	CTATGAAGTT	TGACGTGCGG	CTGCCGTTCC	AGGCCGAGAT	CANCAGGIII	AACCTTATCC	3120
50	TOGTGTTCTT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCCTTGT	CATCCTCTTT	TCAGTCCTGC	ACATTGTCTC	CAGGGTCCTG	ATTCGGGAGC	3240
		GGACAATATC	ACCCAGTCAC		CCACATCACG	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
55	AGCTGCTGGA	TGACAACCAA	AGCATCGCCC	TTTTGTTTAC	CACGGGGGCTG	CGGTGGCTGG	3420
	CTGTGCGGCT	GCAGATTCCC	CCAGCCTATG	COCCUTCTCCC	CATCTCTTAT		3540
	TAACGGGGCT	GTTCCAGTTT	ACCOUNTE	TGGCATCTGA			3600
	COGTOGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCCTT	GGAAGCACCT	GCCAGAATTA	3660
60	AGAACAAGGC	TCCCTCCCCT	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCAG	3720
	AGATGAGGTA	CCGAGAAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAAC"	3780
		GATTGGCATT	GTGGGGGGGA	CAGGATCAGG	GAAGTCCTCG	CTGGCGATGC	3840
	CCCTCTT CCG GTGATATTGG	TCTGGTGGAG	CTCCGAAGCA	GCTGCATCAA	CATTCCTCAA	GTGAGAATCA	3960
65	TGTTCAGTGG	CACTGTCAGA	TORRATTEGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
0.5		CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TTGAATCTCA	AGTGATGGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTCT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
50		AGAGACAGAC	TTATTGATTC	AAGAGACCAT	COGAGAAGCA	TTTGCAGACT	4260
70		GACCATTGCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC CAGAGAACAA	GGTCCTTCTC	AAGGGCTGAC	4380
	GTTCCCGATT	CTATGCCATG TGACGAAGTC	TITGCTGCTG	CAGAGAACAA	CATTCCCTGC	CHAGGGGGGGG	4500
	CCCCTCATCG	CCTCCTCCTA		CCCTTCTCG		TOGCACAGCA	4560
75		GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC			4620
	ATTOCATATT	CATGTAAACA			ATTGCACTCT	AAAAGGTTCA	4680
	CGGAACCCTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	CTTTATTTTA	4800
80	TATTAAAATA	AGCACTGTGC	TAATAACAGT	GCATATTCCT	TTCTATCATT		4860 4920
00	TIGCTGTACT	AGAGATCTGG TGGTTTCACG	TITTGCTATT	AGACTGTAGG	CONTROCK TO	ACCITOTOCC*	4920
	ATACTOCCOC	CTCCGACAGC	COUNTRY	CCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	GACCATCCAG	AGCGCCGTGA	CTTCTCAGGG	CTCCTGCCTT	5100
	CTGTCCTGGT	CTCACTTACT	CITTCTCTCA	GGAGACCAGC	GGGGCGAAGC	CCAGGCCCCT	5160
85	TTTCACTCCC	TOCATOLAGA	ATGGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCCTGCCT	TCTTCTTTTT	CCTGTTGTTT	CTAAACAAGA	ATCACTCTAT	CCACAGAGAG	5280
	TOOCACTGOO	TCAGGTTCCT	ATGGCTGGCC	ACTOCACAGA	GUTCTCCAGC	TECARGACCT	5340

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GTTGGTTCCA	AGCCCTGGAG	CCAACTGCTG	CTTTTTGAGG	TGGCACTTTT	TCATTTGCCT	5400
ATTOCCACAC	CTCCACAGTT	CAGTGGCAGG	GCTCAGGATT	TOGTGGGTCT	GTTTTCCTTT	5460
CTCACCCCAG	TOGTOGCACA	GTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTC	CAACTTTAAG	5520
CACCECTEGC	TAATCAGEGE	CTCACACTGG	CGTAGAAGTT	TITGTACTGT	AAAGAGACCT	5580
ACCTCAGGTT	CCTGGTTGCT	GTGTGGTTTG	GTGTGTTCCC	GCAAACCCCC	TTTGTGCTGT	5640
CCCCCTCCTA	GCTCAGGTGG	GCGTGGTCAC	TGCTGTCATC	AGTTCAATCG	TCAGCGTTGC	5700
ATOTOTORO	CARCTAGACA	TTCTGTCGCC	TTAGCATGTT	TGCTGAACAC	CTTGTGGAAG	5760
CAAAAATCTG	AAAATG TGAA	TARARATT	TTGGATTTTG	TAAAAAAAAA	алааааааа	5820
AAAAAAAAA	AAAAAAA					

Seq ID NO: 194 Protein sequence: Protein Accession #: NP_005679.1

15		11	21	31	41	51	
13	Ť	i	i .	i	1	1	
	MYDIDIGKEY	TTDSDGVBSV	RERTSTSGTH	RDREDSKFRR	TRPLECQUAL	ETAARAECLS	60
	T.DA CMUSOT.R	TIDERHPKCK	VHHCLSALKP	IRTTSKHOHP	VDNAGLFSCM	TFSWLSSLAR	120
	DARRAGET.SM	EDMISTISKEE	SSDVNCRRLE	RLWOEELNEV	GPDAASLRRV	VWIFCRTRLI	180
20	T.CTWCLMTTO	LAGESGRAPM	VKHLLEYTOA	TESNLOYSLL	LVLGLLLTEI	VRSWSLALTW	240
	AT WINDSHOUTET	DOLLITATION OF THE PARTY OF THE	RITERIANIER	KSLGRLINIC	SNDGORMFEA	AAVGSLLAGG	300
	DIRECT CHTY	ADJUST TAKEN OF THE PARTY OF TH	LOSAUPTLPY	PANMFASRLT	AYPRRKCVAA	TDERVOKMNE	360
	ST WAT ABLEM	VANUKARSOS	VOKTREERER	ILRKACYFOG	ITVGVAPIVV	VIASVVTFSV	420
	HART CERT TO	ACA PTUUTUR	NEMPPALKUT	PFSVKSLSEA	SVAVDRFKSL	FLMBEVHMIK	480
25	WWW.CDUTET	DMKNIA TT. AND	SSHSSIONSP	KLTPKMKKDK	RASRCKKEKV	RQLQRTEHQA	540
	UT ADOVOUT.T.	LDCDDDDDDDDD	REEGENTHLG	HLRLORTLHS	IDLEIQEGKL	VGICGSVGSG	600
	WEDT TOXTLO	OMPLURGSTA	TSGTFAYVAO	OAWILNATLR	DNILFCKEYD	EERYNSVLNS	660
	COTTOTAL	DECDITOR	DOMESTICANT	ORISLARALY	SDRSIYILDD	PLSALDAHVG	720
	ARTERICA TRY	UT VOVTUT.DU	THOLOYIADC	DRVIPMKEGC	ITERGTHEEL	MNLNGDYATI	780
30	TRANSFER COMP	DUDINGUEER	SCSOKKSODK	GPKTGSVKKE	KAVKPEEGOL	AGTERICACIO	840
-	TERMETRY CHEVE	ON AGGREGABLE	UTMALEMENV	GSTAPSTWWL	SYWIKOGSON	TIVIRGNETS	900
	WODGMUDAIDU	JAYTSAYVOM	SMAUMILILKA	IRGVVFVKGT	LRASSRLHDE	LFRRILRSPM	960
	www.mmnman	TEMBROYDAD	AUDUBT. PPOA	EMPTONVILV	FFCVGMIAGV	FPWFLVAVGP	1020
	TITTE BOST UT	WEBSIT TREES	PLINTTOSPE	LISHITESSIOG	LATIHAYNKG	OELTHEAGRT	1080
35	T DOMOS PERT.	PTCAMPULAU	REDETSTALT	TTTGLMIVLM	HGQIPPAYAG	LAISYAVOLT	1140
-	OT POPPUPIA	CETEARPTSV	RRINHYIKTL	SLEAPARIKN	KAPSPDWPQE	CEVTFENAEM	1200
	DAMPING DIAT	VVVCDTTVDV	PRICINGPIC	SCKSSLGMAL	FRLVELSGGC	IKIDGVRISD	1260
	TOT ADT BOY!	CTTDOUDVIR	SCTURSNIDE	PNOYTEDOIW	DALERTHMKE	CIAQLPLKLE	1320
	CHIMPATONIE	CHARROLLACT	ARALLRHCKT	LILDRATAAM	DISTRICT	TIREAFADOT	1380
40	MITTAHRLHT	VLGSDR IMVL	AQGQVVEPDT	PSVLLSNDSS	RFYAMFAAAE	NKVAVKG	

Seq ID NO: 195 DNA sequence Nucleic Acid Accession 8: NM_006470 Coding sequence: 228..1922

					41	51	
	1	11	21	31	37	1	
	1	GCCTGAGTAC	moma ocensors	marcance contra	COOR TOTOGO	TOCCATOCAG	60
50	GCTGTCCTGA	CAGTAATGAG	TCTMGCTGCC	moore and a second	COCATCIOCO	ACTTARABATC	120
30	CGCCAGCACA	TGCAATCATC	TGGCCGMGCT	TOUTOTOTO	CACTTGGGCT	GCACAGATCC	180
	TTGCAGCAGC	GACAGAAGAA	TAGGCGTGGT	CCICITOICI	CTCCCAGATG	CCTGAGTTGG	240
	TOGGCCAAGG	TCCAGGGCCA	MONCHOCCIN	CCVCACACACA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCTCTCAGCC	300
	ATCTAATGGC	GTCACCCAGC	COLCUMBUS	CCTCACCCAC	CCCAGTGGAA	GAAGAGGACG	360
55	CAGACTCTGG	GGAGAAGCTT	COMMITCIO	COCKCODACA	GGACAGCGAC	TOTGCAGAGC	420
23	10000010010	TOCTGGTGAG	COGNANGAGG	TOTTOTOTO	CTTCTGCCTT	GATGACACCA	480
	AGGGGGATCC	GGCAGTGAAG	TOCTOTOTAL	CCTGCATGGT	GAATTACTGT	GAAGAGCACT	540
	BOOK GOOGGE	TCAGGTGAAC	ATCABACTOC	AARGCCACCT	CCTCACCGAG	CCAGTGAAGG	600
	3 CO3 C3 3 CTC	COCATACTCC	CONGCICACO	ACAGCCCACT	GTCTGCTTTC	TGCTGCCCIG	660
60	1 TO 1 CO 1 OT C	CATCTCCCAC	CACTCTTCCC	AGGAGCACAG	TGGCCACACC	ATAGTCTCCC	720
00	magamagaga	COCCAGGGAC	A A G C A G C T C	AACTCCACTC	CACCCAGTTA	GACTTGGAUC	780
	GGT B B CTC B Z	CTTCAATGAA	AATGCCATCT	CCAGGCTCCA	GGCTAACCAA	AAGTCTGTTC	840
	MOOROTOOT	CTCAGAGGTC	BAAGCGGTGG	CTGAAATGCA	GTTTGGGGAA	CTCCTTGCTG	900
	omores again	acceptance.	A A TOTOM TOO	TOTTOTTAGA	GGAGAAGGAG	CAAGCTGCGC	960
65	TOROCCEDOCC	CARCGGTATC	AAGGCCCACC	TGGAGTACAG	GACTGCCGAG	ATGGAGAAGA	1020
00	CONNECTOR	CCTGGAGAGG	ATGGCGGCCA	TCAGCAACAC	TCTCCAGTIC	TTGGAGGAGT	1080
	NORGON NOTE:	TARGLACACT	GAAGACATCA	CCTTCCCTAG	TGTTTACGTA	GGGCTGAAGG	1140
	AMARA CECTO	COCCATOOCC	DALGTTATCA	CGGAATCCAC	TGTACACTTA	ATCCAGTIGC	1200
	MOCACA ACTA	TANCABARAG	CTCCAGGAGT	TTTCCAAGGA	AGAGGAGTAT	GACATCAGAA	1260
70	CHICAN CHICAGO	TOCCOPPORT	CAGCGCAAAT	ATTGGACTTC	CARACCTGAG	CCCAGCACCA	1320
, 0	COCARCACT	COTOCALTAT	CCCTATGACA	TCACGTTTGA	CCCGGACACA	GCACACAAGT	1380
	NEOTOCOCCO	GCAGGAGGAG	AACCGCAAGG	TCACCAACAC	CACGCCCTGG	GAGCATOCCT	1440
	NOOCOGROCT	CCCCAGCAGG	TTCCTGCACT	GGCGGCAGGT	GCTGTCCCMG	CAGAGTCTGT	1500
	ACCTROCACAC	CTACTATTT	GAGGTGGAGA	TCTTCGGGGC	AGGCACCTAT	GTTGGCCTGA	1560
75	CVTV2CAAAGG	CATCGACCGG	AAAGGGGAGG	AGCGCAACAG	TTGCATTTCC	GGAAACAACT	1620
	TOTOTOGAG	CCTCCAATGG	AACGGGAAGG	AGTTCACGGC	CTGGTACAGT	GACATOGAGA	1680
	COCCER CINCA S	NOCTOGCCCT	TTCCGGAGGC	TCGGGGGTCTA	TATCGACTTC	CCGGGGGGGGA	1740
	TCCTTTCCTT	CTATGGCGTA	GAGTATGATA	CCATGACTCT	GGTTCACAAG	TTTGCCTGCA	1800
	AATTTTCAGA	ACCAGTCTAT	GCTGCCTTCT	GGCTTTCCAA	GAAGGAAAAC	GCCATCCGGA	1860
80	TTGTAGATCT	GGGAGAGGAA	CCCGAGAAGC	CAGCACCGTC	CTTGGGGGGTG	ACTGCTCCCT	1920
	AGACTCCAGG	AGCCATATCC	CAGACCTTTC	CCAGCTACAG	TGATGGGATI	TGCATTTTAG	1980 2040
	GGTGATTTGT	GGGCAGAAAT	AACTGCTGAT	GGTAGCTGGC	TTTTGAAATC	CTATGGGGTC	2100
	TCTGAATGAA	AACATTCTCC	AGCTGCTCTC	TTTTGCTCCA	TATESTSCIE	TTCTCTATGT	2160
	GTTTGCAGTA	ATTCTTTTT	TTTTTTTGA	GACGGAGTCT	CCCACTGTTG	CCCAGGCTGG	2220
85	AGAGCAGTGG	COCCATCTTC	GCTCACTGC	AGCTCCGCCT	COCCACTTC	AGCAATTCTC	2220
	CTGCCTCAGC	CTCCCGAGTA	GCTGGGATTA	CAGGTGCCTC	CCACCACAC	CAGCTAATGT	2340
	TTTGTATTT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGCC	AGGCAGATCI	CARACTCCTG	2340

WO 02/086443 ACCTOSTGAT GENOCIACOT OSGCCTCCCA AAGTGCTOGG ATTACATGCO TGAGGCACTG 2400
CGCCCTGCCT GTTTGTAGTA ATTTTTAGGC ACCAAATCTC CCTCATCTTC TAGTGCCATT 2460 CTCCTCTCTG TTCRGGTAAA TGTCACACTG TGCCCAGAAT GGATGACCAG GAACCTTAAA GAGTGGCTGA AAAGATTGCA GAGTTATCAT AATAAATTGC TAACTTGCGT Seg ID NO: 196 Protein seguence: Protein Accession #: NP_006461 10 21 41 51 MARLDIMARG PLPRATAGRE APLERDISGER SPINGSASPV BEEDVISSEK LIGRETEEGDS DSABOCDPAG BGKEVLCDPC LDDTRRVKAV KSCLTCMVNY CEBHLQPHQV NIKLQSHLLT RPVKDHNNRY CPANHSPLSA PCCPDOOCIC ODCCORNSCH TIVSLDAARR DKEAELQCTQ 180 15 LDIBERUKIN ENAISELQAN QKSVLVSVSE VKRVAEMOFG ELLAAVKKAQ ANVMLFLEEK EQAALSQANG IKAHLEYESA EMEKSKQELE RWAALSNYVQ FLEEVCKFKK TEDITFFSVY VSUKKUKLSGI RKVITESTVE LIOLLENYKK KLQEFSKEEE YDIFFGVSVAV VQRKYMTSKP 240 300 EPSTREOPLO YAYDITFDPD TAHKYLRIGE ENRKVINTTP WEHPYPDLPS RFLHWRQVLS QQSLYLRRYY FEVEIPGAGT YVGLTCKGID RKGEBRNSCI SGMNFSWSLQ WNGKRFTANY SDMBTPLKAG PFRRLGVYID PPGGILSPYG VEYDTMTLVH KPACKPSEPV YAAPWLSKKE 400 20 540 NATRIUDICE EPECPAPSIC VIAP Seq ID NO: 197 DNA sequence Nucleic Acid Accession #: NM_004316 25 Coding sequence: 433-1149 CCCGAGACCC GGCGCAAGAG AGCGCAGCCT TAGTAGGAGA GGAACGCGAG ACGCGGCAGA 30 GOGGETTCAG CACTGACTTT TGCTGCTGCT TCTGCTTTTT TTTTTCTTAG AAACAAGAAG 120 GOGCURGOGG CAGCCTCACA CGCGAGCGCC ACGCGAGGCT CCCGAAGCCA ACCCGCGAAG 180 CONCORDED TOURSESSED ACCORDING ACCORDING ACCORDING ALLEGANT TOURSTTTTT 240 TEGCTCCCAC TCTAMGARGT CTCCCGGGGA TTTTGTATAT ATTTTTATA TTCCTTAGG GCTCCCGCTT CATATTTCCT TTTCTTTCCC TCTCTGTTCC TGCACCCAMG TTCCTCTGTT 360 35 STCCCCCTCS COOGCCCCGC ACCTCGCSTC COSGATCGCT CTGATTCCGC GACTCCTTGG 420 480 540 CAGCAGCAGC AGCAGCAGCA GCAGGCGCCC CAGCTGAGAC CGGCGGCCGA CGGCCAGCCC 660 4∩ TCAGGGGGG GTCACAACTC AGCGCCCAMG CAAGTCAMGC GACMGGGCTC GTCTTCGCCC GAACTGATGC GCTGCAAACG CCGGCTCAAC TTCAGGGGCT TTGGCTACMG CCTGCCGCAG 720 780 CAGCAGOOGG COCCOTOGO GOGCOGCAAC GAGCGCGAACCCCGT CAAGTTOGTC 840 AACCTOGGCT TTGCCACCCT TCGGGAGCAC GTCCCCAACG GCGCGGCCAA CAAGAAGATG 900 AGTAAGGTGG AGACACTGCG CTCGGCGGTC GAGTACATCC GCGCGCTGCA GCAGCTGCTG 960 45 CACCAGCATG ACCCGCTGAG CGCCGCCTTC CAGGCAGGCG TCCTGTCGCC CACCATCTCC 1020 CCCAACTACT CCAACGACTT GAACTCCATG GCCGGCTCGC CGGTCTCATC CTACTCGTCG 1080 GACGAGGGCT CTTACGACCC GCTCAGCCCC GAGGAGCAGG AGCTTCTCGA CTTCACCAAC 1140 1260 50 1270 1380 1440 GAGCAGCACA CGCGTTATAG TAACTCCCAT CACCTCTAAC ACGCACAGCT GAAAGTTCTT 1560 55 GCTCGGGTCC CTTCACCTCC CCGCCCTTTC TTAGAGTGCA GTTCTTAGCC CTCTAGAAAC 1620 CACTTOCTCT CTTTC

60 Seq ID NO: 198 Protein sequence: Protein Aggession #: NP 004307

70 Seq ID NO: 199 DNA sequence Nucleic Acid Accession #: NM_007015 Coding sequence: 1-1005

11 31 75 ATGACAGAGA ACTOCGACAA AGTTCCCATT GCCCTGGTGG CACCTGATGA OGTGGAATTC TGCAGCCCCC CGGCGTACGC TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120 AAGGTGGGAG CCGTGGTCCT CATTTCGGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT ATCHATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300 80 TTTAAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCA GAATGGCATC 360 ACAGGAATTC GTTTTGCTGG AGGACAGAAG TCCTACATTA AAGCGCAAGT GAAGGCTCGT ATTCCTGAGG TGGGCGCCGT GACCAAACAG AGCATCTCCT CCAAACTGGA AGGCAAGATC 420 480 ATTOCIONES INCOCCOLO INCOCATACIO ACCUTATORI CONTROLO CONT 540 GACARCAGCT TCITGAGTTC TARGGTGTTA GRACTCIGCG GTGACCTTCC TATTTTCTGG 600 85 CTTARACCAR CCTATCCARA AGRARATCCAG AGGGRARGAR GAGRAGTGGT ARGRARATT 660 CTTCCAACTA CCACAAAAAG ACCACACAGT GGACCACGGA GCAACCCAGG CGCTGGAAGA 720 CTGARTARTS ARACCAGACC CASTGTTCAN CAGGACTCAC ARGCCTTCAN TCCTGATRAT

	1110.00	000113					
	WO 02/ CCTTATCATC : ATCIGTTGTA	AGCAGGAAGG					840 900
	GGGGGCTATT	ACCCATGGCC	TTATAATTAT	CAAGGCTGCC	TOTGARATCA	CAGAGTCATC	960 1020
5	CACGTGCTGT .	AAAATAAGAA	CTAGCTGAAG	AGACAACCAA	GCGGTTATTC	TTGACACTCT	1080 1140
	TAACAGAATT	TTTTTAATCG	TTTTCCAGAA	ATTTGTTATT	TGCAAATGCA	ATTGATTTGC	1200 1260
10	CATAAGTCTT AGTTTGCC	CCCTTGCTTG	CATCTTCCAA	AGCTATTTOG	AAATAAACAC	GAAAATTTAC	1320
10	MOTITION						
	Seq ID NO: Protein Acc	200 Proteir	sequence:				
15		11	21	31	41	51	
	Ī		CODDANATA	INDESERRIT.	 KVGAVVIJEG	AVILLEGAIG	60
20	AFYFWKGSDS TGIRFAGGEK						120 180
20	DNSFLSSKVL LNNETRPSVQ						240 300
	GGYYPWPYNY	edsqafnfin QGCRSACRVI	MPCSWWVARI	TOMA	ICCIBCARDI	Incontract	500
25	Seq ID NO:	201 DNA sec	uence				
	Nucleic Aci Coding sequ	ence: 112.	495				
30	7	11	21 	31	41	51 	
30	GTAATAAGAG	CGGGGTCTCC	OCCOGGG LAGG	CGCCCACAGC	AGGTGTGGTG	TTCATCCCGG	60 120
						CATGGGTTTC GGGCAGCCTC	180
							240 300
35	GAGGACGCGC GAGCTGAAGC	GCCTCCTGCT	GGCTGCACTG	TCCAGCTOOG	CTGCCCAGAA	GAGGGCCAGT	360
							420
						GCGCCGCAGG AATCCAATGA	480 540
40							600
							660 720
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							1140 1200
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							1320
	TTGCCTAACT	AAGGTCCCAA	GGTCACAATA	ACCTTATTCT	ATACTTTCTT	GTAAAAGTTT	1380 1440
55						TTGTATAAGG TTCAGTGOCA	1500
33							1560
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						GAATCTCAAA TTAGCTACAT	1680
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00							1860
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65	ATATCTIGIT	TTAATTGTT	ATTGCTAGT	GATAGAAAT	CAATATTTA	AATATTAGGA	2100
•	AAAAAAAA	AAAAAAAA	AAAAAAAA	4			
	Seq ID NO:	202 Protei	n sequence				
70			_		41	51	
	1	11	21	31 	i -	ì	
	MGFRKFSPF	L ALSILVLY	COLORADE	DE STREEDING	AT LSKEDARL	LL AALVQDYVQN	1 60
70	KASELKQEQ	E TOGSSSAAG	K RACNTATO	T HRLAGLLS	RS GCMVKSNF	VP TNVGSKAFGE	120
75	RRRDLQA						

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11

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85

51

85

5	AAGAAAGC CCAGAATGCC TAACTTGATG TTCCTTGTGG GTTGGAAGAC GATGTCATCA TATITTTCCC	AGATCTAAGC AACAAGTTTC GATATGTCCA AACTAAACTC CATGTGGTTT CAGAGGATGT AATCACCTGG GAGCTCCTCT	OCTOCOGTAA ACACGTTCOC GCGACTTCGA CTCCCTTTCC GGTTCCTCC CTCAAACTTC GAAAATACCA GTCCTGCTTC	GAGAGACCAT TTCCTAATTT TGGTGGCTCT AGATGGGAGG GAAAATGAGG	CGCCCTCATG CCCTTCTTGC TTGGGCTGGT AAAGAGAGCA GCCGCTTTGA	TTAGCATGCC ATCCTTCCTA ATTGGTGGCT GGACTCACAG GTCCCCCAGA	360 420 480 540 600 660 720 780
	Protein Ac	cession #: 1	P_001732				
15 20	MKASELEQEQ	11 ALSILVLLQA EREGSSLDSP RPHVSMPQNA	21 GSLHAAPPRS RSKRCGNLST N	31 ALESSPADPA CMLGTYTQDF	41 TLSEDEARLL NKPHTFPQTA	51 LAALVQDYVQ IGVGAPOKKR	60 120
20	Nucleic Ac:	205 DNA sec id Accession Lence: 1-945	1 #: NM_0053	61			
25	GAGGCCCTGG	COCTOGTGGG	21 TCAGCACTGC TGCGCAGGCT	CCTGCTACTG	AGGAGCAGCA	GACCGCTTCT	60 120
30	CCTCCCCACA AGACAATCCG CTGGAGTCCG CTCCTCAAGT	GTCCTCAGGG ATGAGGGCTC AGTTCCAAGC ATCGAGCCAG	AGTTACCTG AGCCTCCAGC CAGCAACCAA AGCAATCAGT GGAGCCGGTC	TTCTCGACTA GAAGAGGAGG AGGAAGATGG ACAAAGGCAG	CCATCAACTA GGCCAAGAAT TTGAGTTGGT AAATGCTGGA	GATTETTEG GTTTCCCGAC TCATTTTCTG GAGTGTCCTC	180 240 300 360 420
35	GTCTTTGGCA TGCCTGGGCC CTCCTGATAA ATCTGGGAGG	TCGAGGTGGT TCTCCTACGA TCGTCCTGGC AGCTGAGTAT	TCCCGTGATC GGAAGTGGTC TGGCCTGCTG CATAATCGCA GTTGGAGGTG	CCCATCAGCC GGCGACAATC ATAGAGGGCG TTTGAGGGGA	ACTIGIACAT AGGICATGCC ACTGIGCCCC GGGAGGACAG	CCTTGTCACC CAAGACAGGC TGAGGAGAAA TGTCTTCGCA	480 540 600 660 720 780
			GCAAGATCTG	GIGCAGGAAA	ACTACCTOGA	GTACCGGCAG	840
40	ACCAGCTATG TACCCACCCC	GTGATCCTGC TGAAAGTCCT TGCATGAACG	ATGCTACGAG GCACCATACA GGCTTTGAGA	CTAAAGATCG	GTGGAGAACC	TCACATTCC	900
40 45	ACCAGCTATG TACCCACCCC Seq ID NO:	GTGATCCTGC TGAAAGTCCT	ATGCTACGAG GCACCATACA GGCTTTGAGA 1 sequence:	CTAAAGATCG	GTGGAGAACC	TCACATTTCC	900
	GTGCCCGGCA ACCAGCTATG TACCCACCCC Seq ID NO: Protein Acc 1 MPLEQRSQHC PPHSPQGASS LLKYRAREPV CLGUSYDGLL	GTGATCCTGC TGAAGTCCT TGCATGAACG 206 Protein cession #: 1	ATGCTACGAG GCACCATACA GGCTTTGAGA 1 sequence; NP_005352 21 21 EALGLVGAQA RQSDEGSSNQ RNCQDFFPVI LLIIVLAIIA	GAGOGAGAG 31 PATESQOTAS EEEGPRMFPD PSKASEYLQL LEGDCAPEEK	41 SSSTLVEVTL LESEFQAAIS VPGIEVVEVV	51 GEVPAADSPS REMYELVHFL PISHLYILVT PEGREDSVFA	60 120 180 240
45	GTGCCGGCA ACCAGCTATG ACCAGCCC Seq ID NO: Protein Acc 1 MPLEGRSQHC PPHSPGCASS LLKYRAREPV CLGLSYDGLL HPRKLIMOU YPPLHERALR Seq ID NO:	GTGATCCTGC TGGAAGTCCT TGCATGAACG 206 Protein commin #: 1 11 KPERGLEARG FSTTINYTLW TKAEMLESVL GDNQVMPKTG VQCNYLEYRQ EGGE 207 DNA sec	ATGCTACGAG GCGACCATACA GCGTTGAGA 1 Sequence: NP_005352 21 BALGLVGAQA RNCQDFFPVI LLIVLATIA VPGSDPACYE GREENCE	GAGGGRGAAG 31 PATEBOOTAS EEEGGPRMFPD PSKASEYLQL IEGDCAPREK FLWGPRALIE	41 SSSTLVEVTL LESEFQAAIS VPGIEVVEVV	51 GEVPAADSPS REMYELVHFL PISHLYILVT PEGREDSVFA	60 120 180
45	GTGCCGGCA ACCACCTATG TACCACCCC Seq ID NO: Protein Acc	GTGATCCTGC TGGAAGTCCT TGCATGAACG 206 Protein commin #: 1 11 KPERGLEARG FSTTINYTLW TKAEMLESVL GDNQVMPKTG VQCNYLEYRQ EGGE 207 DNA sec	ATGCTACGAG GCACCATACA GCCTTTGAGA 1 Sequence, IP_005352 21 EALGLVGAQA ROSDEGSSNO, RNCQDFFPVI LLIIVLAIIA VPGSDPACYE Quence 1 %; NM_0211	GAGGGRGAAG 31 PATEBOOTAS EEEGGPRMFPD PSKASEYLQL IEGDCAPREK FLWGPRALIE	41 SSSTLVEVTL LESEFQAAIS VPGIEVVEVV	51 GEVPAADSPS REMYELVHFL PISHLYILVT PEGREDSVFA	60 120 180 240
45	GTGCCGGCA ACCAGCTATG TACCCACCC Seq ID NO: Protein Act I 	GTGATCCTGC TGCATGAC 205 Protein cession #: b 1 1 1 KPERGLEARG KPERGLEARG FORTINYTHM TKAZMLESVL GUNVMPKTG VQENYLEYRQ EQC 207 DNA sec dd Accession cence: 743-: 1 1 1 AGGAGGAGGAG	ATGCTAGGAG GGCCCATAGCA GGCCTTGAGA 1 sequence: 1P_005352 21 21 21 21 21 21 21 22 22 23 24 24 25 25 25 25 25 26 26 26 26 26 26 26 26 26 26 26 26 26	GRAGGERGAAG 31	41 	51 	60 120 180 240 300
45 50 55 60	GTOCCOGGCA ACCACCTAGE TACCCACCCCC Seq ID NO: FOR IN NO. SEQ ID NO: MPLEDERONG MPLEDERONG LIMYNAME SEQ ID NO: NUCleic Ac: Coding seq I ARAGRANGO I ARAGRANGO CCCCAMACTAA CCCCTTGGGG CCCCTTGGGG CCCCTTGGGG CCCCTTGGGG CCCCTTGG	GTGATCCTGC TGGAAGTCCT TGGAAGTCCT TGGAAGTCCT TGGAAGTCCT TGGAAGTCCT TGGAAGTCCT TGGAAGTCCT TTGGAAGGCCT 11 KKPENGLSARG FSTTINYTLM TKGEMLSEYL GENGVERTLEFRQ EGGE TAGGAGGGA TTGGGAGGGA CTGGTGTGTT CGAGGAGGGAGTCC GGAGGAGTCC	ATGCTAGGAG GGACCATACA GCCTTTGAGA GCCCTTTGAGA IP_GOS352 21 EALGIVGAGA RGSDEGSSNQ RGSDEGSSNQ RGSDEGSSNQ RGSDEGSSNQ 1 + NM_0211 2893 21 AAAGGAGAG TCCTCTGTT TGGCCTCAGG TTGCCCTCTGG TGGCGCCGGG TGGACGGCCG	31 1 PATEBOQTAS BEGGMIFAD FSKASTILQL ITGGOCAPES 15 31 11 TIGGTAPES TIGGOCAPES TIGGOCAPES TIGGOCAPES COCAGA AGCCCCGAGA CCCCACAGA CCCCACAGA CCCCCACAGA CCCCCACAGA CCCCCACAGA CCCCCACAGA CCCCCCACAGA CCCCCCACAGA CCCCCCACAGA CCCCCCACAGA CCCCCCACAGA CCCCCCCACAGA CCCCCCACAGA CCCCCCCACAGA CCCCCCCACAGA CCCCCCCACAGA CCCCCCCACACACA	41 SSSTLWEYTL LESEPQAAIS VPCIEVVEVLEST 41 GGCCLGCCGG GGCCGGCCGG AAGGCCGG AAGGCCGGT CTCCCCGAGG AAGGCCGT CTCCCGAGG AAGGCCGT CCCCGAGG AAGGCCGT CCCCGAGG ACGCGGCGCGAGCCGGAGCCGGAGCCGGAGCCGGAGCGGGAGCGGGAGCGGAGGCGGAGCGGAGCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCACACCCGCACACCCGCACACCCGCACCAC	51 GEVPANDSPS RIGHTS FISHLY ILLY FISHL	60 120 180 240 300
45 50 55	GTOCCOGGCA ACCACCTTICAS ACACCACTATICAS ACACCACTATICAS ACACCACTACACAC APPLEDRAGAC APPLEDRAGAC APPLEDRAGAC APPLEDRAGAC ARAGGRAGAG CACCACTACCAC ACACCACTACACAC ACACCACACAC ACACCACACAC ACACCAC	GTGATCCTGC TGGATGATCT TAGGAGGGC TTAGGAGGGC TGGTGTGTT TGGATGGGATCT TGGATGGATCT TGGATGGATCT TGGATGGATCT TGGATGGATCT TGGATGGATCT TGTGATGATCT TGTGATGGATCT TGGATGGATCT TGTGATGGATCT TGTGATGATCT TGTGATGATCT TGTGATGATCT TGTGATGATCT TGTGATGATCT TGTGATGATCT TGTGATGATCT TGTGATGATCT TGTGATGATC TGTGATGATCT TGCATGATCT TGTGATGATCT TGTGATGATC TGTGATGATC TGTGATGATC TGTGATGATCT TGTGATGATC TGTGATCT TGTGATGATC TGTGATC TGTGATC TGTGATC TGTGATC TGTGATC TGTGATC TGTGAT	ATGCTAGGAG GGCCCATAGC GGCCCTAGC GGCCCTAGC AGGCCCATAGC AGGCCCATA	31 PATESOCYAS BEEGENFFD FEXASEYLG 15 31 TOGTTTAGA TOGTTAGA COLAGATIC COL	41 SSSTLWEYTL LESERGALS VEYLEYPL VEYLEYPL LESERGALS VEYLEYPL VEYLEYPL LESERGALS VEYLEYPL VEY	51 GEVPAADSPS RIGHTEUNFTL PTISELTILV FOR STANDARD SPS RIGHTEUNFTL PTISELTILV FOR STANDARD SPS RIGHTEUNFTL STANDARD SPS RIGHTEUNFT SPS RIGHT SPS RIGHTEUNFT	60 120 180 240 300
45 50 55 60	GTOCCOGGCA ACCACCTOGACA ACCACCTATE ACCACCTATE ACCACCTATE ACCACCTATE ACCACCTATA ACCACCTATE ACCACCTATA ACCACTATA ACCACCTATA ACCACCTATA ACCACCTATA ACCACCTATA ACCACCTATA ACCACTATA ACCACCTATA ACCACCTATA ACCACCTATA ACCACCTATA ACCACTATA ACCACTATA ACCACCTATA ACCACCTATA ACCACCTATA ACCACCTATA ACCACCTATA AC	GTBATCCTGC TGBACTGCT TGCATGACG TGGACTGACG 205 Protein 11 11 12 12 12 13 14 15 15 15 16 16 17 16 17 17 17 17 17 17 17 17 17 17 17 17 17	ATGCTAGGAG GOCCOTAGGAG GOCCOTAGGAG AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	STANAGATCS GAGGORGAAG 31 PATEROQUIAS ER EGRIFFO PARAGATCS GAGGORGAAG 15 11 TIGGTTTAGA CCCCARTAGACC CCAAGATGCACC CCAAGATGCACC GAGCOCCTGAC GAGCOCCTGAC GAGCOCCTGAC GAGCOCCTGAC GAGCOCCTGAC GAGCOCCTGAC GAGCOCCCGAC GAGCOCCCTGAC GAGCOCCCGAC GAGCOCCCCAC GAGCOCCCCAC GAGCOCCCCAC GAGCOCCCCAC GAGCOCCCCAC GAGCOCCCCCC GACCACCTCCAC GAGCOCCCCCC GACCACCCCTC CAAGTCCCCCCC GACCACCCCCCC GACCACCCCCCC GACCACCCCCCCC	41 SSPILNEYTL LESEFOALS SSPILNEYTL LESEFOALS SSPILNEYTL LESEFOALS SSPILNEYTL STRUKYLIST SVKYLIST SVKYLIST SSPILNEYTL STRUKYLIST SSPILN	SI II GEVPAADSPE SINOVELVIER II II GEVPAADSPE SINOVELVIER II	60 120 180 240 300 120 180 240 300 420 480 660
45 50 55 60 65 70	GTOCCOGGOA ACCACTATACA ACCACTATACA ACCACTATACA ACCACCATACA ACCACCATACA ACCACCATACA ACCACCATACA ACCACCATACA ACCACCATACA ACCACCATACACA ACCACCACACA ACCACCACACA ACCACCACACACACACACACACACACACACACACACACAC	GTRATCCTRC TOGATOTAC TOGAT	ATGCTAGGAG GOCCOTACAG GOCCOTAGGAG GOCCOTAGGAG A 1 sequence 1 seque	GRAAGATCA GAGGOGOAAG 31 31 31 31 31 31 31 31 31 31 31 31 31	41	SI SURPANDESSE SERVICE AND S	60 120 180 240 300 60 120 180 240 360 480 600 720 780 840 900

	WO 02/	086443 GACAGGATGA	accompando a	coocaras as oc	A A COR A COPCAC	Carcanacacana	1620
	CGACTCCCTT	CAAACCGAGA	GTGTCCCTTT	TGAGGGCCTG	CTGAGCGAAG	GCAACACCAT	1680
	CCGCATCGAG	TTCACGTCCG	A CCAGGCCCG	GGCGGCCTCC	ACCTTCAACA	TCCGATTTGA	1740 1800
5	CGACCCGACC	AAAGGCCACT TATAACATTG	GGACTATAGT	GGAGTTCACC	TGCGACCCCG	GCCACTCCCT	1860
-	GGAGCAGGGC	CCGGCCATCA	TCGAATGCAT	CAATGTGCGG	GACCCATACT	GGAATGACAC	1920
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	GGGAGAAGAG	AAACGGATCT	TCTTAGATAT	CCAGTTCCTG	AATCTGAGCA	ACAGTGACAT	2100
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	TGAGAAAATT	ATGTACTGCA	CCGACCCCGG	AGAGGTGGAT	CACTOGACCC	GCTTAATTTC	2520 2580
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••	TCGCCTGCCC	CACTGCGTTT	CAGAAGCGGC	AGCAGAGACG	TCGCTGGAAG	GGGGGAACAT	2700
20	GGCCCTGGCT	ATCTTCATCC	CGGTCCTCAT	CATCTCCTTA	CTCCTCCGGAG	GAGCCTACAT	2760 2820
	CTACAGCCAG	ATCACCGTGG	AAACCGAGTT	TGACAACCCC	ATTTACGAGA	CAGGGGGAAC	2880
	COLARACOTT.	PACCOTTOCA	TTTLLALACA	COTACCOTTT	AAAAAAGGGGC	TTGTGAACTC	2940 3000
25	AAAGGCGGGCT	TCCCCGAGAC GTTTTTTGGT	TARACTTTTT	ARCARAGGGT	TACGGGTTTT	TTCCCCGGAT	3060
	TTTATAAATT	TTAAAAGTG					
30	Seq ID NO:	208 Protein	sequence:				
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	1	11	21	31	41	51	
	MAGRAPORDY	SPMALMDKGE	NRL/PGSASEE	SOETITSTII	TTTVITTEOA	PALCSVSFSN	60
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	SYDENTMOSO	POTENTEAPR	CONTRIMER	LILLHDKDRMT	VHSCOTNKSA	LLYDSLOTES	300
40	VPFEGLLSEG	NTIRIEFTSD HSLEQGPAII	QARAASTFNI	RFEAFEKGIC	YEPYIQNGNF	TTSDFTYNIG	360 420
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	SCALIGATES	MEDDACLIEC	KOOGETMNYT	EVERNDECED	1.PRIONCWET	TSHTELVEGA	540
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45	VLIISLLLGG	AYIYITRCRY	YSNLRLPLMY	SHPYSQITVE	TEPDNPIYET	GGTQKV	
	Sea ID NO.	209 DNA 866	mienco				
	Nucleic Ac:	id Accession	#: NM_0013	327.1			
50	Coding seq	uence: 89-63	31				
50	1	11	21	31	41	51	
	h can cacaca	GCTGTGTGTA	COCACAATAC	CACRATACCT	natagaccer.	GACCTTCTCT	60
	CTGAGAGCCG	GGCAGAGGCT	CCGGAGCCAT	GCAGGCCGAA	GGCCGGGGGCA	CAGGGGGTTC	
55	GACGGGCGAT						120
		GCTGATGGCC	CAGGAGGCCC	TGGCATTCCT	GATGGCCCAG	GGGGCAATGC	180
	TGGCGGCCCA	GCTGATGGCC	CAGGAGGCCC	TGGCATTCCT	COCCGGGGGGG	CAGGGGCAGC	
	AAGGGCCTCG GCTGAATGGA	GCTGATGGCC GGAGAGGCGG GGGCCGGGAG TGCTGCAGAT	CAGGAGGCCC GAGGGGCCCC GCGGGGCCAG	TGGCATTCCT CGGCAGAGGT GCGGGGTCCG GGGGCCGGAG	CCCCGGGGGG CATGGCGGCG AGCCGCCTGC	GGGGCAATGC CAGGGGCAGC CGGCTTCAGG TTGAGTTCTA	180 240 300 360
60	AAGGGCCTCG GCTGAATGGA CCTCGCCATG	GCTGATGGCC GGAGAGGCGG GGGCCGGGAG TGCTGCAGAT CCTTTCGCGA	CAGGAGGCCC GTGCCACGGG GAGGCGCCCC GCGGGGCCAG CACCCATGGA	TGGCATTCCT CGGCAGAGGT GCGGGGTCCG GGGGCCGGAG AGCAGAGCTG	GATGGCCCAG CCCCGGGGGCG CATGGCGGCTGC AGCCGCCTGC GCCCGCAGGA	GGGGCAATGC CAGGGGCAGC CGGCTTCAGG TTGACTTCTA GCCTGGCCCA	180 240 300 360 420
60	AAGGGCCTCG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT	GCTGATGGCC GGAGAGGCGG GGGCCGGGAG TGCTGCAGAT CCTTTCGCGA CCGCTTCCCG ATCCGACTGA	CAGGAGGCCC GTGCCACGGG GAGGCGCCCC GCGGGGCCAG CACCCATGGA TGCCAGGGGT CTGCTGCAGA	TGGCATTCCT CGGCAGAGGT GCGGGGTCCG GGGGCCGGAG AGCAGAGCTG GCTTCTGAAG CCACCGCCAA	GATGGCCAG CCCCGGGGGG CATGGCGGCG AGCCGCCTGC GCCCGCAGGA GAGTTCACTG CTGCAGCTCT	GOGGCAATGC CAGGGGCAGC COGCTTCAGG TTGACTTCTA GCCTGGCCCA TGTCCGGCAA CCATCAGCTC	180 240 300 360 420 480 540
60	AAGGGCCTCG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG	GCTGATGGCC GGAGAGGCGG GGGCCGGGAG TGCTGCAGAT CCTTTCGCGA CCGCTTCCCG ATCCGACTGA CAGCTTTCCC	CAGGAGGCCC GTGCCACGGG GAGGCGCCCC GCGGGGCCAG CACCCATGGA TGCCAGGGGT CTGCTGCAGA TGTTGATGTG	TGGCATTCCT CGGCAGAGGT GCGGGGTCCG GGGCCGGAG AGCAGAGCTG GCTTCTGAAG CCACCGCCAA GATCACCCAG	GATGGCCAG CCCGGGGGCG CATGGCGCTGC AGCCGCCTGC GCCGCAGGA GAGTTCACTG CTGCAGCTCT TGCTTTCTGC	GOGGCAATGC CAGGGGCAGC COGCTTCAGG TTGAGTTCTA GCCTGGCCCA TGTCCGGCAA CCATCAGCTC CCGTGTTTTT	180 240 300 360 420 480 540
	AAGGGCCTCG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GGCTCAGCCT	GCTGATGGCC GGAGAGGCGG GGGCCGGGAG TGCTGCAGAT CCTTTCGCGA CCGCTTCCCG ATCCGACTGA CAGCTTTCCC	CAGGAGGCCC CTGCCACGGG GAGGGCCAG CACCCATGGA TGCCAGGGGT CTGCTGCAGGA TGTTGATGTG AGAGGCGCTA	TGGCATTCCT CGGCAGAGGT GCGGGGTCCG GGGGCCGGAG AGCAGAGGCTG GCTTCTGAAG CCACCGCAA GCTCACGCAA AGCCCAGCCT	GATGGCCAG CCCGGGGGG CATGGCGCCTGC GCCGCAGGA GAGTTCACTG CTGCAGCTCT TGCTTTCTGC GGCGCCCCTT	GOGGCAATGC CAGGGGCAGC COGCTTCAGG TTGAGTTCTA GCCTGGGCCA TGTCCGGCAA CCATCAGGTC CCGTGGTTTTT CCTAGGTCAT	180 240 300 360 420 480 540
60 65	AAGGGCCTCG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCCG GGCTCAGCCT GCCTCCTCCC	GCTGATGGCC GGAGAGGCGG GGGCCGGGAG TGCTGCAGAT CCTTTCGCGA CCGCTTCCCG ATCCGACTGA CAGCTTTCCC	CAGGAGGCCC GTGCCACGGG GAGGCGCCG GCGCGGGCCAG GCCCATGGA TGCCAGGGGT CTGCTGCAGA TGTTGATGTG AGAGGCGCTA GTCCAGCACA	TGGCATTCT CGGCAGAGGT GCGGGGCGGAG AGCAGAGCTG GCTTCTGAAG CCACCGCCAA GATCACGCAA AGCCCAGCCTA AGCCCAGCCTA GACTGGCCAG	GATGGCCAG CCCGGGGGG CATGGCGGCG AGCGCCTGC GCCGCAGGA GAGTTCACTG CTGCAGCTCT TGCTTTCTG GGCGCCCTT TTCATTGTGG	GGGGCAATGC CAGGGGCAGC CGGCTTCAGG TTGAGTTCTA GCCTGGCCCA TGTCCGGCAA CCATCAGGTC CCGTGTTTTT CCTAGGTCAT GGGCCTGATT	180 240 300 360 420 480 540 600
	AAGGGCTCG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GGCTCAGCCT GCCTCCTCCC GTTTGTCGCT	GCTGATGGCC GGAGAGGGGG GGGCCGGGAG TGCTGCAGAT CCTTTCGCGA CCGCTTCCCG ATCGACTGA CAGCTTTCCC CCCTCAGGGC CTAGGGAATG GGAGGAGGACA	CAGGAGGCCC GTGCCACGGC GAGGCGCCAG GAGGCGCAG CACCCATGGA TGCCAGGGGT CTGCTGCAGA TGTTGATGTG AGAGGCGCTA GTCCCAGCAC GGCTTACATG	TGGCATTCT CGGCAGAGGT GCGGGGCGGAG AGCAGAGCTG GCTTCTGAAG CCACCGCCAA GATCACGCAA AGCCCAGCCTA AGCCCAGCCTA GACTGGCCAG	GATGGCCAG CCCGGGGGG CATGGCGGCG AGCGCCTGC GCCGCAGGA GAGTTCACTG CTGCAGCTCT TGCTTTCTG GGCGCCCTT TTCATTGTGG	GGGGCAATGC CAGGGGCAGC CGGCTTCAGG TTGAGTTCTA GCCTGGCCCA TGTCCGGCAA CCATCAGGTC CCGTGTTTTT CCTAGGTCAT GGGCCTGATT	180 240 300 360 420 480 540 600
	AAGGGCCTCG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GGCTCAGCCT GCCTCCTCCC GTTTGTCGCT Seq ID NO:	GCTGATGGCC GGAGAGGCGG GGGCCGGGAG TGCTGCAGAT CCTTTCGCGA CCGCTTCCCC ATCGGACTGA CAGCTTTCCC CCCTCAGGGC CTAGGGAATG	CAGGAGGCCC GTGCCACGG GAGGGCCAG GAGGGCCAG CACCATGGA TGCCAGGGGT CTGCTGCAGA TGTTGATGTG ACAGGGCTA GTCCCAGCAC GGCTTACATG Bequence:	TGGCATTCT CGGCAGAGGT GCGGGGCGGAG AGCAGAGCTG GCTTCTGAAG CCACCGCCAA GATCACGCAA AGCCCAGCCTA AGCCCAGCCTA GACTGGCCAG	GATGGCCAG CCCGGGGGG CATGGCGGCG AGCGCCTGC GCCGCAGGA GAGTTCACTG CTGCAGCTCT TGCTTTCTG GGCGCCCTT TTCATTGTGG	GGGGCAATGC CAGGGGCAGC CGGCTTCAGG TTGAGTTCTA GCCTGGCCCA TGTCCGGCAA CCATCAGGTC CCGTGTTTTT CCTAGGTCAT GGGCCTGATT	180 240 300 360 420 480 540 600
65	AAGGGCCTCG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GGCTCAGCCT GCCTCCTCCC GTTTGTCGCT Seq ID NO:	GCTGATGGCC GGAGAGGCGG GGGCCGGAG TGCTGCAGAT CCTTTCGCGA ACCGGTTCCCG ATCGGACTGA CAGCTTTCCC CCCTCAGGGC CTAGGGAATG GGAGGAGGAC 210 Protein ccession #: 1	CAGANGECE GTGCCACCGE GAGGCCCAC GCGGGCCAC GCACCATGGA TGCCAGGGGC TGCTGCAGA TGTTGATGTG AGAGGCGTA GTCCCAGCAC GCCTTACATG 1 sequence: MP_001318.1	TGGCATTCOT CGGCAGAGGT GCGGGGTCCG GGGGCCGAG AGCAGAGCTG CCTTCTGAAG CCACCCCA AATCACCAG AGCCCAGCCT GACTGGCCAG TTTGTTTCTG	GATGGCCCAE CCCGGGGGG CATGGCGGCG AGCCGCTGC GCCGCAGGA GASTTCACTG CTGCAGCTTTTGGT TTCATTGTGG TAGAAAATAA	GGGCCAFTCC CAGGGCAGC CAGGCTCAGG TTGAGTTCTA GCCTGGCCCA TGTCCGGCAA CCATCAGCTC CCGTGTTTTTT CCTAGGTCAT GGGCCTGATT AACTGAGCTA	180 240 300 360 420 480 540 600
	AAGGCCTGG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT TCTGTCTCCAG GGCTCAGCCT GCCTCTCCC GTTTGTCGCT Seq ID NO: Protein Act	GCTGATGGCC GGGCCGGAG TGCTGCAGAT TGCTTCGGAG CCGCTTCCCG ATCCGACAT CCACTTCCC CCTCAGGGC CTAGGGAAT GGAGGAGAC 210 Protein ccssion #: 1 11	CAGAMGECE GTGCCACCCG GAGGGCCCC GCGGGGCCAC CACCATGGA TGCCAGGGT TGTTGATATG AGAGGCCTA GTCCAGCAC GGCTTACATG Bequence: UP_001318.1	TGGCATTCOT CGGCAGAGGT GCGGGGTCCG GGGGCCGGAG AGCAGAGCTG GCTTCTGAAG CCACCOCCNA AGTCACGCCG AAGCCAGCCT GAGTGGCCAG TTTGTTTCTG	GATGGCCAG CCCCGGGGG CATGGCGGC AGCCGCTOC GCCCGAGGA GAGTTCACTG CTGCAGCTCT TGCTTTCTGC GGCGCCCTT TTCATTCTGG TAGAAAATAA	GGGCCAATGC CAGGGGCAGC CGGCTTCAGG TTGAGTTCTA GCCTGGCCA TGTCCGGCAA CCATCAGCTC CCTAGGTCAT CCTAGGTCAT GGGCCTGATT AACTGAGCTA	180 240 300 360 420 480 540 600 660 720
65	AAGGGCTGG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GGCTCAGCCT GCCTCTCCC GTTTGTCGCT Seq ID NO: Protein Ac. 1	GCTGATGGCG GGGCCGGAG GGGCCGGAG TGCTGCAGAT CCTTTGGGA ATCCGACTGA ATCCGACTGA CAGCTTCCC CCTCAGGGC CTAGGGAGT GGAGGAGGAC 210 Protein cession *: 1 1 1 3 STGDADGGGG	CAGGANGCCCG GAGGCCCCG GAGGCCCCG CAGCCATGGA TGCCAGGGGT TGCTGGATGTA AGAGGCGTA AGAGGCGTA CTCCAGCCA GGCTTACATG A sequence: HP_001318.1 21 PGIPDGPGGN	TGGCATTCCT CGGCAGAGGT GGGGGGGGGGGGGGGGGG	GATGGCCAG CCCGGGGGG CATGGCGCTGC AGCCGCAGGA GAGTTCACTG CTGCAGCTCT TGCTTTCTGC GGGGCCCCTT TTCATTGTGG TAGAAAATAA 41 GGGGGPRGAGA	GGGCCAATGC CAGGGGCAC CGGCTTCAGG TTCAGTTCTA GCCTGGCCA TGTCCGCCA TGTCCGCCA TGTCCGCCA TGTCCGCCA TGTCCGCCA TGTCCGCCA TGTCCGCCA TGTCCTTTT CCTAGGTCAT AACTGAGCTA TAACTGAGCTA	180 240 300 360 420 480 540 600 660 720
65 70	AAGGGCTGG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GGCTCAGCCT Seq ID NO: Protein Ac 1 NQAEGGGTGG PRGFHGGAAS	GCTGATGGCC GGGCCGGAG TGCTGCAGAT TGCTTCGGAG CCGCTTCCCG ATCCGACAT CCACTTCCC CCTCAGGGC CTAGGGAAT GGAGGAGAC 210 Protein ccssion #: 1 11	CAGGAMGCCCC GAGGGCCAG GAGGGCCAG CACCATGGA TGCCAGGGT TGCCAGGAG TGTCAATGA GTCCCAGCAC GGCTTACATG a squence: NP_001318.1 21 PGIPDGGGA	TGGCATTCCT GGCAGAGGT GGGGGCCGGAG AGCAGGCT GCTTCTGAAG CCACCOCCAA AGCCAGGCT GACTGCCCA TTGTTTCTG 31 AGGGGGAGAT AGGGCAGAT TTGTTTCTG TLAMBFATTM	GATGGCCAG COCCGGGGGG CATGGCGCCAGGA AGCCGCCAGGA GAGTTCACTG TGCATTCATG GGGGCCCCT TTCATTGTG TAGAAAATAA 41 GGRGPRGAGA GGGGPRGAGA EAGLARRSLA	GGGCCAATGC CGGCTTCAGG TTGACTTCTA GCCTGGCCA TGTCCGCCA CCATCAGGTC CCATCAGGTC CCTAGGTCAT CCTAGGTCAT GGGCCTGATT AACTGAGCTA 51 ARASGPGGGA QDAPPLPVPG	180 240 300 360 420 480 540 600 660 720
65	AAGGGCTGG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GGCTCAGCCT Seq ID NO: Protein Ac 1 NQAEGGGTGG PRGFHGGAAS	GCTGATGGCC GGAGAGGCGG GGGCCGGAG TGCTGCAGAT CCTTTCGGA CCGCTTCCCG CCCTCAGGGC CTCCTAGGGAAT GGAGGAGGAC 210 Protein cession #: 1 1 1 1 JGDADGPGG GLNGCCCGA	CAGGAMGCCCC GAGGGCCAG GAGGGCCAG CACCATGGA TGCCAGGGT TGCCAGGAG TGTCAATGA GTCCCAGCAC GGCTTACATG a squence: NP_001318.1 21 PGIPDGGGA	TGGCATTCCT GGCAGAGGT GGGGGCCGGAG AGCAGGCT GCTTCTGAAG CCACCOCCAA AGCCAGGCT GACTGCCCA TTGTTTCTG 31 AGGGGGAGAT AGGGCAGAT TTGTTTCTG TLAMBFATTM	GATGGCCAG COCCGGGGGG CATGGCGCCAGGA AGCCGCCAGGA GAGTTCACTG TGCATTCATG GGGGCCCCT TTCATTGTG TAGAAAATAA 41 GGRGPRGAGA GGGGPRGAGA EAGLARRSLA	GGGCCAATGC CGGCTTCAGG TTGACTTCTA GCCTGGCCA TGTCCGCCA CCATCAGGTC CCATCAGGTC CCTAGGTCAT CCTAGGTCAT GGGCCTGATT AACTGAGCTA 51 ARASGPGGGA QDAPPLPVPG	180 240 300 360 420 480 540 600 660 720
65 70	AAGGGCTGG GCTGAATGGA CCTCGCCATG GGATGCCCCAA CATACTGACT CTGTCTCCAG GCCTCCTCCC SCG ID NO: Protein Acc 1	GCTGATGGCC GGGCCGCAG GGGCCGCAG GGCCCGCAG CCCTTCCGCG CCCTCCCGC CCCTCAGGC CTACGGAATG CGGATTCCC 210 Protei cession #: 1 1 1 STGDADGPGG GLNGCCCGCA NILTIRLTAA	CAGGANGECCE GAGGACCCA GAGCACCA GACCCATGGA TGCCAGGAGT TGTTGATTG GTCCAGCAC GACTACACC A BEQUENCE BP_001318.1 21 PGIPDGPGGN RGPESRLLEF DHRQLQLSIS	TGGCATTCCT GGCAGAGGT GGGGGCCGGAG AGCAGGCT GCTTCTGAAG CCACCOCCAA AGCCAGGCT GACTGCCCA TTGTTTCTG 31 AGGGGGAGAT AGGGCAGAT TTGTTTCTG TLAMBFATTM	GATGGCCAG COCCGGGGGG CATGGCGCCAGGA AGCCGCCAGGA GAGTTCACTG TGCATTCATG GGGGCCCCT TTCATTGTG TAGAAAATAA 41 GGRGPRGAGA GGGGPRGAGA EAGLARRSLA	GGGCCAATGC CGGCTTCAGG TTGACTTCTA GCCTGGCCA TGTCCGCCA CCATCAGGTC CCATCAGGTC CCTAGGTCAT CCTAGGTCAT GGGCCTGATT AACTGAGCTA 51 ARASGPGGGA QDAPPLPVPG	180 240 300 360 420 480 540 600 660 720
65 70	AAGGGCTGG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GCCTCCTCCC Seq ID NO: Protein Act	GCTGATGGCC GGGCGGGAG GGGCCGGGAG TGCTGCAGAT CCTTTOGGGA CCGCTTCC CCCTCAGGGC CCTCAGGGC CCTCAGGGAC GAGGGTTGC GGAGGAGGAC L10 Protein Ccession #: 1 STGDADGFGG GLNGCCCGGA NILTITLTAA 211 DNA see 211 DNA see 11 ACCCESSION	CAGAMGCCC GAGAGGCCC GAGAGCCCC GAGAGCCCC CACCATGAA TGCCAGAGGCCCC TGCCAGCAG ACAGGCCCCTA CACCACCACCAC CACCACCACCACCACCACCACCACC	TGGCATTCCT CGGCAGAGGT CGGCAGAGGT GGGGGCGGAG AGCAGCAGCAG AGCACACCCA AGCACCACCT AACTGCCAG TTTGTTTCTG 31 AGGGGGAGAGT SCGCAGCT AACTGCCAGACT AACTGCCAG ACTCCACCT AACTGCCAG ACTCCACCT AACTGCCAGCT AACTGCCAGCT AACTGCCAGCT AACTGCCAGCT TTTGTTTCTG 31	GATGGCCAG COCCGGGGGG CATGGCGCCAGGA AGCCGCCAGGA GAGTTCACTG TGCATTCATG GGGGCCCCT TTCATTGTG TAGAAAATAA 41 GGRGPRGAGA GGGGPRGAGA EAGLARRSLA	GGGCCAATGC CGGCTTCAGG TTGACTTCTA GCCTGGCCA TGTCCGCCA CCATCAGGTC CCATCAGGTC CCTAGGTCAT CCTAGGTCAT GGGCCTGATT AACTGAGCTA 51 ARASGPGGGA QDAPPLPVPG	180 240 300 360 420 480 540 600 660 720
65 70	AAGGGCTGG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GCCTCCTCCC Seq ID NO: Protein Act	GCTGATGGCC GGGCGGGGG GGGCCGGGAG TGCTGCAGAT CCTTTOGGGA CCGCTTGCG ATCCGACTGA CAGCCTTCACGGC CTAGCGATGA CAGCCTTCACGGC CTAGCGAATG CGAGGACGAC 210 Protein CCCGGGAGACGAC 311 11 1 1 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	CAGAMGCCC GAGAGGCCC GAGAGCCCC GAGAGCCCC CACCATGAA TGCCAGAGGCCCC TGCCAGCAG ACAGGCCCCTA CACCACCACCAC CACCACCACCACCACCACCACCACC	TGGCATTCCT CGGCAGAGGT CGGCAGAGGT GGGGGCGGAG AGCAGCAGCAG AGCACACCCA AGCACCACCT AACTGCCAG TTTGTTTCTG 31 AGGGGGAGAGT SCGCAGCT AACTGCCAGACT AACTGCCAG ACTCCACCT AACTGCCAG ACTCCACCT AACTGCCAGCT AACTGCCAGCT AACTGCCAGCT AACTGCCAGCT TTTGTTTCTG 31	GATGGCCAG COCCGGGGGG CATGGCGCCAGGA AGCCGCCAGGA GAGTTCACTG TGCATTCATG GGGGCCCCT TTCATTGTG TAGAAAATAA 41 GGRGPRGAGA GGGGPRGAGA EAGLARRSLA	GGGCCAATGC CGGCTTCAGG TTGACTTCTA GCCTGGCCA TGTCCGCCA CCATCAGGTC CCATCAGGTC CCTAGGTCAT CCTAGGTCAT GGGCCTGATT AACTGAGCTA 51 ARASGPGGGA QDAPPLPVPG	180 240 300 360 420 480 540 600 660 720
65 70 75	AAGGGCTGG GCTGAATGGA CCTCGCCATG GGATGCCCCA CATACTGACT CTGTCTCCAG GCCTCCTCCC Seq ID NO: Protein Act	GCTGATGGCC GGGCGGGAG GGGCCGGGAG TGCTGCAGAT CCTTTOGGGA CCGCTTCC CCCTCAGGGC CCTCAGGGC CCTCAGGGAC GAGGGTTGC GGAGGAGGAC L10 Protein Ccession #: 1 STGDADGFGG GLNGCCCGGA NILTITLTAA 211 DNA see 211 DNA see 11 ACCCESSION	CAGAMGCCC GAGAGGCCC GAGAGCCCC GAGAGCCCC CACCATGAA TGCCAGAGGCCCC TGCCAGCAG ACAGGCCCCTA CACCACCACCAC CACCACCACCACCACCACCACCACC	TGGCATTCCT CGGCAGAGGT CGGCAGAGGT GGGGGCGGAG AGCAGCAGCAG AGCACACCCA AGCACCACCT AACTGCCAG TTTGTTTCTG 31 AGGGGGAGAGT SCGCAGCT AACTGCCAGACT AACTGCCAG ACTCCACCT AACTGCCAG ACTCCACCT AACTGCCAGCT AACTGCCAGCT AACTGCCAGCT AACTGCCAGCT TTTGTTTCTG 31	GATGGCCAG COCCGGGGGG CATGGCGCCAGGA AGCCGCCAGGA GAGTTCACTG TGCATTCATG GGGGCCCCT TTCATTGTG TAGAAAATAA 41 GGRGPRGAGA GGGGPRGAGA EAGLARRSLA	GGGCCAATGC CGGCTTCAGG TTGACTTCTA GCCTGGCCA TGTCCGCCA CCATCAGGTC CCATCAGGTC CCTAGGTCAT CCTAGGTCAT GGGCCTGATT AACTGAGCTA 51 ARASGPGGGA QDAPPLPVPG	180 240 300 360 420 480 540 600 660 720
65 70 75	AAGGGCTCG GCTGAATOGA CCTGCCCATC GCATCGCCATC GCATCGCCCATC GCTGCTCCCAC GCCTCCACCC GCTTGTCGCC TTTGTCGCT Seq ID NO 1 1 MQAGGGTGC PROFINGAAS VLLKEFTVS Seq ID NO Seq ID N	GCTGATGGCC GGGAGGGCGC GGGCCGGGAGGCCGGGAGGGCCGGGAGGCCGGGAGGAGGA	CAGGAGGCC GAGGAGGCC GAGGAGCCC GAGGAGCCC GAGGAGCCC CAGGAGCCC CAGGAGCC CAGGAGC CAGGAGCC CAGGAGCC CAGGAGCC CAGGAGC CAGG	TGGCATTCCT GGGGGGGGGG GGGGGGGGGG AGGCAGGGG AGGCAGGGG AGGCAGGGG AGGCAGGGT TTGTTCTQ 31 } AGGGGGAGGAGT THGTTCTQ 31 junece	GATGGCCCAG CACCGGGGGCCCCAGA AGCGCCCTC GCCCCAGGA GATTCACTC TCCTTCTCC GGGGCCCCTT TTCATTCTGG TTCATTCTGG GGGGCCCTT TTCATTCTGG TAGAAAATAA 41 GGRGFRGAGA EAGLARRSIA WITCCFLPVP	GGGCAATCC CAGGGGCAG CORCTTCAGG TTRAGTTCTA GCCTGGCCA TTRAGTCTA GCCTGGCCA CCCTGGCCA CCCTGCTCAG CCCTGGCCA TAGATCTA 51	180 240 360 360 420 480 540 660 720
65 70 75 80	AAGGGCTCG GCTGAATOGA CTCGCCATC GCTGATCGCAC CTCGCCCAC GCATCGCCC CTGTCTCGCAC GCTGCTCGCCAC GTTGTCGCCAC TTGTCTCGCC TTTGTCGCCT TTGTCGCCT TTGTCGCC TTGTCGC TTGTCGCC TTGTCGC TTGTCGC TTGTCGC TTGTCGC TTGTCGC TTGTCGC TTGTCGCC TTGTCGC TTGTCG	GCTGATGGCC GGGAGGGCCG GGGCCGGGAGGCCGC GGGAGGCCGC GGGCCGGGAG TCCCGATCGC CCCT CAGGCA TCCCAGCATTGC CCCT CAGGCA TCCCAGCATTGC CCCT CAGGCATTGC CCCT CCT CCCT CC	CAGAMGCCC CAGAMGCCC CAGAMGCCC CAGAMGCCCC CAGAMGCCC CAGAMGCC CAGAMGCCC CAGAMGCC CAGAMGCCC CAGAMGCC CAGAMGCCC CAGAMGC	TGGCATTCT GGGGGGGGGG GGGGGGGGGA AGCAKAMGTG GGGGCCGAM AGCAKAMGTG GATTCACCCA AGCACCACA AGCACCACA TTTGTTTCTG 31 1 AGGGGGAGA TTTGTTTCTG 31 QUENCE	GATGGCCCAG CACCOCCAGA CACCACAGA CACCACACAGA CACCACACACA	GGGCAATTCC CAGGGGCAC CORCTTCAGG TTRAGTTCTA TTRAGTTCTA TTTAGATTCTA TCTCAGGCAC COCTAGGCAC COCTAGGCAC ST 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	180 240 360 360 420 480 540 600 660 720
65 70 75	AAGGGCTCG GCTGAATOGA CTCGCCATG GCTGAATOGA CTCGCCCATG GCTCAACCG GCTCAACCC GTTGTCCCAG 1 NOAEGRGTGG PRCGTIGGAAC Seq ID NO: PROTEIN NOAEGRGTGG PRCGTIGGAAC COding seq 1 CTCCCTCCCC CTTGTCCCAG CCCCCCCC CTTGTCCCAG 1 CTCCTCTCCCC CTTGTCCCC CTTGTCCC CTTGTCC CTTGTC CTTGT CTTG	GCTGATGGCC GGAGAGGCGC GGGCCGGGAG GGGCCGGGAG CCTTTGGCGA CCTTTGGCGA CCTTTGGCGA CCTTTGGCGA CCTTTGGCGA CCTTTGGCGA CCTTTGGCGA CCTTTGGCGA CCTTGGCGC CCTGAGGGGAG 210 Protei cession #: 1 11 11 21 21 DAN secida ACCTGGGAGAGGAGA ALLTIRLTA 211 DAN secida Accession usence: 52-4: 11 11 11 11 11 11 11 11 11 11 11 11 11	CAGAMGCCC GAGAMGCCC GAGAMGCCC GAGAMGCCCC GAGAMGCCCC GAGAMGCCCC GAGAMGCCCC GAGAMGCCCC GAGAMGCCCC GAGAMGCCCC GAGAMGCCCC TOTTCATCA CAGAMGCCCTT CATCA CAGAMGCCCTT CATCA CAGAMGCCCT CATCA CAGAMGCCCT CATCA CAGAMGCCCT CATCA CAGAMGCCCT CATCA CAGAMGCCCT CATCA CAGAMGCCC CATCACAT CACCAGAMC CACTACATC CACCAGAMC CACCAGAMCC CACCAGAMCCC CACCAGAMC	TGGCATTCT GGGGGAGAGG GGGGGGGGAGA AGCAGAGGGG GGGGGGGAGA AGCAGAGGGG GATGGGGGGGAGAG 31 GGGGGGAGAG GATGGCGAG CGGGGGAGAGAG GATGGCAGAGAG CGGGGGGAGAGAG GATGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GATGGCCCAG CACCAGGAGAGAGAGAGAGAGAGAGAGAGAGA	GGGCAATCC CAGGGGGAC COSCTITCAGG TTAGATTCTA COCTOGGCC COCTOGGCC CCCCCAGGCCC CCCCAGGCCCA 51 AACCCAGGCCA CAACAGCCC CCCCAGGCCA CAACAGCCC CCCCAGGCCAC CCCCAGGCCCA 51 AACCCAGGCCC CCCCCAGGCCC CCCCCCCCCC CCCCCCCC	180 240 300 360 420 480 540 660 720 60 120
65 70 75 80	AAGGGCTCG GCTGAATOGA CTCGCCATC GCTGATCGCATC GCATCGCCATC GCATCGCCATC GCTGCTCCGCAT GCCTGCTCCCGC GTTTGTCGCT I NQAGGRGTGC FRGCHGGCATC Seq ID NO: Nucleic Ac Coding seq I CCCGTGTCCC GAGGGGGGGGGGGGGGGGGGGGGGGGGG	GCTGATGGCC GGGAGGGCCG GGGCCGGGAGGCCGC GGGAGGCCGC GGGCCGGGAG TCCCGATCGC CCCT CAGGCA TCCCAGCATTGC CCCT CAGGCA TCCCAGCATTGC CCCT CAGGCATTGC CCCT CCT CCCT CC	CAGAMGCCC GAGAMGCCC GAGAMGCCC GAGAMGCCC GAGAMGCCA GAGAMGCCC CACAGAMGCCC CACAGA	TGGCATTCT GGGGGGGGGG GGGGGGGGGGGGGGGGGGG	GATGGCCCAM CCCCCGGGGGCC CATGGCGCCAC CATGGCGCCC CATGGCGCCCC CATGGCGCCC CATGGCCCC CATGGCCCC CATGGCCCC CATGGCCCC CATGGCCCC CATGGCCCC CATGGCCCC CATGGCCC CATGCCC CATGGCCC CATGGCCC CATGGCCC CATGGCCC CATGGCCC CATGGCCC CATGGCC CATGGCCC CATGCCC CATGGCCC CATGGCCC CATGGCCC CATGGCCC CATGGCCC CATGGCCC CATGGCC CATGGCCC CATGGCC CATGGCCC CATGGCC CATGGCC CATGGCC CATGGCC CATGCC CATGGCC CATGGCC CATGCC CATGGCC CATGGCC CATGGCC CATGGCC CATGGCC CATGCC CATGGCC CATGGCC CATGCC CATG	GGGCAATTC GGGGGGATC CGGGGTTAGG TTCTGGCAT TTCTGGCAT TTCTGGCAT CCTGGCAT TTCTGGCAT TTCTGCAT TTCTGGCAT TTCTGGC	180 240 360 360 420 480 540 600 660 720

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	ATCAGCTCCT	TGCTTCAGTT CTCTCCAGCA CTCAGGCTCC CTCCTCCCCT	GCTTTCCCTG	TTGATGTGGA AGGCGCTAAG	TCACGCAGTG	CTTTCTGCCC	360 420 480 540
5	GCCTGATTGT CTCAGCTA	TTGTCGCTCG	AGGAGGACGG	CTTACATGTT	TOTTTCTGTA	GAAAATAAAG	600
10		212 Protein cession #: 1	Sos sequence				
	1	11	21	31	41	51	
15	MQAEGQGTGG PRCPHGGAAS FLPVFLAQAP	STGDADGPGG AQDGRCPCCA SGQRR	PGIPDGPGGN RRPDSRLLQF	AGGPGEAGAT RLTAADHRQL	GGRGPRGAGA QLSISSCLQQ	ARASGPROGA LSLLMWITQC	60 120
20	Nucleic Ac:	213 DNA ser id Accession nence: 416.	4: NM_0005	55			
	1	11	21	31	41	51	
		ATGAATGTCG	CAMPGOMCO	OCTACO TOTAL	00000000000	managara an	60
	AGCACAAAGA	CACTGGCTGT	TOCCTGGAGG	CTGTCCCTTT	ARAGGAGAAT	CTTAGTTTAT	120
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	ACTUCCUUTT	CATAGTCATT AGCTCCTTCT	GTACTGAAAT	AGGGGAATTT	TOTCAGGCTA	TOGACTTCATT	300
	TACAACTGTT	AGTCATGTGG	GCATGTGTGA	GGAAACAGAT	GCCAGTTTTA	ATGTATTTAG	360
30	CCCGAAGTTC	CAATTTGATA GGACACTTTG	GGAGCCACTG	TCAGTCTCTG	AGGTTCCACC	AAAATATGGA	420 480
50	GATGAATGGG	TTGCCTAGCC	CCACTCACAG	CGCCCACTGT	AGCTTCTACC	GAACCAGAAC	540
	CTTGCAGGCA	CTGAGTAATG	AGAAGAAAGC	CAAGAAGGTA	CGTTTCTACC	GCAATGGGGA	600
	CCGCTACTTC	AAGGGGATTG GACCTGACGC	CATCTCTCTCT	TGACALCATC	AACCTGCCTC	AGGGAGTGCG	660 720
35	TTACATTTAC	ACCATTGATG	CATCCAGGAA	GATCGGAAGC	ATGGATGAAC	TGGAGGAAGG	780
	GGAAAGCTAT	GTCTGTTCCT TGGTCTGTCA	CAGACAACTT	CTTTAAAAAG	GTGGAGTACA	CCAAGAATGT	840 900
	GGCTAGCAGC	AACAGTGCAC	AGGCCAGGGA	GAACAAGGAC	TTTGTGCGCC	CCAAGCTGGT	960
40	TACCATCATC	CGCAGTGGGG	TGAAGCCTCG	GAAGGCTGTG	CGTGTGCTTC	TGAACAAGAA	1020
40	GACAGCCCAC	TCTTTTGAGC AAAAAACTCT	AAGTCCTCAC	TGATATCACA	GAAGCCATCA	TCCATGATTT	1080
	CTTTGGTGAT	GATGATGTGT	TTATTGCCTG	TGGTCCTGAA	AAATTTCGCT	ATGCTCAGGA	1200
		CTGGATGAAA GCATCCCCAA					1260
45	CCGAAGCAAG	TCTCCAGCTG	ACTCAGCAAA	CGGAACCTCC	AGCAGCCAGC	TCTCTACCCC	1380
	CAAGTCTAAG	CAGTCTCCCA	TCTCTACGCC	CACCAGTCCT	GGCAGCCTCC	GGAAGCACAA	1440
	GAGGGGAGAG	CTGCCTCTGT	CCTTGGATGA	BATTCARGC	TATCATTOTA	GTAGGGTAGT	1560
	TCTGCTCAAG	TGTCCAACAG	GGCTATTGGT	GCTTTCAAGT	TTTTATTTTG	TTGTTGTTGT	1620
50	TATTTTGAAA	AACACATTGT CAGTTACCAA	AATATGTTGG	GTTTATTTTC	CTGTGATTTC	TCCTCTGGGC	1680 1740
	TCCAGGGATG	CAAAATGTGC	TAGTCCATGA	CCTTTCAATG	GARAGCTTAG	GGGCCTGGGG	1800
	TARATTTGCC	CCGTTTAAAT	TTGCCCAAAC	AGTTTTCCTT	TTGTAGAGGG	GTGTTTAAAT	1860 1920
55	ACAAACACAA	TAAAAAGTTT	TCTCTGGGGAA	TCAAGAATGG	TGGAGGACCC	TGGAAGGACA	1920
	GCAAGGCAGC	TCCCCAGCCT	CACTCTTCAC	TCCTGATTGA	GGCCCGGGTT	TGTTGTCCAG	2040
	CACCAATTCT	CCTGGTCAAT	GGGGAGAAAT	AAACCAACAA	CTTATAATTG	TGACACCAGA	2100 2160
	ACATTTCCGA	AGAGTTTATA	AAGCACAGTG	AATTCCTGGT	CAATCTCTCC	ACTGAGGCAA	2220
60	TTTGGAATCA	ATAAGCAATT TGTCTAACAT	GATAATAGTT	TOGAGTAAGG	GACTTCATAT	ACCTGATTCC	2260
	TOTACCATTC			CACTGAAAAC			2400
	GGTCTGACAC	CTTTCAGTCT	CTTTTTATAG	CAAGAAATCA	ATATOCTTTT	TATAAAAATT	2460
65	CATGTCTCTA	TTTCAGGACC AAAACACATG	AMACTOTTCA	ACCAGAAAAA	AAAAAAAAAA	CCGAAGAATA	2520 2580
	ATGTTATTTA	GAAATTATGC	TGTCACTGCC	AAACAGTAAC	CTCCAGGAGA	AAACAAGATG	2640
	AATAGCAGAG	CCCAATTCAA	TAGAATCAGT	CTARTATAT	CTTTTTAACA	ATTATGCTTG	2700 2760
	ATATTTTAAG	CAACTCTTTT	TATCTATAAT	CCTAATATTT	CATACTGAAG	ACACAGAAAT	2620
70	CTTTCACTTG	TCTTTAACAT	TAGAAAGGAT	TTCTCTTTAC	TAAGGACTGA	TCATTTGAAA	2880
	GCCCATANTG	TCTTTTGAGA GCAAAAACAA	CTAATTTTAA	TTGAAGGTCT	TOCTTGCCAN	TCCTGTGTTG	2940 3000
	GCTTTNACCA	ARTATAAAAA	TTCCCTTATT	CCTTGGTAAT	GGTGCAAATN	TTTGGAAAGG	3060
75	CACAGCATCC	AAACCAAGCT TGAGCTTGCT	GCTGTTTGGC	TACTGAATGG	TOGGLOCOC	TROCTCCACT	3120 3180
, ,	GTGTGTGTGT	CTGTGCATCT	GCAGCTGCTT	CAAAATTAAG	ANATACTACA	AGACACCCCT	3240
	GTAATGGATT	CGTGCCAACT	GGGTGGCACT	GCTGATGTGC	ACTGTGTAGG	GGGGAACCCA	3300
	ACATTTTOGG	CGTATCTCAA TTCAAGAAAA	GTGAGATGAT	GGTAGTACTG	GTTTCTGGTG	AAATTGAAAA	3360 3420
80	ACCCCAAATG	ATGAGGATCT	CTTTTTGCCC	CCTCTCCTTT	TTTTGTAAAC	CCATTCAAAA	3480
	CCATTAATAA	CCCCATTTTA NAACATTTTG	CTAANCCCCT	ATTTCTTTCT	AGAAGCTCAG	GGTTTNCTTA	3540
	GGGCATAAAG	AATOGTGGGA	GGCCTGATTT	TAAAATTCAG	GCCAGAACCC	CCAATGACTC	3660
85	CACCCATAGT	NTCACTITAG	GTCTCATTTA	GTCCATCACC	TTTATTTTAA	GTTGAGGAAG	3720
05	ACACTAGOTO.	TARAGAGCAG TNTGAGTATT	TOTTOGATTO	COGTATATOT	ACTACTAGAA	BATACCABAT	3780 3840
	GGATATATTT	TCTTTAGGAT	AACCTITGAA	CCAACAATNT	TCAATAACAA	TAGTACATCT	3900

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	TCCATCITAC	TTTTAATCGA	GTATAAGGAA	ATGTTTCTTT	ATGOCCATTT	TOGAGGGAGC	3960
	DADTADDDDA	OCTTOOCATA	GTCCAAAATT	TARGICTOCA	ATABTTABTT	GCATTITAAA CTGAGCTCCT AGTTCCATTG	4020
	macmanan	mnoccoon on	THE PARTIES A	mmmommmoom	CATACON CANADA IN	COURT COUNCES	4000
	HULLIAM	TIGGCCCACT	TICKNOGCKA	1111111111111111	GIGICIGIAN	CIGNOCICCI	4000
-	CCACCCCTGT	CATTCACTTC	CAATTTTACC	CAATCCAATT	TTAGCACTCA	AGTTCCATTG	4140
5	TGTTAATTTT	TGCACGGTCT	ACACACATCA	AGTCAGCAAG	CATTTGCCAC	CACTCCCTAT CTCTTGCTTG GAAGGGGAAA	4200
	ACTTCTCCCCT	CTTTTTTACA	CACACACACA	CACACACACA	CACAATCCAT	CTCTTGCTTG	4260
	TTCCTACCTC	CCTCATTTTT	CTTCCCTACA	CARATACARA	TACCCCACAAA	CARCOCOGANA	4320
	************	maccamaga	CTCCCCTACA	3.3.0mmqsms.s	OTTA CTTA TITO I	CTAGGGGTAA TAGCATGACT TTTTCTAGCT	43.00
	AIGIAIAIAI	1000001000	CIGNACAACI	MACTICATAN	GIAGIATIAN	CINGGOSIAN	4300
1.0	ATTGAGAGAA	AAGCTCCTTT	TCTCTTCACT	GTTTTGGAAA	GGATAGCCAT	TAGCATGACT	4440
10	GCTTTGTGTC	CTTATGGACT	TTAGTATTAG	CCTAGATTGA	ATTATAGCGT	TTTTCTAGCT	4500
	1001111001	CACACACACAC	TARROTTA STOP	TOCCOOR NOOT	CACACACCCTC	GCTGGGGGCAG CACTAAGTAG	4620
	AGGMANCCOM	CMCACAGAGG	IMMOIMIL	TCCCCGGGGT	CHCHCHGCIG	GCIGGGGCNG	1020
	GATTGGGTTT	ACAACCCACA	TCTCCTGGCT	CITATICCAG	GGCCTTTTCC	CACTAAGTAG	4680
	TATTGCCTTC	CATTAGGCTC	CTGAGAGTTA	TTTCTCAGGG	TCATGTTGCA	TCTTGGAGCC	4740
15	ACATGCTGCT	GCCCTGATCT	CAGTGGGAAA	TNCACCCAGC	AACCTAATAC	AGCCCCTTTT AGAGTGAGGC	4800
	CCCTCCATTC	ACCTGGTTCC	CATCCACATG	COTTOTAGAT	OTCOTTGAMO.	AGAGTGAGGC	4860
	**************************************	1001001100	Amoooooooo	maacammama	Chronosamo	ACCR CAMCAC	4020
	ATTUMOUSCC	MINOSHUCA	ALGOOGICCC	IGGCCITGIC	CATCIONITIC	MOGNONICAC	4960
	TGCTCCATCG	TGAGGAGCCC	TCTGAATAGC	CCCCCACTGA	ATGCTTGCCT	TGCCCCAAATG	4980
	GAATGGAGGA	AGATTGATTT	TCTCCATCAG	TTCACCTTGT	GTCATCTCAT	AGGAGATCAC TGCCCAAATG AATGGTTGGT GAGTGGAACA	5040
20	CTTTCCAGGC	TGAGGGAAAT	GTTTCTTGTT	TOCAHAGTAN	AAAAAAGAAA	CACTCCAACA	5100
	Ama lacomonom	meamooma a c	TOROTO A CAT	COORDINATED	CATTTANANA	GAGTGGAACA AAACTAGTGT TAGAGAAAAT CTGCTNTGAT TOGCTGATGT ACACTCTTCC CAAAAGGTC TATTTATTAG	5160
	ATANCTTTGT	TCATCCTAAC	TITCIGAGAI	GGCTTTTCAN	CATTIMANA	MMCIAGIGI	2100
	GGTACCATTC	ACTOGCANGA	TTTNTTTTAG	AATATGGGAG	TAAGATGAGG	TAGAGAAAAT	5220
	AACCTGGTCT	CACTGTGGTT	GCCCTCATCC	ACAATGTCCC	GANAGCCATC	CTGCTNTGAT	5280
	CACCACAATT	TOTAGGTATA	AGCAAGGGGC	TTTGTGAGAA	ABATOTACYC	TOGGCTGATGT	5340
25	mana and	ODGGGGGGGG	maga aga a a a	macca a como	TOTAL CONTROL OF THE PARTY OF T	LONGTOTOG	5400
23	TANACATTOO	CICCIGIGIT	TOCACCADOOL	TAGCIDIGCEG	TOTOCICIAL	MCMCICITCC	5400
	CATCGTCTTG	TGTACACTGC	TCCTGTGGCC	TTCCACAGCA	GAAACCAGGG	CAAAAGGGTC	5460
	CAAACACATG	GTTTTCCTTG	CTGCAAGGCT	NTTCCTGGGA	ACTAAGGGGG	TATTTATTAG	5520
	TTCAGTTNTA	AGAGACCTCC	TECTOGGCTT	ACCCCACTCC	TCAGGTACTT	CTCTCTCCTT TGTAGCTATT TCTTAGACCA	5580
	aamaamaaa	OTTOGRACACITICS	A CONNECTION A CIC	A NOOS A COTTO	AND CHOCATO	2000 CORN 27	5640
30	CCICCITCIC	CICCACABIC	ACMIGIANCE	MAGGAMECTIG	MANGIGGAIG	IGINGCIALL	5040
30	TGAAGAAGGC	AAGGAACCCT	GAGATTCTTC	TTTGAATCCT	TTAGTCCANG	TCTTAGACCA	5700
	GTGATTGGTG	CTTACCTTGA	ACAAAATTTT	GTCTGTGTTC	CTAATCCCTT	CARTACTNTG	5760
	GGTACARTGC	TOYCGARTCAC	CCTGCACATT	TGATTCTAAA	TOGCTTTTAT	TTTTTAAAAA	5820
	TOCATATIONS	TACCACAAGA	MARCACCATO	COTATATATOOC	Chananghor	TOTAGONORG	5000
	ICCAIMICCO	INCONCHAGA	INACAGGATG	COMINICOC	COUNTRACE	- CCAGGACAC	5000
35	TGATGGGAAT	GATCCCCAANG	ATCACCCCAC	CICAGAAAAC	GTCTGTGCCA	CAATACTNTG TTTTTAAAAA TCCAGGACAC ANAGACTTCC CCAGTTTGCT TTGGCCACAT	5940
33	CCAGATAGAA	NCACTGGGAC	AGTGGTTTGA	ACGACTTCTT	TTATGGTTGT	CCAGTTTGCT	6000
	ATGGAAATAA	AAGGCATTGA	TTTTTTTAAAA	AAGATGATTG	GAACCTGTCT	TTGGCCACAT	6060
	AGGGGGGACTT	GGATCCATTT	CCACCCCTTA	CTCATATATT	COUNTRACTO	AAGGGCTTTTG	6120
	ACCOUNTY ACCOUNTY	CONTCONTT	OMAGGE LOMA	*********	CONTRACTOR	manmanaaa	C100
	GCTTTWAGTC	CCAGACTGGT	CICCCAMGIG	MACCATAMOT	GITTIOONGC	TCATCIGGGG	0100
40	TGAGGCATGA	GAATGTTGCC	CCATCTATCC	CTTCAGGAAA	AGGTGCCTTC	TTGGCCACAT AAGGCTTTG TCATCTGGGG CCTCCCTTTC GGTCTTTATA ATGCANACCT CTTTTTTTT ACAATCTTGG CTCAGTCTCC TTATTATTATA	6240
40	TCCTAAAGCC	TOGTCCCCAA	AAATTGTTTT	TOTOTOCAAA	AGTCTAGTAT	GGTCTTTATA	6300
	CACCCANACT	CTTAGTGTTG	CGTCCTGCCT	TGTTTCCTTG	TTAAGGATCT	ATGCANACCT	6360
	CCCCCTTTGC	CTTAGCTAGC	GTCACATTCC	CTATCATTTC	ACABGACTAA	CTTTTTTTTT	6420
	CCCGCTTTGG	CITAGCIAGC	GIGMENTIGG	CIMICALITO	ACIDISACIAN	CITITITI	0420
	TITITITI	ACTUMUTETE	CCTCTGTCAC	CINGGCIGGA	GIGCHGIGGC	ACAMICTIOG	6460
4.0	CTCGCTGCAA	CCTTCACCCT	TCACCTCCCA	GGTCGAAGCG	ATTCTCCTGC	CTCAGTCTCC	6540
45	CGAGTAGCTG	GGATTACAGG	CGTGCGCCAC	CARATCTGGC	TATTTTTTTA	TTATTATTAT	6600
	TTTTAGTAGA	GATGGGGTTT	CACCATGTTG	COCACACTOC	TOTTGE ACTO	TTARTATAT TTOGCCTCAA ACCATGGCATCAGA CAATTGGTAA TCAGATGCA TTCTCATTAC TTTTGTATAC CTATGTTAT GTCTCTCCCT TCAATCAGCC TCAATCAGCC TCAATCAGCC TCAATCAGCC TCAATCAGCC TTTGTGGTT TCATTGGGTT TTTGTGGTT TTTGTGGTT TTTGTTGTT	6660
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	ATTATCTGCC	CACCICGGCC	TOCCAMMOTO	CIGGGATIAC	MUDICATOMOC	MCCMIGCCCM	0720
	GCTGACAAGA	CTAATTTTTT	ATCCCTTGGT	TTATTGGCTT	CAACATCTTC	TGGAATCAGA	6780
	GGTGATTTTT	TCTTACCTTG	GATGCCTGAG	ACTAGGGGAG	TATAGAATTC	CAATTGGTAA	6840
50	22110000100	THEORGANICA	TOATCAGAAG	COCNOCTTAG	TTGGGLGLGLGG	TORGATION	6900
	CARCINCALCO	CACCOMMOMAA	ORDAGOCRAN	CACTETICANO	CONTRACCOR	TECTOS TESO	6060
	CHONOMONOT	CHECTIGIAN	GIANGGUANA	CACTITORNO	GCMITMOCOI	TICIONITAC	0,00
	TTAGGTCAAT	AACCITGAGG	GAATCAATGG	CITTITIGCC	GCTCTAGGTC	Trigigiarc	7020
	TCTTTGACTT	TTCTTTCTCT	GTCTAGTTTC	CTCTGTTCTC	AGTTTATATT	CTATGTTATC	7080
	PULLACACAL	TOTACAGTAC	ABACATCCAT	COTTTCTCCT	GTGCAATTCT	GTCTCTCCCT	7140
55	Omma mma mom	Seremento Inc	memoracopore	Omerca care	ACCCMPROSE	CATIOTICOCTIC	2200
-	CITATIATOL	TIMITIOING		CICCCICICI	A000111000		7000
	TTCTTAGCCT	GTGATTTTGC	CTTGGGGACTG	ATGATAAATT	ATTTCCAGAT	TCAATCAGCC	7260
	CTGGTCCTAC	COCAGTOCAA	TCAGAAGTAT	GTTGGTGGGG	AATCAACCTG	ATCCTGGCCC	7320
	TTTCTTCTTC	TOCATTITCA	TTCGTAATCC	CCCTCAGCAG	ATCTTTACAA	GCAGTTTCCT	7380
	PATROCTORT	GTATOTTAG	GEOFFEGGGE	TOTALOGUE	GTACACAATA	CTTTCTCCTT	7440
60	COMMOND OF	0201017700	0101110001	ar a cocomocom	CT CT CT CT CT	LMC1 CONORT	7500
00	CCTTTTTMGT	CTGACATTTT	GIGGMSCAGI	GMGCGTGCT	CHUMUNCHIN	AT CAGCTONA	7500 7560
	CAGAAAAAAT	CCACCCATGG	ATTTATATCA	GCTAAATACT	AATAATTGAT	TTTGTTTGAT	7560
	GTGCCCATAA	TTTTTTAAAGC	TGCAATATAA	TATAATGAGG	GACCACAGGT	AATTTCTCCT	7620
	GTCATTTGTT	TTGGCTGGAT	GGGGGTGGGG	GAGTAATTGC	TTAAAGTTTT	ACCATTACAC	7680
	ATTENDACTOR	CTATABATABAT	CONCENTRACO.	COTTOCTABO	TOTTOLOCTO	TTTTTLLCTLL	7740
65	GRGARARAT GTGCCCATRA GTCATTTGTT ATTRAACTCT ACTGGTAGGC ARAGAGACAT CTTGACACCA	************	C110111000	********	MODE I CANADA	TIT DOLCTION	7800
05	ACTOSTAGGC	ANTOGONGTT	GATTIMARIG	AMAGNINAT	TTANCANATC	TATACTATAA	7600
	AAAGAGACAT	TTGCTTAATT	GACATGTATT	TTTTCCTTCT	GAGTCACCIA	AACATTTACT	7860 7920
	CTTGACACCA	ACTGTTCATG	ATACTGAATA	GACAGTCCAT	ATAAGAGAAA	TTAGTGGACC	7920
	TARROTTO	ACATTOTAGO	TYTTTAATTTA	TTREACNORS	TTGCADAGCC	CTTCCGABATG	7980
	0010000000	CONTRACTOR	1011011111	111111111111111111111111111111111111111	10010000	CTTGGAAATG TTTATAAGTT	0040
70	TCACTGCTTG	GCAMTACCAT	ATGGCA: GCC	MARKETINCA	MIGNOTITIE	TITALANGIT	6040
/0	ATCCAAAAGG	GATTTGAACA	AGTAAGAGGT	TATGCCAAAA	TGTCTCCAAT	GTATGGTCCT	8100
	GTAATATATT	GCAGCTTGAA	GCCAATGATC	CCTTATGACT	TGTATACAAC	GTATGGTCCT TAATGCATGT GATCACCTTT	8160
	TTTATTGAAT	TTTGCATTTC	CCACCTGTGG	TARGECTETA	AAATGTTTTT	GATCACCTTT	8220
	vmamagan mm	A A A COMPOSTA C	ACA A A A COMM	THINK TOOCCO.	PROPERTY AND	CACAAACTES	0200
	WIGIOCCATT	Change of T	ACCOUNT OFF	TIME OF CALL	Man or small	GAGAAAGTTT GTACCTGTAG TGACTAGCTT	0240
75	AMAATGGAAA	CHUCCCACCC	TITCIGCCCT	ATMGCTGTAG	TINGMATIGA	GIACCIGTAG	0340
75	CAAAACAGCT	GTAATTOGTG	GTTGTAGTGT	TAGAGGTGTT	AGCTTGCTAG	TGACTAGCTT	8400
	TGGAGAGTAA	ATGCATGGTA	TTGTACATCA	CATTTCTTAA	CTCGTTTTAA	CCTCTGAAAA CTCCCTGCTC CCAAGTAAAG	8460
	CARTATATEC	TOTOTOTOTA	ACCARCATOR	CACCOCCTTG	CCCACACCC	CECCCAGCAG	8520
	COLORAGE	- AGIATOTAG	1001101100	maca cocci io	AME I CHOOSE	CCBACTRABEC	9590
	CCAGITGICT	ACAGITGTA	AA IATCTGAT	TTGMGGCCCCA	MIMACIGITG	COMMUTANAG	6580
00	TCAGCAAACA	ACANACAAAC	CAAAATGTGG	GUANAAGGCA	TTTCTCAACC	ATCTCTCAGC	8640
80	AGTTATTGAT	CATTTCTTAA	GGAACAGCAT	TGTGATCAAA	GACTCAACTT	TACGTAAAAA	8700
	TYACTGCTAR	ATTOGGGTTV	TATTIGGCCAT	TGATTACATT	CAGGATTGAB	TAGTTITCAG	8760
	DAMES CARE	2.00000110	Chambacani	TO A DO TO THE LAND OF THE LAN	TATCY/TOOM	OCTOMMENT :	0070
	ANTUACATOT	ANT CCAUNGA	CHUTHUGTAG	TOMIGICOUT	ATCCCTGCA	GCZGTTTTAA	0020
	GATAGAGACC	TCAGAAGACT	CTGCTTGACC	GATGACCAAT	AATTATTICA	AAAAAAAAGA	8880
	ARARATGAGA	GARATARAAC	AGATATTTAA	GAACTTTAGC	CACCTATTTA	GARTACTTAT	8940
85	AGCCAGADAD	AAAAACAAGG	GCATGAGTTC	ANATGCATTA	CTATCAGTGT	CCTAGGCAAT	9000
	ACCTARCOM	Coccopana	COCATTCASA	ACCACUATES.	CAAGAGGCA	al/od/Asisteleanu	90.60
	ACCIMACCIA	CICIOMANTT	GIGHTICHM	MANAGEMENT T	OCCUPATION TO	COLOCULITY -	9000
	TUGTTTGCTG	ACCOCACTTG	GACTGGTAGG	TTTGGTGAGG	CCCCCATAAA	CCAGCTARAG ATCTCTCAGC TACGTARAAA TAGTTITCAG GCTGTTTTAA AAAAAAAAA GAATAGTAT CCTAGGCAAT TCTCCTTTTT CCAGCTGGAG	9120

5	TAAGGTGCTG	/086443 TEATCTCTG TTCTTGGGTC TGAACTGTGA GCAATTATTT CAAGATGTGT	AGAGGACTTC GTGCTGAAGA TGGCTCTCAA	TTCGCAGCAT	AGAGAAGTTT TCAATACCAG TCATCGCATT	GCCATGTGTG GCAGCCAAAG CTCATTTCTG	9180 9240 9300 9360
10	Seq ID NO: Protein Ac	214 Protein cession #: 1	sequence: P_000546				
15	GDRYFKGIVY EGESYVCSSD LVTIIRSGVK	11 RDKTSRNMRG AVSSDRFRSF NFFKKVEYTK PRKAVRVLLN ACGPEKFRYA ANGTSSSQLS	DALLADLTRS NVNPNWSVNV KKTAHSFEQV ODDESLDENE	LSENINLPQG KTSANMKAPQ LTDITEAIKL CRYMKGNPSA	VRYITTIDGS SLASSNSAQA ETGVVKKLYT TAGPKASPTP	RKIGSMDELB RENKDFVRPK LDGKQVTCLH OKTSAKSPGP	60 120 180 240 300
20							
25	Mucleic Ac	215 DNA sec id Accession wence: 312.	n #: NM_1304	31	41	51	
30	CTTTOCAACA GTCTTCCTGG TCCTGTGGCA CCCAGGTCGT	AGAGCTCTGC TCTTCGTTCT TAATTTAGTT CAGTCCGTGG GATGCAGGCG TATGAGTGAG	TTCTCACTGA GTGAGTGAAT CTTTGAGGGA CCATGGGCCG	CCCAGACTCA GTGTGGAGGA AAAGGGCCTC GTAATCGTGG	GCCGGTAGGT GCCAGCGGGC GCGGTGGTCC CTGGGCTGGA	TTAGGACAGG TTAGGACAGG TCCGCCTTCC ACGAGGGAGG	60 120 180 240 300 360
35	AAGAAGAGA AAGAAGAGACACC TTAAGATAGA	CCAGCCAGTT ACCACCAACT TGCTGTTCAA GGATGCACCT TAAAGTGCTG	GGACCTGTGA GATAATCAGG GGGACTGATG GGAGATGGTC	TTGTCCAGCA GTATTGCACC TGGAAGCTTT CTGATGTCAG	GCCCACTGAG TAGTGGGGAG TCAACAGGAA GGAGGGGACT	GAAAAACGTC ATCAAAAATG CTGGCTCTGC CTGCCCACTT	420 480 540 600 660
40	ATGAAGACTG	AAACCAAGAA TTACAGTTTT	TATTGTTCTT	ATGCTGGAAA	TTTGACTGCT	AACATTCTCT	720
45		216 Protein					
50	1 MSEHVTRSQS AVQGTDVEAF	11 SERGNDQESS QQELALLKIE	21 QPVGPVIVQQ DAPGDGPDVR	31 PTEEKRQEEE EGTLPTFDPT	41 PPTDNQGIAP KVLEAGEGQL	51 SCEIKNEGAP	60
55	Nucleic Ac Coding seq	217 DNA sec id Accession mence: 82	1 #: NM_0014 135				
60	TGAGATTCAT CCAAGGCGCT GATGAAGTGG	11 TGTGAGGCAG CTGTGTGAAA ATGTACAGCC AACCAGCAAC	TATGAGTTOG TCCTGAAGTG ACCTGAAGAA	CCACCAAGAT ATTGGGCCTA GGGGAACCAG	CGACCTATTA TGCGGCCCGA CAACTCAACG	TTGGCCTAGA GCAGTTCAGT TCAGGATCCT	60 120 180 240
65	GCTGATAGCC GGGCAGGAGG CAATCACAGT	AGGAGGGAGA AGGAACAGGG TGGACCOGCC GTTAAAAGAA AAATTCTCCC	TCACCCACAG AAATCCAGAG GACACCTTGA	ACTGGGTGTG GAGGTGAAAA AATGATGCAG	AGTGTGAAGA CGCCTGAAGA GCTGCTCCTA	TGGTCCTGAT AGGTGAAAAG	300 360 420 480
70	Seq ID NO: Protein Ac	218 Protein cession #: 1	sequence: IP_001467.1	31	41	51	
75	 MSWRGRSTYY DEGASAGQGP	 WPRPRRYVQP KPEADSQBQG	 PEVIGPMRPE HPQTGCECED	QFSDEVEPAT GPDGQEVDPP	 PEEGEPATQR NPEEVKTPEE	 QDPAAAQBGB GEKQSQC	60
-	Nucleic Ac	219 DNA sec id Accession sence: 90-36	#: NM 0014	176			
80	1	11 	21 	31 	41 	51 	
85	AGACAGAGAC GCTTCTCGCT ATGGGAAGTC	GCAGAGTGAG TGAGCGGCCC CCTCCTGCCC CAGCCAGTGT CAACTGCAAT	GGCACCGCCA GCAGCCCGGG ATCTTTGATC	TGCCTGCGCT CCACCTCCAG GGGAACTTCA ATGGCATTCA	CTGGCTGGGC GAGGGAAGTC CAGACAAACT CTGCGAGAAG	TGCTGCCTCT TGTGATTGCA GGTAATGGAT	60 120 180 240 300 360

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CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG 420 CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG 480 ACCACAGACT CCTAGACTCC AACTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG ACGCCGGCCG CTGTGTCTGC AAGCCAGCTG TTACTGGAGA ACGCTGTGAT AGGTGTCGAT CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG 660 GGCATTCAGC CAGCTGCCGC AGCTCTGCAG AATACAGTGT CCATAAGATC ACCTCTACCT 720 TTCATCAAGA TOTTGATGGC TGGAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC AATOGTCACA GCGCCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT TTGTGGCTCC TGCCAAATTT CTTGGGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCCT 900 10 TTGACTACCG TGTGGACAGA GGAGGCAGAC ACCCATCTGC CCATGATGTG ATTCTGGAAG 960 GTGCTGGTCT ACGGATCACA GCTCCCTTGA TGCCACTTGG CAAGACACTG CCTTGTGGGC 1020 TCACCAAGAC TTACACATTC AGGTTAAATG AGCATCCAAG CAATAATTGG AGCCCCCAGC 1080 TGAGTTACTT TGAGTATCGA AGGTTACTGC GGAATCTCAC AGCCCTCCGC ATCCGAGCTA CATATGGAGA ATACAGTACT GGGTACATTG ACAATGTGAC CCTGATTTCA GCCCGCCCTG 15 TETETGGAGE CCCAGCACCC TGGGTTGAAC 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TCTCTCTTC CTCCACCCAT AATAGAGGAA TGTTCCTACT 4560 4620 4680 TRACCICCAT CONTECTIC ARCATATATT TATTERGIAC CTACTOTOT COMCOGCIE GIGGRACAGE GEGRACATA TECTERECCI CARRACATTRI TITRICTAGE GRAGALAGA ARCATITITA ARARAMANT TRANCITAC ARCITICIT TOTOCCAGAI GEGRAFICA 4740 4800 75 GCAATAACCG CTTGGTTTGC AACCTCTTTG CTCAACAGAA CATATGTTGC AAGACCCTCC 4920 CATGOCOGCA CITGAGITIT GGCAAGGCIG ACAGAGCTCT GGGTIGIGCA CATITCITIG 4980 CATTCCAGCT GTCACTCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040 TARCACCAGT GGGAATTGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGGAAGACTA 80 TOGTOCTOCC TIGCTTCTGT ATTTCCTTGG ATTTCCTGA AAGTGTTTTT AAATAAAGAA CAATTGTTAG ATGCC

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21

31

51

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50	Seq ID NO: Protein Act 1 1 1LGRAGAGRG TIREDPDSVP YLGASTPDLQ Seq ID NO: Nucleic Act Coding sequ	224 Proteinession #:	n sequence: AAR17001.1 21 RQGGSIHSGR QGGDYFYSFG quence n #: NM_0214 110 21 TCAGGGCTGC	31 IAAVHNVPLS GCHRYAAYQQ 448 31 ATGCCTGAAG	41 VLIRPLPSVL LQRETIPAKL 41 AGATCTTCA	DPAKWQSLVD VQSTLSDLRV 51 ATCCCAAAGT TGCTTCATCA	60 120
50 55 60	Seq ID NO: Protein Acc I ILGRADAGEG TIREDPDSVP YEGASTPLIQ Seq ID NO: Nucleic Aci Coding sequ I ATGCCTCGAG GAGACACAGG	224 Proteinession #: 11	n sequence: AAH17001.1 21 AQGGSIH9GR QGGDYFYSFG quence n #: NM_0214 110 21 TGAGGGGTGG	31 TAAVHNVPLS GCHRYAAYQQ 448 31 ATGCCTGAAG CCCCTGGAAG	41 VLIRPLPSVL LQRETIPAKL 41 AGATCITCA TOGAGGAGGA COTOCTCCTC	DPAKWQSLVD VQSTLSDLRV S1 ATCCCAAAGT TGCTTCATCA	120
50	seq ID NO: Protein Acc I I I ITLGRAGAGG TIREDDDSVP YLGASTPDLQ Seq ID NO: Nucleic Ac: Coding sequ I I ATGCTCGAG GAGACACAGG TCCACTTCCA TCCTCCTGGT TCCAACTTCCA	224 Proteinession #: 11 APEGPGPSGG PIDVLNIKGA 225 DNA se id Accessionence: 11 CTCCAAAGGG GCTGGAGGGCTCAACGTGAGGGCTCAACGTGAGGGCTCAAAGGTGCTCAAAGGTGCTCAAAGGTGCTCAAAGGTGCTCAAAGGTGCTCAAAGGTGCTCAAAGGTGCTCAAAGGTGCTCAAA	n sequence: AAH17001.1 21 AQGGSIHSGR QGGDYPYSFG Quence n #; NM_0214 110 21 TCAGGGCTGC TGCACAGGGCT ACCAAGGAC TCAGGTAGACC TCAGGTAGACC TCAGGTAGACC TCAGGTAGACC TCAGGTAGACC	31 IAAVHNVPLS GCHRYAAYQQ 48 31 ATGCCTGAAG CCCTGGCTG CCAAGGAGGAGG TOCTCTTCCCT	41 VLIRPLPSVL LQRETIPAKL 41 AAGATCITCA TOGAGGAGGA CCTCCTCCTC TTCTGCTCA CCTCGTCGTC	51 Interpretation of the control of	60 120 180 240 300
50 55 60	Seq ID NO: Protein Act I I TLGRAGAGRG TIREDDBSVP YLGASTPUL Seq ID NO: Nucleic Aci Coding sequ I ATCCTCGAG GAGACACAGG TCCACTTCGA TCCCCTGGT CCCAATCCTG	224 Protei pession #: 11 APROPOSOS PIDVLNIKOA 225 DNA se dd Accessio ence: 11 11 CTCCAARGCG CCNGCTCCTC ATCCCCTAARCC CCNGCTCCTC ATCCCCTAARC CCCAACTGG AATCCCCCAACTGG AATCCCCAACTGG	n sequence: AAH17001.1 21 AQOSIBSCR QGDYFYSFO QUENCE TCAGCGCTGC TTTTCCATCC TCAGAGGTT TCAGCAGGCT TCAGAGAGGCT TCAGAGAGGCT TCAGAGAGGCT TCAGAGGGT TCAGGGT TCAGAGGGT TCAGAGGT TCAGAGGGT TCAGAGGT TCAGAGGGT TCAGAGGT TCAGAGGGT TCAGAGGT TCAGAGG TCA	31 IAAVHNVPLS GCHRYAAYQQ 446 31 ATGCCTGAAG TCTTTTCCCT CCAGAGGGG TGCTCCTCCCC TGCTCTCCCC	41 ULIRPLPSVL LQRETIPAKL 41 AAGARCHTCA TGGAGGAGGA CCTCCTCTCTCTCTTTTTCTGCTGA CCTCGGTCGTA AGGAGGAGGA CCTCGGTCGTA AGGAGGAGGA CCTCGGTCGTA AGGAGGAGGA CCTCGGTCGTA AGGAGGAGGA CCTCGGTCGTA AGGAGGAGGAGGA CCTCGGTCGTA AGGAGGAGGAGGA	51 ATCCCAAAGT TGCTTCATCA TGCTTCATCA TGCTTCATCA TGCTTCCTT TGATGAGACA TGCTTCCCTT	60 120 180 240 300 360
50 55 60	Seq ID NO: Protein Acc I ILGRAGAGRG TIREDDESVP YLGASTPDLQ Seq ID NO: Nucleic Ac: Coding sequ I I ATCOCTCUAG GAGACACAGG TCCAACTCCA TCCTACTGCT CCAACTCCC CCATTAGATC CAGGTCCTCC CAGGTCCTCC	224 Protei pession #: 11	n sequence: AAM17001.1 21	31 LANYENVPLS GCHRYAAYQQ 46 31 ATGCCTGRAG CCCCTGRAGCCCCAAAAAAAAAACAAAAAAAAAAAAAAAA	41 VILRELESVL LQRETIPAKL 41 AAGATCTTCA TGGAGGAGGA CTTCTGCTGA CCTCGGTGCT AGGAGGAGTC	51 I ATCCCAAAGT TOCTCCTC TGATGAGACA TOCTCCTT TOCTCCCTT AGCACCTTA AGCACCTA	60 120 180 240 300
50 55 60	Seq ID NO: Protein Acc L	224 Frotei ression #: 11 AREGPGPSGG PIDVLNIKGA 225 DNA se id Accessio ence: 11 CTCCAAAGCG GCCTCAAGCA ACCACCACTA ATCCCACTA ATCCCACTAT ATCCCACTAT TOTATACACA TCTCCACATAT TCTCACATAT TCTCACATAT TCTCACATAT TCTCACATAT	n sequence: AAMH7001.1 21 AQOSSIBSCR QGGDYFYSFO Quence n #: NM_0214 Commonwealth	31 LANYRNYPLS GCHRYAAYQQ 46 31 ATGOCTGAAG CCCCTGGCTG TCTTTTCCT CCAGAGCAG AGCCARAAGG AGCARAAGG ATGAAGGAGG	41 ULIRPLPSVL LQRETIPAKL 41 AAGARCTICA TOGGGRAGGA CCTCCTCCTC TITCTGCTGA CCTGGGGGTC TAGAGGAAGA CCATCACAAAA CCATCACAAAA	51 	60 120 180 240 360 420 480 540
50 55 60 65	Seq ID NO. Protein Acc I LIGRAGAGAG TIREDDSVP TLOASTPUL Seq ID NO. Nucleic Acc Coding seq I ATOCTOMA AGAGACAGAG TCCMCTTOMA TCCMCTTOM TCCMATTCCT COMATTCCT TOMATCCT	224 Protei pession #; 11 ABERGADESGO PIDVLWIKGA 225 DNA se id Accessio pence: 11 CTCCAAAGCG CCMGCTCCTC ACCCCAAAGCG CCMGCTCCTC ACCCCAAAGCG CCMGCTCCTC ACCCCAAAGCG CCAAACTCTCTCAAAGCA CCACAAACTCTCTCAAAGCA CCACAAATCTCTCTCATTTCTCCTCTTTCTCTCTTTCTCTCTTCT	n sequence: AARH7001.1 21	31 IAVENUPLS GCHRYANYQQ	41 VLIRELESVL LQRETIPAKL 41 AAGATCHTCA TOGGGAGGA CONCOCTOCT THICTOCTGA CONCOCTOCT TAGATGAGAA TOTTGTTAG TOGATCHCAAA	51 I ATOCCAAAGT TOCTTCCTCC TOCTCCTCC TOCTCATGAGGACACTAGTGACTGACTGACTGACTGACTGAC	60 120 180 240 360 420 480 540 660
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50 55 60 65 70 75	Seq ID NO. Protein Acc LARAGAGNA THEODRAY Seq ID NO. NULLAISTAN ATOCTOLAG ARACCICA COATMANACT COAT	224 Proteinession 8: 11 APROPRIES AND RESEARCH STATE S	n sequence: n sequ	31 IANYHWYPLS GGRYANYQQ GGRYANYQQ 148 31 ATOOCTGANG GCCCTGACG GCCGGGGGGGGGGGGGGGGGGGGGGGGG	41 VLIRELPSVL LQRETIPAKL 41 AAGARCITCA TOGAGGAGGA TOGAGGAGGA TOGAGGAGGA TOGAGGAGGA TOGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	SI ATOCCAAAOT TOCTCOTOCT TOCTCOTOC TOCTCOTOC TOCTCOTOC TOCTCOTOC TOCTCOTOC TOCTCOTOC TOCCOCT TOCCOCT TOCCOCT TOCCOCT TOCCOCT TOCCOCTCO T	60 120 180 240 480 540 660 6720 780 840 990 990
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TPEGVIWSAL NNGLYPGME HLIYGEPRKL LTODWYDRNY LEYROVPGSD PARYEFLMGP 240 300 RAHAEIRKMS LLKFLAKVNG SDPRSFPLWY EBALKDEBER AODRIATIOD TTAMASASSS 360 Seq ID NO: 227 DNA sequence Nucleic Acid Accession #: NM_005025.1 10 Coding sequence: 82-1314 GOGGAGCACA GTOCGCCGAG CACAAGCTCC AGCATCCCGT CACGCGTTGC ACCTGTGTGC GAGGCTTGAA ACTGTTACAA TATGGCTTTC CTTGGAGCT TCTCTTTGT GCTTCTGCAA AGTATGGCTA CAGGGGCCAC TTTCCCTGAG GAAGCCATTG CTGGTTGTGT AGTGAATATG 15 120 180 TATAATCGTC TTAGAGCCAC TGGTGAAGAT GAAAATATTC TCTTCTCTCC ATTGAGTATT 240 OCTOTTGCAA TGGGAATGAT GGAACTTGGG GCCCAAGGAT CTACCCAGAA AGAAATCCGC 300 CACTCLATCO CATATORCAC COTALABAT COTCARCAT THICTTOTT CARCACTT 260 20 TCAAACATGG TAACTGCTAA AGAGAGCCAA TATGTGATGA AAATTGCCAA TTCCTTGTTT 420 GTGCAAAATG GATTTCATGT CAATGAGGAG TITTTGCAAA TGATGAAAAA ATATTITAAT 480 GCAGCAGTAA ATCATGTGGA CTTCAGTCAA AATGTAGCCG TGGCCAACTA CATCAATAAG TGGGTGGAGA ATAACACAAA CAATCTGGTG AAAGATTTGG TATCCCCAAG GGATTTTGAT 600 GCTGCCACTT ATCTGGCCCT CATTACTOCT GTCTATTTCA AGGGGAACTG GAAGTCGCAG 660 TTTMGGCCTG AAAATACTAG AACCTTTTCT TTCACTAAAG ATGATGAAAG TGAAGTCCAA ATTCCAATGA TGTATCAGCA AGGAGAATTT TATTATGGGG AATTTAGTGA TGGCTCCAAT 720 780 GARGCTOGTG GTATCTACCA AGTCCTAGAA ATACCATATG AAGGAGATGA AATAAGCATG 840 ATGCTGGTGC TGTCCAGACA GGAAGTTCCT CTTGCTACTC TGGAGCCATT AGTCAAAGCA 900 ATOCTOGTIC TOTCHAGACA GRAGITCUT CITECTACITC TESPASUCATI ANTORANAS, ACGICIGETTE AMAGATOSIC AMACTETISTA AMAGATOSITT AMAGTGAGANT ATACCISCOC AGGITCACHE TOGAACAGAR ANTORATITA ANAGATOTIT TRANGGICTE TOGAATACT GRAATITTCA TCAAAGATCA CACCITCICTE ATAATAAGGA GATTITTCTT TCCAAAGAA TTCACAAGCT CITCCTAGAG GITAATGAGA AAGGICTCAGA AGGICCTGGT 960 1020 1080 GUCLOGGGA TGATGGGAT TAGTAGGATG GUCGTGCTGT ATCCTCAMGT TATTGTGGAC CATCCATTT TGTTTGTTAT CAGRAACAGG AGAACTGGTA CAATCCTAT CATGGGAGG GUCATGCATC CIGAAACAAT GAACCAGGT GACATGATT TGGAGACT TAGTAGTAGT 1200 1260 35 1320 TTATTTGAAT AACAAGGAAA ACAGTAACTA AGCACATTAT GTTTGCAACT GGTATATATT 1380 TAGGATTTGT GTTTTACAGT ATATCTTAAG ATAATATTTA AAATAGTTCC AGATAAAAAC AATATATGTA AATTATAAGT AACTTGTCAA GGAATGTTAT CAGTATTAAG CTAATGGTCC 1500 TGTTATGTCA TTGTGTTTGT GTGCTGTTGT TTAAAATAAA AGTACCTATT GAACATGTG Sec ID NO: 228 Protein semience: Protein Accession #: NP 005016.1 45 MAPLOIFFIL VLOSMATGAT PPERAIADLE VNNYNRIRAT GEDENILFSP LSIALAMGMM ELGAÇGETÇK EIRHEMGYDE LKNGEEFEFL KEFSNMVTAK ESQYVNKIAN SLFVQNGFHV NEEFLOMMKK YFNAAVNHVD FSONVAVANY INKWVENNYN NLVKDLVSPR DFDAATYLAL 180 INAVYFKONW KSOFRPENTR TESPTKDDES EVOLPMNYOO GEFYYGEFSD GSNEAGGIYO 240 50 VLEIPYEGDE ISMMLVLSRQ EVPLATLEPL VKAQLVEENA NSVKKQKVEV YLPRFTVEQE IDLKOVLKAL GITEIPIKDA NLYGLSDNKE IFLSKAIHKS FLEWNEEGSE AAAVSGMIAI 300 SRMAVLYPOV IVDHPFFFLI RNRRTGTILF MGRVMHPETM NTSGHDFEEL Seg ID NO: 229 DNA sequence 55 Nucleic Acid Accession #: NM_003695 Coding semience: 12-398 60 CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGCAGC CCTGGCTGTG GCTACAGGGC
CAGCCCTTAC CCTGGCTGC CACCTGTGCA CCAGCTCCAG CAACTGCAAG CATTCTGTGG 120 TOTGCCCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA ATCTOUTGAA GARGGACTGT GCGGAGTOGT GCACACOCAG CTACACCCTG CARGGCCAGG TCAGCAGCGG CACCAGCTCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300 ACALOGORAC ACCOLOGOS ACCOCOCASOS CONTAGRAS CONTAGRAS ACCORDANAS 360 TGAGGCTCCT GGCGTCATC TTAGCCCCCA GCCTGTGACC TTCCCCCCAG GGAAGGCCCC
TCATGCCTTT CCTTCCCTTT CTCTGGGGAT TCACACCTC TCTTCCCCAG CCGCCAACGG 420 480 GGGTGCCAGG AGCCCCAGGC TGAGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG 540 CATGGAATGC TGATGACTTG GAGCAGGCCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600 70 ACAGAGGATG CAGCOCCCAG CTGCATGGAA GGTGGACGAC AGAAGCCCTG TGGATCCCGG GATTCACAC TCCTTCTGTT TTGTTGCCGT TTATTTTGTA CTCAAATCTC TACATGGAGA 660 TARATGATTT ARACC Seq ID NO: 230 Protein sequence: 75 Protein Accession #: NP 003686 MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCPA SSRFCKTTNT VEPLRGNLVK 80 KDCAESCTPS YTLQCQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHSA LSLGLALSLL AVITLADEL.

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: Eos sequence Coding sequence: 126-752

WO 02/086443 COGGOCAGOT GGCTCATGCT CGGGAGCCTG GTTGAGCGGC TGGCGGGGTT GTCCTGGAGC AGGGGGGGAG GAATTCTGAT GTGAAACTAA CAGTCTGTGA GCCCTGGAAC CTCCACTCAG 120 AGAAGATGAA GGATATCGAC ATAGGAAAAG AGTATATCAT CCCCAGTCCT GGGTATAGAA 180 GTGTGAGGGA GAGAACCAGC ACTTCTGGGA CGCACAGAGA CCGTGAAGAT TCCAAGTTCA 240 GGAGAACTCG ACCGTTGGAA TGCCAAGATG CCTTGGAAAC AGCAGCCCGA GCCGAGGGCC 300 TCTCTCTGA TGCCTCCATG CATTCTCAGC TCAGAATCCT GGATGAGGAG CATCCCAAGG 360 GARACTACCA TCATGGCTTG AGTGCTCTGA AGCCCATCCG GACTACTTCC ANACACCAGC 10 ACCOMPTIGA CARTGOTGGG CTTTTTTCCT GTATGACTTT TTCGTGGCTT TCTTCTCTGG 480 CCCGTGTGGC CCACAAGAAG GGGGAGCTCT CAATGGAAGA CGTGTGGTCT CTGTCCAAGC 540 ACGACTETTE TGACGTGAAC TGCAGAAGAC TAGAGAGACT GTGGCAAGAA GAGCTGAATG 600 AAGTTGGGCC AGACGCTGCT TCCCTGCGAA GGGTTGTGTG GATCTTCTGC CGCACCAGGC TCATCCTGTC CATCGTGTGC CTGATGATCA CGCAGCTGGC TGGCTTCAGT GGACCAAATT 720 15 TTCAGGATGG CTGTATTCTG CGGTCAGAAT GAGAGAGTCA AGCTGGGCAG AATCTCTCGC 780 CAMGAGTICA GCCTTCCTTT GGGGCTGCT CCATCAGTCC COAGCTGTGT GGGACAGGC TTCACTGCAC CGCCATCTTA CTGAGTTGCT TCACGTGAG AAAAGGGGGC TTTGGCCCTG 940 900 TGACTCAGTT CCACATTTTG GATTGCATAC TGGAAAAGAA GCCAATCTTC TTGCTAGTAA 960 ACCAGCAGC CGCCTGTATA CACTOGTGAC CCAAGCAATG GATATAAACC TAAAAATCTG 20 AGGCAGGGGA GAGGTGGAAT ACAGTAGTTC TTGGAATCTG AAGTCTCCTA TTTGATCAGG 1080 TTATTTCCTG GGACTTOGCA AAAATCTGAT TOGTGGGGAT CTCCTAGGAC CTAGTGGACA 1140 TOTGOTATTA ATTTAATOTO AGGNANANCA AGANATTAAC COAGAGAGAG TOTGGGTTTT 1200 GGAATTCAGC GTAGCTACCT CCAGACCGTG GTGTCTGGCC TCCATTTTTG TCTGTCATTC 1260 AGCTCTGACT TACAGCTGCA GTCACCTTTG CTATAAGGCA CCTGGGTAGA AGGGTGGATG 25 GGCTCACAT CAATTTTTT CTTCCTTTAG GGTGGGGGAT TGGTTTGGCT TTCTFTTGTT 1380 GTGGTTTTTT GTTTATTTT TGTCAAGATT GATTTTTAGA TGCAAGGACT TGAAAAGACC 1440 CAGAAGGATG CCACCAGTTT TTCCTTGAGG CCTAGGATTT TTTATTCTGT CCCGAGCAGA 1500 GGTAATCCT CACAACTIAG TGCACCAGTA GCACCAGCCA TITTGAGCAG AGTACCTCTT
TGGGGAGCTT TTCGTTTTGT TTTGTTTTTA ATTCTCTTTC CTTAGCAGCA AGGTCTTTTT 1560 1620 30 TCCTAGAGAA TCTACTCCGT TGCAGAATCA TTGCAACCTC AGGAGCCCTC ACTGATTGAG 1690 TGCTGTCAGC CTGATATACT ACTITGGACT CTGGAAACAG ATATGGGTTC TATTCTCTAT TTCTACTGTG TGTCGTTAAA CAACCGTCGG AGACCAGATG ACCTGTTAGA TGGCTAGTCC 1740 1800 TGTATAACTC GACTCTGTAT GTTTCAATGT ATGTTACTGG AATGCTTCAC CTGCTGTACA GTGTTTGTGG GATGCTCTTT GAAGATGGTA CTTTTATATT T 35 Seq ID NO: 232 Protein sequence: Protein Accession #: Eos sequence 21 31 41 40 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH ROREDSKFRR TRPLECODAL ETAARAEGLS LDASMHSQLR ILDERHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR 120 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RIMQEELNEV GPDAASLRRV VWIFCRTRLI LETUCIATEO LAGREGINEO DOCTURSE Seg ID NO: 233 DNA seguence Nucleic Acid Accession #: CAT cluster 50 TTTTAATGGT GCTCATATAT ACTGTATTIT TTGTTGTTTA GTTTTACTTA TTGAGAGTGT CACAACATGA ATCACATAAT CATGATTITT TITTITTACT TITACTCCCC AAATTATTCA 120 TGTTTCTTAG ATCGTAGTCA TTGAGAAGTC CCAATAACTC TAAACTTTTG AGTTATAACG 180 TAGTARACTT CICTUTCATC TUTGTGTTAG CICTGTAGTC TTAACCIGGA TITTAATTIT 55 TTTGTTTCCA AAGTCACAAT TGAATTATTC TTAGATACCT TAAGCCACTG AATTCAGTTC TOTTTGACTO AAAGCAAAAC AACOTGACAG TTTATTTTCA AACACTAACT TCTTGATATT 250 TTGTTATGGT ATATCTTTTT ATTANATATT TATTTCACT AAGCTTTCAT AAAATATTTG AAGCTATTTT AATCATCAAG TATGGAAAAC AAATTACTAT TGCATTTTCC TATATATGCA 420 TATATTATO ATTACCAGA ATTOTATOAT TITTOGCCTA ATGACTATOA ATAAACATAA ATTACCCTAC TATACTATA ATAAACATTA CAATTAAAC TACTACATTA ATAACCTGAA AATAGCTTAA AAACTACTTA CAATTAAAC TACTACTTA ATACCTGAT TITTTCTTG 60 400 660 AATIAAAGTA CATTITAAAT GAGCTITATA ATACCITAAA AAGTIGGITC TAATITAAAA 720 TATGARAGET CTGGCTATCA TCCTGGGATA GTAATTCTA ATTATATAT ATTTCAARAC TATATATTTT TEAGTECTT TGACATAACT AATTTCTAAT TATATATGT TCAARACCA 780 840 65 TATCCTGTAT TTTTTTAAG AATTGTTTTA TAAATAGGTC ATAAGATACA AGGTCTGCAT 900 TAGAAGACCC ACTOTTACTA GGTTCCCTAA GGATCTGCCA TAGATTTTTT TITTTTTTTT 960 TTTTTTTAG GTAGTTAAA GCAAGCACTG ATACCAGTGG GAGTTGGTCT TGATCTAGGA 1020 CAMPOROUS ACCAPOLAN ANCARCOT ANTECACET CTTACCTTAT CSCTTCTGAC 1.080 TCCGGGTANA AGATGGAGAA TACCTCATGT ACTGTGACTT GAAAATGAAT TCTTAAAATT 1140 70 CTTAGGCTCT CTCCATGTAT CTTTCTTAAG GAAAAGTTTC TGAGTGTGAT CTCTCTTTTG CCATAGTATC ANGTGGAGGG TAGTTCAGAA AAGTTAATAG GAAATCTITT GTGACAGCAG 1260 ACTATANTAG ANGTITGAGT AATATITTAA TAAATITATA TAATICAANT GATANAANTG 1320 TATCAATGIT ATCCAATGAT TITTATTAAA AAATTACCIT ATTATTAGAA CIGTGCCTAT TACATBAAAA GIGCTCATGT ATTIGAATIT TAAATAATIT ATTIAAATCA AGACCACCAT 1380 1440 75 AAGTCATTAA TAATTTAATA ATTGTTTTAA ATCAGTGGTT TTCAACCCTC ACTTCATATT 1500 AGAATCATCT GAGGACTTTT AATATGGAAT CCACCTCATA ACAATTAAGT CTAAATTTCT 1566 GGAGGATGGA GCCATGCTTG TTTTTCCAAA AGCTCTTTGA GTGATTCTAA TTTGTAGTCA GAGTTGAAGA CCACTGCTCT AAATTAGTGC AGGAAAATGC TTTTATTTCT CCCATGTTAA 1620 1680 CUTUTAAARC TAGTAATGTA CCCAGTTAAG TITTGATGGT TTAAATTCCA CTAAAGAACA 1740 80 TATTCTTCTA ATAACTAGCA TETATTACAT GARATTEAAG AGTTTAAGTT CCATCAAACT AGCCCTTGTG TAAGATTATT ATTTCTTCTC TATAACTTCA AAATAGATAT TTCATTCAAA 1860 CTGTTCAGGT GAGAAAACAT AATGGATTTT TTTTTTTTTC CTCTGGAGCT GCCTGTTCAG 1920 TORGATOGRA GRIGTOGGAR CATITARGGT CRETTCACTA ACCTATGGTT CAGAGTTCTG ATCATATGGA AGTTTOGRAR AGRAGACCITA TCACAGGTTT GTATGCTGGT GRATGGRAGA 1980 2040 85 TITTAATICT CACTOTOTCA AMAGAGAATC AGCTOTOCAG CAGTTOTAGA AMAGOTTIGA 2100 CRATCCCCAA GGGGCAGTGT TACCTTACTC CTTCACTGCT TCTTAGAAGG TAGAATTAAG 2160

TITCTGGAAT TGCACCTACA TGTTTTCTTA TTAACATTCA GAATTGGGAA TATTAATTTT

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TCCACTGAGT ACTTTTCTGA AATTGGTAAC TTGGAGAGTA AAATAACGTA TTTTGCTTTT CAATTTTGTG TTTGTTTACT TTTATGTAAA AATTTGATAT GTGAATTACA CAGTTCTAAT 2340 ARRACCTUAT GCCTTTTCAT TACATCUART TYGRACTCYC ARCTTCAGTG CCAGRAGTGC 2400 TITARAGATO CITTARIGAR ARGIATTARO ARANIATATA GATTIGIATO TORGITTATA 2460 CTTCAGRAAT CCATATATT GTCATATTA TTTTTTTTAGA AACCTCTAA TTGGATAACT AGATGGTATT TAAAATGAAT GCCCAARAAT ATCTTGTAGC TTTGTCCAAR AGTTATCTG TTGGAAGCGC CCACCCATTC ATCTTAGAGA TTTATTAGGA AATAATTTA AATTGTATGT 2520 2580 TYGGAGCG COCCOCKT KYTHAGAGA TYTHATAGAA ANTANTTAN ANTUGANTY KYTTHATHA TATAGATAGAT (TOTAGACO TATTCATAG TATAGATAT ANANTOTIA CHICKTANA COCHACCAT CHICACTT ANOTHER ANTOTIA KARCATTAN CHARACTC TOCCOCKT ANOTHER CHICAGAT CATCOCKT COCACATANA CARCACCAG ACACTCAG TOCCATTA ANTOTICAGAT CATCOCKT COCACATANA CARCACCAG ACACTCAG TOCCATTA TOCTAGAAT CATCOCKT TOTCOCTOCI ACCOCCTOTO COCKAGATA CACAMATCA COCCATACT TOCTAGAAT CATCOCKT 2700 2760 10 2820 2880 2940 CCTTCATCAA GCACITGCCA ACACATTCAC CTCTAACTTG TACAACCTTA CCAACTCACC 3060 15 3120 OCCCARACAC ARRACCACTA ARTCATARCO ACCACACACG CCACACACCA CACACCCACC 3180 CACACAAOCA ACACACCACG ACCAAACACC CCACCACAAA CAACCTAACA ACCACAAACA 3240 GACAACACAT CACATACACT CACTACCCCC CCATACTCCC ACCCACCA

20 Seq ID MO: 234 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 27-281

- 25 ACCACCACGA CAGCTOCCGG GAAGACATGC ACCCCTTGAA GACCCAGAGA GAGGCCGTCT ROCHORGON CHOCTEREDS GARGACHEC MCCCTICAR CACCAGAS GARGACHAT TECTESCOCC TROCTCATT GOSGCTGAG GCATTITAGG CCTCAGGCCA TCTGCACCCA 120 OCCCTCACT GAAACAGTGT GTTGCTCCAC ACCGCCTTGT TTTGCTTGTT GGCGCCCCTCT 240 30 CAGGOTTCCS ACCANTOCAA GAGCCTTGCA GAAAGCATTA ACGTGCTTTT CTCTTTGGCA 300 360 GAGTITITCT TIGCTCIGAT CITGGAGACA TCCCTCTGCC TAGTGGAAAC ATAAGGAATA CAGANAGAAT GCAAGGAGAT AGACCAACGT GAGATTCTCC TTCATGCACT CAAGAGAAAG 420 ATCTTGCAGG AAGAGCTAGT CTTTCAGGCT GGGCTGGTGA CCTGAGAAAG AATGTCCAGC 480 TTTTCTCTC CACTTOCCAT ATCAAGAGCC AGGCGTGGAA GACTAAAACA GGAAATGTTT 540 35 ATRABARCTO TTCROCCOTT CGCCRACRAC RAGTOGTARA GTRGCRARAR TGGGGATGGA GATGCCRGGA GGRARGGATGC CRGGGGTARA GTGGGRARAT GGGRARCCTGA RGCCRGGAGG 600 660 TCAAGCCAAG CCAACAGGTG TTCTGTTTTT CATCACAGAA CTAATAAGTG GTGCTGAGGA 720 CTCARACCOS GGGRAGOCCA CTCTAGRACO CATGOTGGTC ATCCATATOC CCAAGGCCCT GOTCAGAACA CAGCTAAGCA GATGGCTTGG GTCATCAGGA CGTCCATTAC ATCCAAAGGA 840 COTMONAGO CAGCTANGOS GATOSTITES SICATONISS GUILLATINA HICLANSISS ARACHACCES TORACOTITOS HAROCARAS TOCOCTACAS GCONTIGNAS CINCACTORI TOCACTATO TRACOCCAS TORACAGASIC TACCOCCALA ACTRALARA MARAGOSPIA CATARACAC TANCAGCAG AGCHATRATT ARACATGAG TOKARACAST TANGANANA GORRAGOTT COTOTOGNOS TITTATITIT AGGGRARCAS GANGARAGA CARTANTIT 40 900 960 1020 1080 TOTTTTGATG ACTOTATATO CARCTOTGAG GITTGATTAA AGANATGACO TIGAACCACA 1140 45 GCAAAGAAA ATAAAAGACA ATTTCCAGTA AGTATGCCAG TTCGAATTAA TGATTTACTT 1200 1260 TTTATTTTTA AACTGAATTC AGCAGAGATT TACATGCATT ACGATGATTA ACATCTGAAA TITGACCITG ARATASTCIT TACATIGTAR ATTOTTANTS ATCARANCAR GOTTCICKST 1320 GATTALAACA TATTACTAAT TAATTATTAA AGGAGAATAA TTGCAAATAC AACATTCCTA 1380 ARATCTCARG OCTTTTARAG CATTTGTACA ARTGACTGGA CATTTTTTAA ATTTGAAAAA 1440 50 AAAAAAAGC CCTCCATCTG ATTCTCATTT TCATTGTCAG TGCAACAACA AAAAAGGTAT 1500 GCACTTCTCT TCTCATTTTC CACTGTCTCG CAAGCTAGAA ATTCTCACGA CTACCTTTGA TCCCATCAAA GCCAAAGAAA GAAAAGAAAA TTCTTCTGTA CAGATATATC ACATTAAAAA 1560 ATABTCCC
- 55
 Seq ID NO: 235 Protein sequence:
 Protein Accession #: Bos sequence
- 65 Seq ID NO: 236 DNA sequence Nucleic Acid Accession #: NM_002075 Coding sequence: 406..1428
- 31 70 CCACAATAGG GGCAGACCTG TCCATCCTTC TCTGTGGGTC CCCTGTACCT TTCTCCCCCA ACACGATCMS ACCCAGAGGC AGCIGOTTGG GGTTTGTCGA GAAGAAGGAT TATCCAGATC 120 AGTOCTITOT AATOTCAGGT COTGOCTGTA COCTOCGATA CTCACCAAAC COTCTTCCCC ACTRICTTY ANTOTOAGOT CONGESTA CONCECUATA CONCEGAGO CONCEGAGO CONCEGAGO ACCACACA CONCEGAGO ACACATITAGA CONCEGAGO CONC 75 COTCGCAGCT GAGGGAGTAA GGAGGCTCCC AGGAACCGGA GCTGGAAACC CGGCCGAGGT 360 CCAGCCAGAG CCCAAGAGCC AGAGTGACCC CTCGACCTGT CAGCCATGGG GGAGATGGAG 420 CARCTECGTC ROGRAGOGGA GCAGGTCARG MAGCAGATTG CAGATGCCAG GAAAGCCTGT GCTGACGTTA CTCTGCCAGA GCTGGTGTCT GGCCTAGAGG TGGTGGGACG AGTCCAGATG COGACOCCOC GUACOTTANG GGGACACCTC CCCAAGATTT ACGCCATGCA CTGGGCCACT 600 80 GATTCTARGC TGCTGGTAAG TGCCTCGCAA GATGGGAAGC TGATCGTGTC CGACACCTAC 660 ACCACCAACA AGGTGCACGC CATCCCACTG CGCTCCTCCT GGGTCATGAC CTGTGCCTAT 720 GCCCCATCAG GGAACTITGT GGCATGTGGG GGGCTGGACA ACATGTGTTC CATCTACAAC 780 CTCANATCCC GTGACCCCAN TGTCANGGTC AGCCGGGACC TTTCTGCTCA CACAGGTTAT CTCTCCTGCT GCCGCTTCCT GGATGACAAC AATATTGTGA CCAGCTCGGG GGACACCACG 900 85 TOTOCCTTGT GGGACATTGA GACTGGGCAG CAGAAGACTG TATTTGTGGG ACACACGGGT 960 GACTICIATGA COCTOGOTOT CTCTCCTGAC TTCAATCTCT TCATTTCGGG GGCCTGTGAT 1020 GCCAGTGCCA AGCTCTGGGA TGTGCGAGAG GGGACCTGCC GTCAGACTTT CACTGGCCAC

WO 02/086443 GACTOGGACA TORACGCCAT CIGITICITC CCCAATGGAG AGGCCATCTG CACGGGCTCG 1140 GASTICASIA TRANSCORT CHETTICTIC CLCARIGNAM ASSCRITTO GASSIANICA GATRACCETI CONCOCCUT GITTACCTC COSSCRIANICA ASSACCIANI CRICTICTIC CACARAGACA TANTICIOSI CATOLATICO GIGOCOTICT COCTOLATIGA COSSCRITTO CATOLATICA GASTICATA GATRACARA GATRACAR 1200 1260 1320 1380 GCTCTCGCCA CAGGTTCCTG GGACAGCTTC CTCAAAATCT GGAACTGAGG AGGCTGGAGA 1440 AAGGGAAGTG GAAGGCAGTG AACACACTCA GCAGCCCCCT GCCCGACCCC ATCTCATTCA 1500 OCTOTICCE TCTATATICC GOSTOCCATT CUCNCTARGE TTTCTCCTTT GAGGGGATG
GGGACATGG GACTGTGCCT TGGGGGGCA GCATCAGGGA CACAGGGGCA AGAGGCGCC
CCATCTCTCT CCATGGCCT CCCTCCCACA AGTCCTCACA CCCTCCCCCT TAATAGCAA 1620 10 1600 GGACAACCTG CCCCTCCCCA GCCCTTTGCA GGCCCAGCAG ACTTGAGTCT GAGGCCCCAG 1740 GOCCTAGGAT TOCTCCCCCA GAGCCACTAC CTTTCTCCAG GOCTGGGTGG TATAGGGCGT 1800 TIGGCCCTGT GACTATGGCT CTGGCACCAC TAGGGTCCTG GCCCTCTTCT TATTCATGCT TTCTCCTTTT TCTACCTTTT TTTCTCTCCT AAGACACCTG CAATAAAGTG TAGCACCCTG 1920 15 Seq ID NO: 237 Protein sequence: Protein Accession #: NP 002066 20 31 MGEMEOLROE AEOLKKOIAD ARKACADVIL ABLVSGLEVV GRVQMRTRRI LRGHLAKIYA MENATDSKLL VSASQDGKLI VNDSYTTNKV HAIPLRSSWV MTCAYAPSGN FVACGGLDNM CSIYNLKSRE GNVKVSRELS AHTGYLSCOR FLODNNIVTS SGDTTCALND IETGQQKTVF 180 25 VGHTGDCMSL AVSPDFNLFI SGACDASAKL WDVREGTCRQ TFTGHESDIN AICFFPNGEA 240 ICTGSDDASC RLFDLRADQE LICFSHESII CGITSVAFSL SGRLLFAGYD DFNCNVWDSM 300 ESERVICTION HONRYSCLGY TADGMAVATG SHOSFLKINN Seg ID NO: 238 DNA sequence 30 Nucleic Acid Accession #: CAT cluster TECCAATGTG THGAACCTAC CATAAATTCT TTTCTTACHG GACAATCTTA THCTAANCAA TACCETTICC TITTAAGGCA GATAATCCTC CAAGTTITCT AATGATATCT GAAACTATTA 35 120 ACTGATTCTG TGAATTATGA AATCTGAAAA GGAATTGGAA GTTGCTAAAA ATCTATCATT TGCATTGACC AGTGTGGAGC ACAGTGGAAT GAGAATGCGT GCCCTGACAC CAAAGAAAAA TAAGTGACTG GAAAGCTGAA GAATCACCGG CTTCAGTGAC ATGGAACCCA GTGATTGAT 180 240 420 AAGAAAGAAA AATAAAATAC ACAATATGGA CGATGGAGAA AAACAGTTAC ATTTCTTTAT 480 GGATCAAGAA GITTGTGTAC ACATAATCTC ATTTTGAGAT ATATAACTAT TTTTGTCTTT 540 CAGAAGTGAA TCAAAATATT TCAAAATGCT GTCTTATGAA ACTACAATAT TCTCACAGAT 600 TAGAAAAGTT TITCTGTAAA AGTCAGATAG TAAATATTIT AGGTTTTGCA GTGTCTTTTG CAACTACTCA ACTITCCTAC TGTAGCACAA GAGTAGCTGT GGTACTGTGC AAATAAATTG 720 CTTGTGTTCC AATAAAGCTT CATTTACAAA AACATGCCAT GGGCCATATT TGGCCTGTAC 780 ACTOTTOTTT GCCAAGTCCT AATATAGITG CTTAGCAAGT ATTGTGAGCT ATTTGAGGAA 840 GACATGAAAG TTCATTGGGT TGCTAAAAAG TATGTAGAAA TTCAAAGGAA AATTAAAATT TAGGCTAAGT TATAATACAC TGTTTTAACA ATTGTAAAAT GTAAGAGAA TTTACAAATA 50 AAAATCCCAA ATAAAA Seq ID NO: 239 DNA sequence Nucleic Acid Accession #: NM_001786.1 Coding sequence: 130-1023 55 31 41 . GGGGGGGGGG GGCACTTGGC TTCAAAGCTG GCTCTTGGAA ATTGACGGA GAGGAAGCG GTTGTTGTAG CTGCCGCTGC GGCCGCCGC GAATAATAAG CCGGGATCTA CCATACCCAT TGACTARCTA TGGAAGATTA TACCAAAATA GAGAAAATTG GAGAAGGTAC CTATGGAGTT 60 180 GTGTATARGG GTAGACACAA AACTACAGGT CAAGTGGTAG CCATGAAAAA AATCAGACTA 240 GIGITATAMOS CHARACACAN ANCHACHOT CANGIUSTAS CATOMANA ANCONCAT.
BANASTONA GAGAGAGGSI TOCIAGATA GANATOSAO ANTICOT ATTANAGAA
CTICOTCATC CANATANOT CASTITICAS GATTGCTTA TOCMOGATIC CANGITATA
CICARCTITIC ASTITICTTC CATGGATCTS ANGANATIC TOCATICTAT COCCOCTATO
CASTIACATOS
CASTICATOS ATTCTTCACT TOTTANGAST TATTATACC ANATOCTACA 06968ATGIS 300 420 480 65 TITTGTCACT CTAGAAGAGT TCTTCACAGA GACTTAAAAC CTCAAAATCT CTTGATTGAT 540 600 GACADAGGAR CARTTARACT GGCTGATTTT GGCCTTGCCA GAGCTITTGG AATACCTATC ACAGTATATA CACATGAGGT AGTAACACTC TOSTACAGAT CTCCAGAAGT ATTGCTGGGG 660 TORGOTOSTI ACTORACTOC ASTESACATI TOSACTATAS GOACCATATI TGCTGAACTA GCAACTARGA AACCACTTIT COATGGGGAT TORGAAATTG ATCACTCTT CAGGATTITC 720 780 70 AGAGCTATICA CACACTATT CONTISSION TORSIONAL TORSIONAL AGAGCTATOR AGAGCTATOR CONTISSION AGAGCTATOR CONTISSION AGACTAGCAT COCATGCAT COCATGCAT AAACTTGGAT 040 900 GRAMATOSCT TGGATTTGCT CTCGAMANTG TTANTCTATG ATCAGCCAA ACGANTTCT GGCAMANTGG CACCAGATCA TCCATATTTT ASTGATTTGG ACANTCAGAT TANGAMANTG TAGCTTTGTG ACANAAGATT TCCATATGTT ATGTCAACAG ATAGTGTGT TTTATTGTT 960 1020 75 1080 ARCTOTIGTO TATTITTETO TTATATATAT TTOTTTGTTA TOAAACTTCA GOTGIACITO 1140 GTCTTCTAAT TTCAAAAATA TAACTTAAAA ATGTAAATAT TCTATATGAA TTTAAATATA ATTCTCTAAA TCTGAAAAAA AAAAAAAAA AAAAA

Seq ID NO: 240 Protein sequence: Protein Accession #: NP_001777.1

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	PPKNKPGSLA	SHVKNLDENG	LDLLSKMLIY	DPAKRISGKM	ALMHPYFNDL	DNGIKKW	240
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15	ATTGACTAAC	TATGGAAGAT GGGTAGACAC	TATACCAAAA	TAGAGAAAAT	TGGAGAAGGT	ACCTATGGAG	180 240
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25	AAAACTTGGA	TGAAAATGGC TGGCAAAATG	TTGGATTTGC	TCTCGARART	GTTAATCTAT	GATCCAGCCA	780 840
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	AGCTGTACTT	CGTCTTCTAA	TTTCAAAAAT	ATAACTTAAA	AATGTAAATA	TTCTATATGA	1020
30	ATTTAAATAT	AATTCTGTAA	ATGTGAAAAA	AAAAAAAAA	AAAAA		
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35	1	11	21	31	41	51 	
	MEDYTKIEKI	GEGTYGVVYK MQDSRLYLIF	GRHKTTGQVV	AMKKIRLESE	EEGVPSTAIR	EISLLKELRH	60 120
	SARYSTPVDI	NSIGTIFAEL	ATKKPLFHGD	SEIDQLFRIF	RALGTPNNEV	WPEVESLQDY	180
40	KNTFPKWKPG	SLASHVKNLD	ENGLDLLSKM	LIYDPAKRIS	GKMALNHPYF	NDLDNQIKKM	
		243 DNA sec		e1 1			
	Coding sequ	uence: 221-					
45							
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	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTGG	AGCITCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CGCGGGCGCC CCTTCCTGGG CCTATGCCGG	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACATC	COGGGGGGGG TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA GCACTGCCCT AGGCCATGTA	120 180 240 300 360
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	GASCRACCTC CGACCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCTG TGACTCCTTG CATCCTCTG	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTGA GGAGTGATAG	ATCCAGACTC GGCGGCGCAG GGAGTCCGG CGCGGGGCGC CCTTCCTGGG CCTATGCCG GCTGTCGG GCAGCACATT CAATCTTTGT	CAGCGCCCCC CCAGCACGCCC CCAGCACACCCC CCAGCGACCACCCC CCACCACCACCCC CCACCACCACCCCC CCACCA	COSSIGNACIONE COSSIGNACIONE CONTROL CO	ACCCCRACCC ARCTTCCTCC COCCTTCTGC COCCTTCTGC COCGCCTCCA GCACTGCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG	120 180 240 300 360 420 480 540
50	GAGCAACCTC CGACCCAGAG GGGGGGCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCTG TGACTCCTTG CATCCTCTGC CTTGGAAGAC TCTTGCAAGAC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTGA GAGGGGTGA GATGAGGTGC CTGGCTATTT	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CGCGGGCGCC CCTTCCTGGG CCTATGCCGA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTTGGCAC	CAGCGCCGCC CCAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACAT GAGCACCGGG GCAAGCAACC GGCCACCGTT AGCATGGCTGTC AGCATGGTTC AGCATGGTTAT	COSSIGNING TO CONTROL	ACCCCAACCC AACTTCCTCC CCCCTTCTGC CCCCCTCTGCCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAACTC TGGTAGATTTCT TGGTTGTTCT	120 180 240 300 360 420 480 540 600
50	GAGGRACCTC CGACCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCT TGACTCCTG CATCCTCTG CTTGGAAGAC TCTTGCAAGGT ATTCTATGAC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTGA GATGAGTGC CTGGCTATTT CCTATGACCC	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CGCGGGGCGCC CCTTCCTGGG CCTATGCCGG GCGTGTCGCA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTTGCCAC CAGTCAATGCACCAC	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCAGGTGTC CGACAACATC GAGCACCGGG GCAACAACC GGCACCGTT GATGGCTGTC AGCATGGTATC AGCATGGTAT	COGGGGGGGGGGGCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT CAGATCAGT ATTGGGGTG ATTGGGGTG GGCAATAGAA TTTGGTCAAG	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TCGTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAGA CCTCTTCAC	120 180 240 300 360 420 480 540 600
50	GAGGAACCTC GACCAGAG GCGGGGCCA ACCTGCACC GCTGTTGGGC GCCCAGTGG GCCCAGTGG GATCCTCG CATCCTCG CTTGAAGAC ATTCTATGAC TGGCTGGGCT ATTCTATGAC TGGCTGGGCT CCGAAAAACA	AGCTTCTAGT CTTCTCCAGC GCCAGCCTTG CCTGAGCCAG TTCATTCTGS AGGATTACT TGGATGTCGT CTGAATGTCGT GGGGTGATAG GGTGATATT CCTATGACCG GCTGCTTTTCC ACCTCTTAGC	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG GGAGTCCGGG CCTTCTGGGG CCTATGCGGG GCGTGTCGCA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTTGCCAC CAGTCAATGC TCTGCCTTCT CAACACCAAG	CAGCOCCCCC CGAGCAGGCC TTGCCCACCT CGAGCAGGCC TTGCCCACCT CGACCACCT CAGCACCCGG CCAACCACC GGCACCCT CACCACCC AGCACCCT CACCACCC AGCACCCT CACCACCC AGCACCCT CACCACCC AGCACCCT CACCACCC AGCACCCT CACCACCC AGCACCCT CACCACC AGCACCCT CACCACC AGCACCCT CACCACC AGCACCCT CACCACC AGCACCCT CACCACC AGCACCC ACCACC ACCACC ACCACC ACCACC ACCACC	I COGGGCGGG TCCCCGCCTT GCAAACTCTC ATGCCAACG GCCATCGTCA GTGACCGCC CAGATCCAGT GGGCATCAAGT ATTGGGGTG GGCATTAAAA TTTGGTCAGG CTACTTTGCT AJACCTGCAC	ACCCCAACCC ACCCCAACCC ACTCCTCC COCCTTCTCC COCCTCTCC CGCGGCTCCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTC TCGTTCTAAGA CCCTCCAAGA CCTCCTTCCAC CTTCCTGCG	120 180 240 300 360 420 480 540 600 660 720 780 840
50	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCT TGACTCCTTG CATCCTCTG CATCCTCTG CATCCTCTGCAGGT ATTCTATGAC TCTTGCAGGT ATTCTATGAC GGAAAAACA GAAGACTAC GGACATTGAG	AGCTTCTAGT CTTCTCCAGC GCCACCTTGG CCTGAGCCAG TCCATTCTCTG AGGATTTACT TGGATGTCCT TGGATGTTCG GGATGTAG GATGAGAG GGTGATAT CCTATGACC GCTGCTATTT CCTATGACCC GTGGGCACA ATACTATCAT	ATCCAGACTC GGCGGCCAG GGAGTCCGGG GGAGTCCGGGGCGCC CCTTCCTGGG CCATCCTGGG CCATGCCGG GCACCACATT CAATCTTGGT AGAGGATGAG TAGTTGCCAC CAGTCATGCCAC CAGTCATGCCAC CAGTCATGCCAC CAGTCATGCCAC CAGTCATGCCAC CAGTCATGCACACATTAGGG AGGCAAAAG CAGCCAAAG CAGCCAAAG CAGCCAAAG CAGCCAAATTAGGA	I CAGCOCCGCC CGAGCAGGGC TTGCCCACCT CGAGCAGGTC ATGGATCGGC GGACAACATC GAGCACCAGGC GCCAACCATC ATGGATTGGAT	COGGGGGGGG TCCCCGGCTT GCAACTCTC ATGCCCACG GCCATCGTCA GTGACGCCC CAGATCCAGT GGGATGAAGT ATTGGGGTG GGCATGAAGA TTTGGTCAGA CTACTTTGCT AACCTGCAC TTTTGGAACA	ACCCCAACCC ACCCCAACCC COCCTTCTGC COCCTTCTGC COCCTTCTGC CCACGCCTGCA GCCAACGTCTT TGCTGCTTGG GTATGAAGTC TTCGTTCAAGA CTCCTTCAC GTTCCTTCAC GTTCCTTCAC GTTCCTGTCC CTTCCAGOGG AACCGAAAAT	120 180 240 300 420 480 540 600 660 720 840 900 960
50 55 60	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CCAGAGGCTT TGACTCCTTG CATCCTCTG CATCCTCTG CATCCTTGCAGGT ATTCTATGAC TCTTGCAGGT ACTCTATGAC GGAAAAACA GAAGACTAC GGACATTGAG	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG GCCACCTTCG AGGATTAGT TGGATGTCCT TGGATGTCCT CTGAATCTGA GGATGATAG GGATGATAG GATGAGGTCC CTGCATTCCT CTGCATTTCCT ACCTCTTACC GTGTGACACA ATACATCTACT ACAAAACAAA	ATCEMBACTC GGCGCCCAG GGAGTCCGGG GGAGTCCGGG GCGGGGGCCC CCTTCCTGGG GCAGCACATT AGAMGATGAG AGAGATAAG CAATCTATG AGAMGATGAG AGAGCAAAT CTGCCTCC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAGCCAAG AGGCAAAAG AGGCAAAAG AGGCAAAAG AAGACAAAC TAACATTAGG CAAACAACT TAACATTAGG TAACATTAGG TAACATTAGG TAACATTAGG TAACATTAGG TAACATTAGG TAACATTAGG TAACATTAGG TATATCTT TATCTTTCTT TTATCTTCTT TTATCTTCTT TTATCTTCTT TTATCTTCTT TTATCTTCTT TTATCTTCTT TTATCTTTCTT	CAGCOCCCC CRACCAGGC CTGCCCACC CGAGCAGGC CTGCCCACC CGAGCACCAC CGACACACC CGACACACC GGCCACCGT GATGGCTGC GGCACCGT GATGGCTGC GGCACCGT GATGGCTGC GGCACCGT CAGGATCGCA AGCATGGTAC CAGGATGGTAC CAGGATGCAA AGAAAATCCA ACCTTAGAAT AAAAACCCAT TCCTCAATAT	COGGGGGGG TCCCCGCTT GCAAACTCTC ATGGCCAACG GCATCGTCA GTACCGCCTCGA GGCATCAAGT ATTGGGGTG GGCATAAGA ATTGGGGTG GCAATAGA TTTGGTCACC AAACCTGCAC TGTTGAAACA TTTGGGTAT TTTGGGTAT TTTGGGTAT TTTGGGTAT AACCTGCAC	ACCCCAACCC AACTTCCTCC COCCTTCTGC CGCOCTGCTGC CGCACTGCCCT AGGCCATGTA GCAAAGTCTT TCGTGGTTGG GTATGAAGT CCGTAATATTCT TCGTCTAAGA CCTCTCACG GTTCCTGCC CTTCCAGGG AACCGAAAT CTAATGTAAA ACTCAGTGGT AATTTTAACAT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50	GAGCAACOTC COACCOAGA GGGGGCCA ACCTGCCACG GCTGTTGGGG GCCCAGTGG GCCCAGTGG CAGCCCCAGTGG CAGCCCAGTGG CAGCCCCGAGTGG CATGCAGGA ATTCTATCAGGA ATTCTATCAGGA ATTCTATGGAGCT GGACATTGGG GGACATTGGG GGACATTGGG GGACATTGAG GGACATTGAG TTGTATTTATT AAACATGGGT TTGTATTATT TTGTATTATCT	AGCITCTAGT CTTCTCCAGC GCCACCTTCG GCCACCTTCG AGGATTACT TGGATGTCT TGGATGTCT TGGATGTCT CTGAATCTGA GATGAGTGC CTGCTATTA CCTATGACC GCTGCTATTA ACCTATTACC GTGGACAC ACCTCTTACC GTGGACAC ACCTCTTACC GTGGACAC ATACAT CAT ACACACTAT CAT ACACACTAT CAT C	ATCEAGACTC GGCGCCCAG GGAGTCCGGG GGCGCGCCCC CCTTCCTGGG GCGGGCGCCC CCTTCCTGGG GCAGCACATT AGAAGATGAG AAGATGAG AAGATGAG CAATCTTGT AGAAGATGAG CAGCCAATT CCTGCCTTCT CAACCCAAG GAGGCAAATAG TCTGCCTTCT CAACACCAAG GAGGCAAATAG TAACATTAG CAACACCAAG GAGGCAAATAG CAACACAAG GAGCAAATAG CAACATTAGTTCTT GAGTAATCTTCTT GAGTAATCATTCT	Tagoscocc Craccagge Trecoract Trecoract Argaract Craccagge Craccagge Craccagge Golacate Agoractaga Agoractaga Golacate Agoracaa Golacate Agoracaa Golacate Agoracaa A	COGGGGGGGG TCCCCGGCTT GCAAACTCTC GCAAACTCTC GCAATCGACC GCCATCGTCA GCCATCGTCA GCCATCGTCA GGCATCAAGT ATTGGGGGTG GGCAATAGAA ATTTGGGGTG GCCATAGAA ATTTGGTCAGG CTACTTTCGT TTTGGTAAACT TTTGGTAAACT TTTGGTAAACA TTTGGAAACA TTTGGAAACA GGGAAGGAA GGGAAGGGAA	ACCCCAACCC AACTTCCTCC COCCTTCTTCC COCCTTCTTCC CCCCCCCC	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020 1080 1140
50 55 60	GAGCAACOTC COACCOAGA GGGGGCCA ACCTGCCACG GCTGTTGGGG GCCCAGTGG GCCCAGTGG CAGCCTTGAGCC CTGGAAGAC CTTGCAGGT ATTCTATAGC TGGGACATTGGGG GAAGACTAC GGACATTGGG GTATGTATTACT TTGTATTACT TTGTATTACT TTGTATTACT TATATTAGG	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG GCCACCTTCG GCCACCTTCG TCATTCTCG AGGATTTACT TGGATGTCGT GGATGTCTG GATGAGTG CTGATGTCTC CCTATGACC TCCATATC CCTATGACC TCCATATC CCTATGACC TCTATCTCC ACCTCTTACC GTGTGACACA ATACTTATCT ACTATCACAT TAGTACTATA TAGTACTATA TAGTACTATAT TGTTCCATT TGGTTGCATT TGGTTGCATT	ATCCAGACTC GGCGCGCAG GGAGTCCGGG GGCGCGCCC CCTTCCTGGG GCGTGTCCCAG GCGTGTCCCAG GCGTGTCCCAG GCGTGTCCCAG AGAGGATGAC TAGATGATGCAG CAGTCAACA TAGACACAAG TAACACAAG TAACATTTGC TAGACCAAG TAACATTTGC TAGACCAAG TAACATTAGA TAACATTAGA TAACATTAGAT TACATTTAAAA	CAGCOCCCC CGAGCAGGC TTGCCCACCT TGCCCACCT TGCCCACCT TGGCCACCT CGAGCAGCT CGAGCAGCT CGAGCACACC GGCCACCT CAGCACCCGG GCAACCACC GGCCACCT AGCATGCACC GGCCACCT AGCATGCACC GGCCACCT AGCATCCACC GGCCACCT AGCATCCACC GGCCACCT TCCTCATAT TCCTCATAT TCTCAATAT TCTCAATAT TCTTAAATG	COGGGGGGGG TCCCCGCCTT GCAAACTCTC GCAAACTCTC GCAATCGTC GTGACCGCC CAGATCACA GGGATCACAT GTGCCCTTGA GGGATCAGAT TTTCGTCAAACT TTTCGTAAACT TTTCGTAAACT TTTCGTAAACT TTTCGTAAACT TTCGGTAAACA TTCGGGAT AACCTGCAC GGGAGGGGGAACACACAAAACACAAAAAAAAAA	ACCCRACCE AACTTCCTCC COCCTTCTGC COCCTTCTGC CCCCGGGCTGCA GCACTGCCT TGGTGGTTGG GTATQASTGC GGATATTTC TCGTTCAGA CTCCTCTCA CTCCTGCC CTTCCAGC GTACCTGCA ACCGAAAAT GTAATCTGAA ACCCAGTGCT ACTTCAGC ACTTCAGA AAATACTAGT ACTCAGTGCT AAATACCTATA	120 180 240 360 420 540 600 660 720 780 840 900 1020 1080 1140 1200 1260
50 55 60 65	GAGCAACOTC GAGCACCACC GAGCACCACC GCCOTTOGGC GCCCACTGC CCTGGACAC TCTTGCAGGC TCTTGCAGGC TCCCACAAACA GAAAGACTAC GGACATTGAG GTATGGTATT TATATTATAGA CTCATTATGGC TATGTATTATT TATATTATAGA CCCATTTATGT CCATATTGT CCATATTT CCATATTT CCATATTT CCATATTT CCATATTT CCATATT CC	AGCTTCTAGT CTCATCTAGT CTCATCTCAGC GCACCTTCAGC GCACCTTCAGC GCACCTTCAGC GCACCTCAGC CTGAATGTCCT TGGAATGTCCT GGATGACCG GATGACGTGATGACCG GCTGCTTATC CATGACCA ACAAACAAA TAAACTTAT CCTTCCCATT TATGATATAT TGATACTAGT GAAGATGTT	ATCCAGACTC GGCGCGCAG GGACTCCGGGGCGCCC CCTTCCTGGG GCGGGCCCC CCTTCCTGGG GCGTGTCCCC GCGTGTCCCC AGAGAGATGAG TAGTTTGCCAC CAGTCAATGC CAGCCCAAG GAGGCAAAG CAACCAAG GAGGCAAAG CAACCAAG CAACCAAG TAGTTAGCT TAGTTATCCT TAGTTATCCT TAGTTATCCT TAGTTATCT TACATGTTTT TACATGTTTT TACATGTTTT TACATGTTTT TACATGTTTT TACATGTTTT TACATGTTTT TACATGTTTT TACATGTTTATA	CAGCOCCICC COAGCOACGC COAGCOACGC COAGCOACGC COAGCOACCC COACCC COAGCOACCC COAGCOACCC COAGCOACCC COACCC CO	COCCEGOGOGO TCCCOGCCTT GCAAACTCTC GCAAACTCTC GCATCGTCA GTGACCGCC CAGATCCACC GGATCCATG GGCATTGAC GGCATTGAC GTGCTTTA GGCATCACT TTTTGCT AACCTGCAC TGTTGAAACA TTTGGTTAAAA AGGAGGGGT ATGGGAAGGGGT ATGGGAAGGGGAT ATGGGAAGGGAT ATGGGAAGGAT ATGGGAAGGAT ATGGGAAGTA ATAGGAAGTA ATAGGTAAAT ATAGGTAAAT	ACCCCAACCC AACTTOCTICC COCCTICTOC	120 180 240 300 360 420 480 540 600 720 780 840 900 1020 1020 1140 1200
50 55 60	GAGCAACCTC GRACCAGAG GCCGGCCACA ACCTGCCACC GCCGTTGGGC GCCCGGTGGCC CGAGGGCCC CGAGGGCCC CGAGGGCC CGAGGAGCACC GAAACCTGCCT TTGGAGGCT TTGGAGGCT TTGGAGGCT TTGGAGGCT TTGGAGGCT TTGGAGGCT TTGGAGCT CCATATTGGC CCATATTGGA	AGCTECTAGE CTTCTCCAGE CTTCTCCAGE CTCCAGCCAGE CCCCAGAGCCAG TCCATTCTCCAG CCCCAGAGCCAG TCCATTCTCCAG CCCCAGATCTCAG CCCCATCAGCCCAG CCCCATCAGCCC CCCCCTATCTCC CCCCATCTCCC CCCCCTTCTCC CCCCTTCTCC CCCCTTCTCCCCTT TAGATCTTACT TCCTCCCCTT TAGTTATCTCC CAGACATCTTT CCCTTTACTCC CAGCCCTT TCCTTTACTCC CAACACTTTT CCCTTTACTCC CAACACTTCCC CCCCCC CCCCCC CCCCCC CCCCCC CCCCCC	ATCOMBACTIC GOCGOCGOM GOCGOCGOM GOCGOCGOM GOCGOCGOM GOCGOCGOM COTTOCTOM COTTOCTOM COTTOCTOM COACACACT CARTICTTO ARACATTRICA GAGGACACA TACATTRICA CARGACACAM GAGGAAANA TACATTACT GAGGAAANA TACATTACT TACATCT TACTTCATTA TCCTTCATTA	CAGCOCGGC COAGGAGGG TTOGCCAGCT COAGGAGGGC TTOGCCAGCT COAGGAGGGC COACACACT GAGCACCGGG GCCACCGGT GGCACCGGT AGCATGGTAT AGCATGTAT AGCATGTA	COSSIGNOSCIA TOCOGGCTT GOAACCTCT ATOGCCAACC GOAACCTCT ATOGCCAACC GOCATCTCA GOACCCACC CAGATCCAC GOACCCAC GOACCAC GOACCCAC GOACCAC GOACCCAC GOACCAC GOACCAC GOACCCAC GOACCAC	ACCOMACCE AACTICCITIC CONCINTENTS CONCINTENTS CONCINTENTS CONCINTENTS COLARIZATION OF THE TOTAL CONTINUE OF TH	120 180 240 300 360 480 540 600 720 780 900 960 1020 1140 1260 1320 1380 1440
50 55 60 65	GAGCAACCTC GAACCAGAG GCGGGGCCA ACCTGCCAGG GCGGGGCCC ACCTGCCAGGGGGCCC ACCTGCCAGGGGGCC CCCAGTGG CCCCAGTGG CATCGCTGT CATCGCTGT CATCGCTGT CATCGCTGTG CATCGCTGTG CATCGCTGTG CATCGCTGTG CATCGCTGTGG CATCGCTGTGG CATCGCTGTGG CATCGCTGTGG CATCGCTGTGG CATCGCTGTGG CATCGCTGTGG CATCGCTGTGG CATCGCTGTGG CATCGCTGT CATCGCTGTGG CATCGCTGT CATCGCTGTGG CATCGCTGT CATCGCTGTGG CATCGCTGT CATCGCTGT CATCGCTG CATCGCTGT CATCGCTG CATCGCT CATCGCTG CATCGCT CATCGCTG CATCGCT CATCGCT CATCGCT CATCGCTG CATCGCT	AGCTTCTAGT CTTCTCCAGC GCCAGCTTCC CTCAGCCAG GCACCTTCC CTCAGCCAG GCACCTTCC CTCAGCCAG AGGACTTACT TGGATGTCC CTCAACTCC CTCAACTCC CTCAACTCC CTCAACTCC CTCAACTCC CTCAACTCC CTCAACTCC ACTCTTACC GTTCTACC GTTCCACTTTACC GACACTCTTACC GACACTCTTACC GACACTCTTACC GACACTCTTACC GACACTCC CTCACTCC CTCACCTCC CTCACCTC CTCACCTCC CTCACCTC CTCACTC CTCACCTC CTCACCTC CTCACTC CTCACCTC CTCACTC CTCACTC CTCACCTC CTCACTC CT	ATCAGACTE GGCGGCGAG GGCGCGAG GGAGTCCGGG GGAGTCCGGG CGCGGCGAG CGCGGCGCACAT AGAGGATGCGG GCAGCACAT AGATGCGG GCAGCACAT AGATGCGG GCAGCACAT AGATGTGCGAC CAGTCAATC CAATCTTTCT AGAACCAG GGGCAAATC TATCTTCCAT AGAGGAATGAT ATCATTCCT AGAGGAATGAT ATCATTCCT AGAGGAATGAT ATCATTCCAT AGAGGAATGAT ATCATTCATTAAAA ATTGGTTAAAA ATGGTTAAAA ATGGTTAAAAA ATGGTTAAAAAA ATGGTTAAAAA ATGGTTAAAAA ATGGTTAAAAAA ATGGTTAAAAAA ATGGTTAAAAAA ATGGTTAAAAAA ATGGTTAAAAAA ATGGTTAAAAAA ATGGTTAAAAAA ATGGTTAAAAAAAA	CAGCOCCGCC CAAGCAGGGC TTGCCCACCT CAAGCGAGTC TTGCCCACCT CAAGCGAGTC TTGCCCACCT CAAGCGAGTC TAGCACCAC CACCACCACCACCACCACCACCACCACCACCAC	COSSIGNATION OF THE CONTROL OF THE C	ACCORACCE AACTICCTCC COCCTTCTCC COCCTTCTCC COCCTTCTCC COCCTTCTCC COCCTTCTCC AGCCANTTA CCAACTCTTCAC COCATCCCC COCTTCTCCAC COCCTTCTCAC COCTTCTCAC COCCTTCTCAC COCCTTCTAA AACCCACTCT COCCTTCAC COCCTTCTAA AACCCACTCT COCCTTCTAA AACCCACTTCAC COCCTTCTAA AACCCACTTCAC COCCTTCTAA AACCCACTTCAC COCCTTCTAA AACCCACTTCAC COCCTTCAC COCCTTCTAA AACCCACTTCAC COCCTTCTCAC COCCTTCAC CO	120 180 240 300 360 420 480 540 600 720 780 840 900 1020 1140 1200 1200 1320 1380 1440 1560
50 55 60 65 70	GAGCAACCTC GAACCAGAG GCGGGGCCA ACCTGCCAGG GCGGGGCCA ACCTGCCAGGG GCCCAGTGG GCCCAGTGG CATCGTGGAAGAC CTATCGTCTT CATCGTAGAAGAC TCTTTCCAGG ATTCTTTCCAGG GAAGAGCTTAGA CGAATTAGG GGAAGATTAGG CGAATTAGG CCATATTAGG CCATATTAGC CCATAT	AGCTTCTAGT CTTCTCCAGC GCCAGCTTCC CTCAGCCAG CTCAGCCAG TCCAGCCAG AGGATTTACT TCGATTCCC CTCAGCAG AGGATTACT GGATGCCC CTCAGCATTT CCTATCAGCC GCTCAGCT CCTCAGCT CCTCAGCC CCTCAGCT CCTCAGCT CCTCAGCT CCTCAGCT CCTCAGCT CCTCAGCT CCTCAGCT CCTCAGCT CCTCATCCC AATTATTAC CATATATTAC CATATATTAC CATATATTAC CCTCATCCCC CCTCTTCAGCC CCTCTTCAGCC CCTCTTCAGCC CCTCTTTCACC CATTTTTATCC CATTTTTATCC CATTTTTATTAC CCTCATCTCC CCTCTTCACCC CCTCTTTCACC CATTTTTTATCC CCTCTTTCACC CATTTTTTATCC CCTCTTTCACC CATTTTTTACCC CATTTTTACCC CATTTTTTACCC CATTTTTTACCC CATTTTTATCC CCTCTTTCACCC CCTCTTCACCC CCTCTTTCACCC CCTCTTCACCC CCTCTCACCC CCTCTTCACCC CCTCTCACCC CCTCTCACC CCTCTCACCC CCTCTCACCC CCTCTCACCC CCTCTCACCC CCTCTCACC CCTCTCACC CCTCTCACCC CCTCTCACCC CCTCTCACC CCTCTCACC CCTCTCACC CCTCTCACC CCTCTCACCC CCTCTCACC CCTCC CCTCTCACC CCTCTCACC CCTCTCACC CCTCTCACC CCTCTCTCC CCTCTCC CCTCTCC CCTCTCC CCTCTCC CCTCTCC CCTCTCC CCTCC CCTCTC	ATCCAGACTE GGCGGCGCAG GGCGCCGCAG GGAGTCCGGG GGAGTCCGGG GGGGGCGCC CCTTCCTGGG CCTTCCTGGG CCAATCTTTGT AGAAGATGAG TAGTTGCCAG GGAGCACAT TAGTTGCCAG GAGCAATAT TAGTTGCCAG GAGCAATAT TAGTTGCCAG TAGTAGCAG TAGTAGTAGAA TAGTAGTAGT TAGTTGCAGTAG TAGTAGTAGAA AATTGGGAGAG AATTGGGAGAG TAGTAGTAGAA AATTGGGAGAG AATTGGGAGAG TAGTAGAGAGAG	CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA CAGCACCAC CAGCACCACCAC CAGCACCACCAC CAGCACCACCAC CAGCACCACCACCACCAC CAGCACCACCACCACCACCACCACCACCACCACCACCACC	COSSIGNATION OF THE CONTROL OF THE C	ACCORACCE ASCITICATE COCCITICATE COCCITICATE COCCITICATE COCCITICATE COCCITICATE ASSOCIATA ASSOCIATA ASSOCIATA COTATOANOT COTATOANOT COTATOANOT COTATOANOT COTTOCAS CITICATOR COTATOANOT COTTOCAS CITICATOR COTATOANOT COTTOCAS COTATOANOT COTATOA	120 180 240 360 420 480 540 600 660 720 780 900 900 900 1020 1020 1140 1200 1260 1320 1380 1440 1500 1560 1680
50 55 60 65	GAGCAACCTC GAACCAGAG GOOGGGGCCA ACCTGCCAGCA ACCTGCCAGCA CCCTGCCAGCAG CCCCCAGTGG CCCCCAGTGG CCCCCAGTGG CATCGCTGT CAATCCCTCT CATCGCTGT CATCGCT CATCGCTGT CATCGCT C	AGCTTCTAGT CTTCTCCAGC GCCACCTTCC CTCAGCCAG CTCAGCCAG TCCATCAGCAG AGGATTAGT TCGATGTCC CTGAATCTCA GATGAGCTG CTGAATCTCA GATGAGCTG CTTCATCTCC CTGAATCTCA CATCAGCTC CTGAATCTCA CATCAGCTC CTGAATCTCA CATCATCAC CTGATGACC CAATCATTACC CTGATGACC CAATCATTCATC CTGATGACC CAATCATTCATC CTGATGACC CAATCATTCATC CTGATGACC CAATCATCATC CTGATGACC CT	ATCOMBACTO GGGGGGGGA GGGGGGGGA GGGGGGGGG CCTTCCTGGG GGGGGGGGC CCTTCCTGG GGGGGGGG	CAGCOCCOCCO CAGCOCACCO CACCO CACC	COSSIGNOS TOCOGOCTY COSSIGNOS CANACTECT ATRISCICARCO GOCAMICTOC GO	ACCCARACCE ASCITTCTCC COCCITTCTUS COCCITTCTUS COCCITTCTUS COCCITTCTUS COCCITTCTUS COCCATOCAS COCCAT	120 180 240 300 360 420 480 540 660 720 980 900 960 1020 1140 1260 1320 1320 1340 1500 1500
50 55 60 65 70	GAGCIAACCTC GAACCAGAG GCGGGGCCCA ACCTGCCAGAG ACCTGCCACA ACCTGCCACA CACCACCAGAG CCCACCACA CCCACCACACA CCCACCACACA CCCACCA	AGCTTCTAGT GTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	ATCOMBACTO GOGGOCOM G	EMGOSCOSCO COAGGOGGO TTOGCOCACT COAGGOGGOT TTOGCOCACT COAGGOGGOT TTOGCOCACT COAGGOGGOT COAGCOGGOT COAGCOGGOT COAGCOGGOT COAGCOCACT COAGCOGGOT COACCOGGOT C	COSSIGNOS TOCOGCOTTO CONTROL TO C	ACCOMAGNO ACTORNO ACTORNO ACTORNO ACTORNO ACCOMAGNO ACCO	120 180 240 300 420 480 540 600 720 780 960 1020 1140 1260 1320 1380 1440 1560 1560 1680 1740 180
50 55 60 65 70	GAGCIAACCTC GAACCAGAG GCOSGGCCAC ACCTGCCAGAG GCOGGGCCAC ACCTGCACACCAGAG GCOGGGCCAC GCAGAGAG GCOGGGCCAC GCAGAGAGAG GCAGAGAGAG GCAGAGAGAG	AGCTTCTAGT GTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	ATCOMBACTE GOCGOCCOM GOGGOCCOM GOGGOCCOM GOGGOCCOM GOGGOCCOM GOGGOCCOM CONTROL	ENGOGOGOGO CORACOAGGO TTOGOCOGO CORACOAGGO TTOGOCOGO GACAGAGO TTOGOCOGO GACAGAGO GACACAGO CACAGO CAC	COSSIGNATION OF THE CONTROL OF THE C	ACCOMAGNO ACTROTOCTOC COCOTTOCTOC COCOTTOC COCOTTOCTOC COCOTTOC COCOTTOC COCOTTOCTOC COCOTTOC	120 120 240 300 420 480 500 660 720 900 1020 1120 11260 1320 1560 1560 1570 1680 1740 1860 1960 1960 1960 1960 1960 1960 1960 19
50 55 60 65 70	GAGCIAACCTE GAACCAGA GCCGACCAGA GCCCCCAGAG GCCGGCCCAC GCCGCCCAGAG GCCCCACCAGAG GCCCCACCAGAG GCCCCACCAGAG GCCCCACCAGAG GCCCCACCAGAG GCCCCACCAGAG GCCCCACCAGAG GCCCCACCAGAG GCCCCACCAGAG GCCCCACACCAG GCCCCACACCAG GCCCCACACCAG GCCCCCACACCAG GCCCCCACACCAG GCCCCCACACCAG GCCCCCCACACCAG GCCCCCCACACCAG GCCCCCCCACACCAG GCCCCCCCC	AGCTTCTAGT CTTCTCCAGC GCACCTTCCCAGC GCACCTTCCCCCC CTCGACCCAGC CTCGACCCACC CTCGACCACC CTCGACCACCACC CTCGACCACC CTCGACCACCACC CTCGACCACC CTCGACCACCACC CTCGACCACCACC CTCGACCACCACC CTCGACCACCACCACC CTCGACCACCACCACCACCACCACCACCACCACCACCACCAC	ATCOMBACTIC GOGGGGCAMA ATCOMBACTATO ATCOMPANA ATTOMBACTATA ATACACTATA ATACACTATACACTATACACTATACACTATA ATACACTATACACTATACACTATACACTATACACACTAC	ENGOGOGOGO CONGONGOS TITOCONCO CONGONGOS TITOCONCO CONGONGOS TITOCONCO CONGONGOS CONGOS CONGONGOS CONGOS CONGONGOS CONGOS CONGONGOS CONGOS CON	COSSIGNATION CONTROL OF THE CONTROL	ACCOMAGNO ACTIONOS ACTIONOS ACTIONOS ACTIONOS ACCOMINATOR ACCOMINA	120 180 240 300 420 480 540 600 780 840 900 900 1020 1140 1200 1200 1200 1200 1380 1440 1500 1660 1740 1680 1740 1680 1740 1680 1740 1680 1740 1890 1890 1990
50 55 60 65 70	GAGCAACCTC GAACCACAGAG GCGGGGCCCAC GACCACAGAG GCCCGATTGGGC GCCCGATTGGGC CAGAGGGCCCC CAGAGGGCCCC CAGAGGCCCCAC CAGAGGCCCCAC CAGAGGCCCCAC CAGAGGCCCCAC CAGAGGCCCCAC CAGAGGCCCCAC CAGAGGCCCCCAC CAGAGGCCCCCAC CAGAGGCCCCCAC CAGAGGCCCCCCCC	AGCTTCTAGT AGCTTCTAGT CTCTCCAGC GCACCTTCC CTCTCCAGC GCACCTTCC TCCATCTCCAGC GCACCTTCC TCCATCTCCAGC GATCAGC GATC	ATCOMBACTIC GGCGGCGCM GGGGCCCM GGGGCCCM GGGGCCCM GGGGCCCM CCTATGCCCM CCTATGCCCM CARTCHITC CARTCHITC CARTCHITC CARCCTRAT CARCCT	ENGOGOGOGO COMAGNAGA TITOCOCACO TITOCOCACO COMAGNAGA TITOCOCACO COMACNAGA GARCACATA GARCACOGO GOCACACATA GARCACOGO GOCACACO GOCACACO GOCACACO GOCACACO GOCACACO GOCACACO GOCACACO GOCACACO GOCACO GOCACACO GOCACAC GOCACACO GOCACAC GOCACACO GOCACAC GOCA	COSSIGNATION OF CONTROL OF CONTRO	ACCORACIC AACTTCATCATCATCATCATCATCATCATCATCATCATCA	120 160 160 160 160 160 160 160 160 160 16
50 55 60 65 70 75	GAGCAACCTC GRACCAGAG GCGGGGCCC GRACCAGAG GCCCGATGGG GCCCAGTGGG GCCCAGTGG ATTCTAGG GCCAGTGGG GTAGGTGG GTAGGTGG GTAGGTG GCGCAGTGAGAG GCGCAGTGAGAG GCGCAGTGAGAG GCGCAGTGAGAG GCGCAGTGAGAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAGTGAG GCGCAG GCGCAG GCGCAG GCGCAGTGAG GCGCAGTGAG GCGCAGTGAG GCGCAGTGAG GCGCAGTGAG GCGCAGTGAG GCG	AGCTTOTAGE GOACCITICO COTTOTACT COTT	ATCOMBACTIC GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CAGOGGOGGO COMOCAGGO COMOC	COSSIGNATION COSSI	ACCOMAGNO ACTION ACTION ACTION ACTION ACTION ACCOMAGNO A	120 160 240 300 420 420 450 540 660 660 660 780 900 1020 1120 1120 1120 1120 1138 1140 1150 1150 1150 1162 1162 1162 1162 1162 1162 1162 116
50 55 60 65 70	GAGCAACCTC GAGCAACCTC GAGCACACCTC GAGCACCACCC GCTGTTGGGC GCCCACTCC GCTGTTGGGC GCCCACTCC CACCCC GCTGTTGGGC GCCCACTCC CACCCC CACCC CACCCC CACCCC CACCC CACC CACCC	AGCTTCTAGT AGCTTCTAGT CTTCAGCAGC CTTCAGCAGC CTTCAGCAGC CTTCAGCAGC CTTCAGCAGCAGC CTTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	ATCOMENTATION ATTOMATOMATICATION ATCOMENTATION ATCOMENTATION ATCOMENTATION AGAINST AGAINST ATCOMENTATION AGAINST AGAINST ATCOMENTATION ATCOMEN	EAGOSCOSCO COMOCASSO COMOC	COSSIGNOSCONTINE COSSICNOSCONTINE COSSIC	AGCOGNACOC AACTICCTOR	120 240 300 360 420 540 540 660 660 660 720 720 720 720 720 720 730 1020 1020 1030 1020 1030 1030 1040 1050 1050 1050 1050 1050 1050 105
50 55 60 65 70 75	GAGCAACCTC GAGCAACCTC GAGCACACCTC GAGCACCACCC GCTGTTGGGC GCCCACTCC GCTGTTGGGC GCCCACTCC CACCCC GCTGTTGGGC GCCCACTCC CACCCC CACCC CACCCC CACCCC CACCC CACC CACCC	AGCTTCTAGT AGCTTCTAGT CTTCTCCAGC CTTCTCCAGC CTTCTCCAGC CTTCTCCAGC CTTCATCTCAGC AGCATTCTCAGC AGCATCTCAGC CTCAGCTCAG	ATCOMENTATION ATTOMATOMATICATION ATCOMENTATION ATCOMENTATION ATCOMENTATION AGAINST AGAINST ATCOMENTATION AGAINST AGAINST ATCOMENTATION ATCOMEN	EAGOSCOSCO COMOCASSO COMOC	COSSIGNOSCONTINE COSSICNOSCONTINE COSSIC	AGCOGNACOC AACTICCTOR	1200 1200 1200 1200 1200 1200 1200 1200

	GCACTGGTGT AGCAAGGCAT CTGATCTTCC	/086443 CTGGAGACCT TTGGCTGCTG CACCTCACAG	TARGCTTATT	GCTTCATCTG	TAAGCGGTGG GAGATAGAAT	ACATGTAAGT	2520 2580 2640 2700
5	CGTTTTGGTG GCCTTAACCA AAGATTCTGA ACAGATGTAA	AATTIGAAAA TIGCTTTTCA GTCTCTCAAG GGAAGTCTTA TGGGAAGAAA	AATGTTTGAA TGATGAGACA TCTTCTGCAG TAAAAGCCTA	AATAAAAAA GTGAAGTAAA TGAGTATGGC CGTGTTGGTA	TGTTAAGAAA ATTGAGTGCA CCAATGCTTT AATCCAACAG	TGGGTTTCTT CTAAACGAAT CTGTGGCTAA CAAGGGAGAT	2760 2760 2820 2880 2940 3000
10	TGTTAGCTGG CTACACAAGG TGCCTTCCAA ATACATAGAT	TAATAACTCA CAGCTGACGC AAAGTCAGCC ACCTGAGAAT CTTCATGATG	TGCTAGGATA ACCGTGTCTT ATATGCTTTT TGTGAGTGTA	GTTAGTTTGG ATGAGGAATT GGAAGTTAAA ATTCCATGIG	AAATGGTACT GGACCTAATA ATTTAAATGG GATATCAGTT	TCATAATAAA AATTTTAGTG CTTTTGCCAC ACCAAACATT	3000 3060 3120 3180 3240 3300
15	TTTGATCTTT	TTTATGGCCC TTATATTCPT AATTTGTATA AAAAAAAAAA	CTACCACACC	TGGAAACAGA	CCAATAGACA	TTTTGGGGGTT	3360 3420
20		244 Protein cession #: i					
	1	11	21	31	41	51	
25	QIQCKVFDSL	FILAFLGNIG LNLSSTLQAT LAILVATANY TSYPTPRPYP	RALMVVGILL GNRIVQBFYD	GVIAIFVATV PMTPVNARYE			60 120 180
30		245 DNA sec id Accession	a #: CAT clu				
	1	11	21	31	41	51	
35	TTAATGGTTA AGCATGGTCC TTTTCTTCCT	TTTTTTTTT AATGCTGTTT CGAGAGTCTG GAGATTTAGT GAAGAATGCA	ACCAAGTGAC ACAAACCTCA TTCTTCATCG	CCAGAGGCAG GTTCAAATCC TTAACAATGA	CGTGGTTTAG TTCTTTTGTC GGATATTAAT	TGGTTTCAAC TTCACTTAGT ATGTTTCACA	60 120 180 240
40	AGGTGGGGAG TTAATAGCCA GTCCTACGCC	CTCCACTTCA CTCCACTTCA CACGGAGTCT	CCCAGGAATT GCCTGGGCAA CGCTGATTGC	CAAAGCTGCA TGTAGTAAGA	ATGCATTATG TCCCATCTCT	ATTACAGCTG GGCTCGGAGG	360 420
45	Nucleic Aci	246 DNA seid Accession lence: 897-	n #: XM_058 1400	1553.2			
	1	11	21	31	41	51	
50	TAAATGTATT GTGAAACCAT CTGTTATCCA	AGTTTCGTAT TAGTCTCAGT TTCTCTTTTA TAATATGGAC TGAGTATTAA	ATGTTTCACA AGTTCTTGAG	AGAGATTTCT TTCCTGTTAC TCCTAACATT	AGATTIGTTC GAGAGGTTTT	TOTTGTGACT CCCTTAGTGC	60 120 180 240
55	TOGGATGAGA GATCATGTTT GTTGAGTGTA ACTGGTAACC TTATTTCTGT	GGAGGTGAAA AAGAAAAGTC TACTGTCTGT TGCCTATCTG GTTTATGTAT	CCTCACTAGA ATGAAAATGG CAAAGACTTC TATTTTTAAG AAGGGGTTTT	AAAAGGGACA TGAACTAGTG CAGCATTTCC AACCCAGGAG TTGTTTTTT	ATGTTAGTGT TTTCCAAGCA AGGTCCTAGA GAAAGCTTTA AAAGACAGGA	GGCCCTTCCT TATTGGAAGG GAGGAACAAG TAATAGAACA TCTCACTCCA	360 420 480 540 600
60	TTGTCCAGGC GCCTTTGCCT TTTTTTTGTT TAGTCTTGCT	CARGTGCART CCTGAGTAGC TGTTTGTTTG TTGTTGCCAG	GGCACGAACC TGGGACTACA TTTGTTTTTG GCTAGTCTCA	TCATAGCTCC GGCATGAGCC GGGGGGGTTG AACTCCTGGC TTCCATTCAG	TOGACTTAAG CCCATGCCTG TTTTGTTTTT TTCAAGTGAT	TGATCTGCCT GCTAGTTTG TGTAGAGACG CCTCCTGCCT TCCAACATGG	660 720 780 840 900
65	AAGAAACTTA ACCATCAAAT CTGATGTTGC CTGAAATTAG	CACCGACTOC CAGGGCTTGC AAGCAAATTG TCATCATATC	AGGTTTCCTT GCTACTTGTC TCAAGCTGTG	AGAAGCTATT ATCATCTTAT CCTTCAATGC ATGACAGAAG	GCAATGCCCC CAAGTGCAGA TOGCCACCAG TTGTATTGAG GAGCACTTGAG	TATGACAAAA AAGAATCATC GTTCCTCGAG CAAGATGTTG CAGTGCCCTC	960 1020 1080 1140 1200
70	GCACAACTCA ATAACCTGGC ACAATGGAAA	AGACTGGGAT CTACTCTGAC TTCAGGCATG TGCACAGTAA	AAGATTTGT AACAACAGCC CGAGTTCCCA CTGAATACCT	GGGAGCAGAC CTGCGAGCAA AATCTCTGCC ATCTCATCAA	CAGCACCICA CATAGTTACA GTATGTTCTG ATGCCAGACC	TTTGTCTGGG GAACATAAGA CCATGGAAAA CTAGAAGACT	1260 1320 1380 1440
75	AACTCCCTGT	CTTCTACCAG GACTTTCCAA GAACOCTCAT	ACTGACAAGC	ACACTTTTTT	CCTCCCCCCT	TGAATCCTCA	1500 1560
80		247 Protein cession #: :					

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MESTYTOSILO PEKLLOCYD DCHICHACAS; PULILIKERU INI PIDVASELAT CPENARHQVP 60
RESISHINIS CIDRACIECO VVNOTRSLAG ETLASSINOC PPCDEDDOKO LNEOTSTPFV 120
NOTTHISDIN SYARNIVTEH KONIASOKRV KELPYULPH KNHIGKAR

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Seq ID NO: 248 DNA sequence
Nucleic Acid Accession #: NN_003392
Coding sequence: 758..1855

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							120
10							180
		CCCCCGCGCT TCCCGTGCTC					240 300
	OCCCCMOOTE	ADDADAGOOD	COGREGERE	CCCCAGCGG	TTCCTGAGTG	AATTACCCAG	360
	GROOGE CHICE	CCACACCACC	BROTRORGAG	COGTCAGGGG	GTGCGGGACT	CGAGCGAGCA	420
15							480 540
	TCGCTGGCGT	GCCCCGCGCA	CAGGATCCCA	CTATATCTTC	CCATCAAAAA	TGAGGTTGCG ACTCACGGAG	600
	CACAACCCCA	CTCARTCARC	DOTABACTTA	AGAGACCCCC	CATGCTCCCC	TGGTTTAACT	660
~~							720 780
20	GTCCATTGGA	ATATTAAGCC	CAGGAGTTGC	TTTGGGGATG	GCTGGANGTG	CAATGTCTTC TAATTGAAGC	840
	CARPOTTOO	TOOTYCCTAG	GTATGAATAA	CCCTGTTCAG	ATGTCAGAAG	TATATATTAT	900
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25							1020
25						ACACCTCTGT CCGTGAGCGC	1140
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							1260 1320
30	CGACAACATC	GACTATGGCT	ACCCCTTTGC	CAAGGAGTTC	CTCATCATC	GCGAGCGGGA TGCACAACAA	1380
30	CONCOCCOCC	CCCACCACCG	TOTACAACCT	GGCTGATGTG	GCCTGCAAGT	GCCATGGGGT	1440
	ORCOGGGGGGA	TOTACOCTOA	ACACATGCTG	CCTGCAGCTG	GCACACTTCC	GCAAGGTGGG	1500
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35							1680
55							1740
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	COCK CCCKCC	ACTUACUCC	CCTCCCAGGA	COCGCTTATT	TATAGAAAGT	ACAGTGATTC	1920
40	TOOTTTTTOO	TTTTTTAGAAA	TATTTTTTAT	TTTTCCCCCAA	GAATTGCAAC	CGGAACCATT	1980
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							2220
45	TOCCATCATA	TGGGATGGGT	AGGTTCCAGT	TGAAAGAGGG	TGGTAGAAAT	CTATTCACAA AGGTCTTGGG	2280
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50	AATAGCTCAT	GAAATTTGGG	TETGALOCTO	TTATAAGAAT	TGGGATTCCA	AAATTTAAAA GATTTGTAAA	2640
							2700
							2760 2820
55	TACATGAATC	CCATTCACAG	GTTTCTCMGC	CCAAGCAACA	AGGTAATIGC TOBALTOCAC	GTGCCATTCA	2880
55	A CA CTCACCC	CTICTICTICATT	CCTCCGTGTT	GTGATGTGAT	GCTGGCCACG	TTTCCAAACG	2940
	CONCETCON	TOGGGTCCCCT	TTGGTTGTAG	GACAGGAAAT	GAAACATTAG	CAGCTCTGCT	3000
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60							3180
00							3240
	GGTTTAATGG	TGCCTGATAT	CTCAAAGTCT	TTTGTACATA	ACATATATA	ATATATACAT TTACAGCTTA	3360
	CTCTGGGGTT	ATOTOTOTOT	CTAGAGCATT	GTTGTCCTTC	ACTGCAGTCC	AGTTGGGGATT	3420
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	GCACGACGAA	GCAACCTCGT	TTCTGAGGA	GAAGCTTGAG	TTCTGACTC	CTGAAATGCG	3540 3600
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	ATTCAARACT	CAGAAGCATO	AGCAATGTT	CTCTTTTCTT	AGTTCATTCT	GCAGAATGGA ATATTCAGCC	3720
70	AACCCATGCC	TATTAGAAAT	GACAGTACTI	ATTAATTGAG	TCCCTAAGG	ATATTCAGCC	3780 3840
	ar accordence	A B TT B TT CT	TATCTCAGAC	THE CONTROL OF	TTAAAAATTT	C TCTTTCCAAA C GGAAAGATAC	3900
	ACA TOTTTTO	ATACCCCCCC	TTAGGAGGT	GGGCTTTCAT	* ATCACCTCAC	CCAACTGTGG	3960
7.5	CTCTTABTTS	ATTOCATABL	CATATCCAC	TCAGCCAACT	GTGGCTCTT	CAATTTATTGC	4020
75	ATAATGATAT	TCACATCCCC	TCAGTTGCAG	TGAATTGTGA	GCAAAAGATG	TTGAAAGCAA	4140
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							4260
80						GCTTATTCT	4320 4380
80	ANTIGGAAGAS	ATTTGTATA: CAGAATATAAJ	ATABARCOT	ACTIGIAAA	AAAAAAA	COLLABOR	2500
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Seq ID NO: 249 Protein sequence: Protein Accession #: NP_003383

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	SOCOKKICHI.	FLVALAIFFS YQDHMQYIGE VVNAMSRACR	GAKTGIKECO	YOFRHRRWING	STVDNTSVFG	RVMOIGSRET	60 120 180
_	PUDARERERI	HAKGSYESAR	ILMNLHNNEA	CRRTVYNLAD	VACKCHGVSG	SCSLKTCWLQ	240
5	LADFRKVGDA GSLGTQGRLC QFVCK	LKEKYDSAAA NKTSEGMDGC	MRINSRGKLV BLMCCORGYD	QVNSRFNSPT QFKTVQTERC	TQDLVYIDPS HCKFHWCCYV	KCKKCTEIVD	300 360
10	Nucleic Aci	250 DNA sec d Accession tence: 561	#: NM 0140	158			
	1	11	21 	31 	41 	51 	
15	TGACTTOGAT	GTAGACCTCG	ACCTTCACAG	GACTOTTCAT	TGCTGGTTGG	CAATGATGTA	60
	CGTCATCTTC GAGATATAAT	GTGGTGAGGG ATATCCCTGA CAAAAGAAGA	TTGTCCTGGC CCTACAATTA	AGTGTGCATT CTATAGCACA	GGACTCACTG TTGTCATTTA	CAACTGACAA	120 180 240
20	ACTATATGCT	GAGTTTGGCA GIGAAAAATG	GAGAGGCTTC	TARCAATTTT	ACAGAAATGA	GCCAGAGACT	300 360
20	TCAGGTTATC	ARGITCAGIC	AACAGAAGCA	TOGACTOTTC	GCTCATATGC	TGTTGATTTG	420
	TAGATTTCAC	TCTACTGAGG	ATOCTGAAAC	TGTAGATAAA	ATTGTTCAAC	TIGTITIACA	480 540
	TGAAAAGCTG	CAAGATGCTG AAGACAGAAA	CAGACAGCTA	TARAGUAGAT	TGCTGCGGAA	CACGAAGAAG	600
25							660
	GCCCTGGCAG	GCTAGCCTGC CTTGTGAGTG	AGTGGGATGG	GAGTCATCGC	TOTGGAGCAA	CTGCCAGATG	720 780
	GACTGCTTCC	TTTGGAGTAA	CAATAAAACC	TTCCAAAATG	AAACGGGGTC	TCCGGAGAAT	840
30	AATTGTCCAT	GAAAAATACA GTTCCCTACA	AACACCCATC	ACATGACTAT	GATATTTCTC	TTGCAGAGCT	900 960
30	TGAGTTTCAA	CCAGGTGATG	TGATGTTTGT	GACAGGATTT	GGAGCACTGA	AAAATGATGG	1020
	TTACACTCAA	AATCATCTTC	CACABGCACA	GGTGACTCTC	ATAGACGCTA	CAACTIGCAA	1080 1140
	TGAACCTCAA	GATGCATGCC	ACCCCATAAC	TGGAGGACCA	CTGGTTAGTT	CAGATGCTAG	1200
35	AGATATCTGG	GATGCATGCC TACCTTGCTG	GAATAGTGAG	CTGGGGAGAT	GAATGTGCGA	AACCCAACAA	1260
	GCCTGGTGTT	TATACTAGAG	TTACGGCCTT	GCGGGACTGG	ATTACTTCAA	GOTGTGGAGG	1320 1380
	CCATTTTTAG	AGATACAGAA	TTGGAGAGA	CTTGCAAAAC	AGCTAGATTT	GGTGTGGAGG GACTGATCTC	1440
40	artaractgt	TTGCTTGATG	сахалалала	A			
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45	1	11	21	31	41	51	
45	1	11 I	21	Ĭ.	Ĩ.	i	60
45	1 MYRPDVVRAR DKLYAEFGRE	11 KRVCNEPWVI ASNNFTEMSQ	21 GLVIFISLIV RLESMVKNAF	LAVCIGLTVH YKSPLREEFV	YVRYNQKKTY KSQVIKFSQQ	NYYSTLSFTT KHGVLAHNLL	120
	1 NYRPDUVRAR DKLYAEFGRE ICRFHSTEDP	11 KRVCNEPWVI ASNNFTEMSQ BTVDKIVOLV	21 GLVIFISLIV RLESMVKNAF LHEKLODAVG	LAVCIGLTVH YKSPLREEFV PPKVDPHSVK	YVRYNQKKTY KSQVIKFSQQ IKKINKTETD	NYYSTLSPTT KHGVLAHNLL SYLNHCOGTR	120 180
45 50	1 MYRPDUVRAR DKLYAEFGRE ICRFHSTEDP	11 KRVCNEPWVI ASNNFTEMSQ EIVDKIVQLV	21 CLVIFISLIV RLESMVKNAP LHEKLQDAVG	LAVCIGLTVH YKSPLREEPV PPKVDPHSVK DOSHBCGATL	YVRYNQKKTY KSQVIKFSQQ IKKINKTETD INATWLVSAA	NYYSTLSFTT KHGVLAHNLL SYLMHCOGTR HCFTTYKNPA	120 180 240 300
	1 MYRPDVVRAR DKLYAEFGRE ICRFHSTEDP RSKTLGQSLR RWTASFGVTI SYEFOPGDVM	11 KRVCNEPWVI ASNNFTEMSQ ETVDKIVQLV IVOGTEVEBG KPSKMKRGLR FVTGFGALKN	21 GLVIFISLIV RLESHVKNAF LHEKLQDAVG EWFWQASLQW RIIVHEKYKH DGYSQNHLRQ	LAVCIGLTVH YKSPLREEFV PPKVDPHSVK DGSHRCGATL PSHDYDISLA AQVTLIDATT	YVRYNOKKTY KSOVIKPSOO IKKINKTETD INATWLVSAA ELSSPVPYTN CNEPQAYNDA	NYYSTLSPTT KHGVLAHNLL SYLWHCCGTR HCPTTYKNPA AVHRVCLPDA ITPRMLCAGS	120 180 240 300 360
50	1 MYRPDVVRAR DKLYAEFGRE ICRFHSTEDP RSKTLGQSLR RWTASFGVTI SYEFOPGDVM	11 KRVCNEPWVI ASNNFTEMSQ EIVDKIVQLV	21 GLVIFISLIV RLESHVKNAF LHEKLQDAVG EWFWQASLQW RIIVHEKYKH DGYSQNHLRQ	LAVCIGLTVH YKSPLREEFV PPKVDPHSVK DGSHRCGATL PSHDYDISLA AQVTLIDATT	YVRYNOKKTY KSOVIKPSOO IKKINKTETD INATWLVSAA ELSSPVPYTN CNEPQAYNDA	NYYSTLSPTT KHGVLAHNLL SYLWHCCGTR HCPTTYKNPA AVHRVCLPDA ITPRMLCAGS	120 180 240 300
	1 MYRPDWVRAR DKLYAEFGRE ICRFHSTEDP RSKTLGQSLR RWTASFGVTI SYEFQPGDVM LEGKTDACQG GI	11 KRVCNEPWVI ASNNFTEMSQ ETYDKIVQLV IVGGTEVBEG KPSKMKRGLR FVTGFGALKN DSGGPLVSSD	21 GLVIFISLIV RLESMVKNAP LHEKLQDAVG EWFWQASLQW RIIVHEKYKH DGYSQNHLRQ ARDIWYLAGI	LAVCIGLTVH YKSPLREEFV PPKVDPHSVK DGSHRCGATL PSHDYDISLA AQVTLIDATT	YVRYNOKKTY KSOVIKPSOO IKKINKTETD INATWLVSAA ELSSPVPYTN CNEPQAYNDA	NYYSTLSPTT KHGVLAHNLL SYLWHCCGTR HCPTTYKNPA AVHRVCLPDA ITPRMLCAGS	120 180 240 300 360
50	1 MYRPDUVRAR DKLYAEFGRE ICRFHSTEDP RSKTLGQSLR RWTASFGVII SYEPQPGDVM LEGKTDACQC GI Seq ID NO: Nucleic Aci	11 KRVCNEPWVI ASNNFTEMSQ ETVDKIVQLV IVOGTEVEBG KPSKMKRGLR FVTGFGALKN	21 CLVIFISLIV RLESNVKNAF LHEKLQDAVG EMPMQASLQM RIIVHEKYKH DGYSQNHLRQ ARDIWYLRGI Quence 1 #: NM_003	LAVCIGLTVH YKSPLRESEV PPKVDPHSVK DGSHRCGATL PSHDYDISLA AQVTLIDATT VSWGDECAKP	YVRYNOKKTY KSOVIKPSOO IKKINKTETD INATWLVSAA ELSSPVPYTN CNEPQAYNDA	NYYSTLSPTT KHGVLAHNLL SYLWHCCGTR HCPTTYKNPA AVHRVCLPDA ITPRMLCAGS	120 180 240 300 360
50	1 MYRPDUVRAR DKLYAEFGRE ICRFHSTEDP RSKTLGQSLR RWTASFGVII SYEPQPGDVM LEGKTDACQC GI Seq ID NO: Nucleic Aci	11	21 CLVIFISLIV RLESNVKNAF LHEKLQDAVG EMPMQASLQM RIIVHEKYKH DGYSQNHLRQ ARDIWYLRGI Quence 1 #: NM_003	LAVCIGLTVH YKSPLRESEV PPKVDPHSVK DGSHRCGATL PSHDYDISLA AQVTLIDATT VSWGDECAKP	YVRYNOKKTY KSOVIKPSOO IKKINKTETD INATWLVSAA ELSSPVPYTN CNEPQAYNDA	NYYSTLSPTT KHGVLAHNLL SYLWHCCGTR HCPTTYKNPA AVHRVCLPDA ITPRMLCAGS	120 180 240 300 360
50 55	1 MYRPDUVRAR MYRPDUVRAR DKLYAEFGRE ICRFHSTEDP RSKTLOGSLE RWTASFGVTI SYEPOPODVM LEGKTDACQC GI Seq ID MO: Nucleic Ac: Coding sequ	11 KRVCNEPWVI ASNNFTEMSQ ETVDKIVQLV IVGGTEVESG KPSKMKRGLR FVTGFGALKN DSGGPLVSSD 252 DNA sed d Accession ence: 71-1:	21 CLUIFISLIV RLESNVKNAF LHEKLQDAVG EMEWOASLOW RIIVHEKYKH DGYSQNHLRQ ARDIWYLRGI Quence 1 #: NM_003 771 21	LAVCIGLTVH VKSPLRESFV PPKVDPHSVK DGSHRCGATL PSHDYDISLA AQVTLIDATT VSWGDECAKP	YVRYNOKKTY KSQVIKFSQQ IKKINKTBTD INATWLVSAA ELSSPVPYTH CNEBQAYNDA NKPGVYTRVT	NYYSTLSFTT KHGYLAHNLL SYLMHCGSTR HCFTTYKNPA AVERVCLPDA ITPRMLCAGS ALRDWITSKT	120 180 240 300 360 420
50 55	1 NYRPDVVRAR DKLYAEFGRE ICRFHSTEDP REXTLOGSLR RWTASFGVTI SYEPOPODVM LEGKTDACOC GI Seq ID NO: Rucleic Aci Coding sequ	11 KRVCNEPWVI ASNNFTENSQ ETVDKIVQLV IVGGTEVESG KPSKMKRGLR FVTOFGALKN DSGGPLVSSD 252 DNA sec d Accession ence: 71-1*	21 CLVIFISLIV RLESMVKNAF LHEKLQDAVG ENFWQASLQW RITUHEKYKH DGYSQNHLEQ ARDIWYLAGI Quence 1 #: NM_000771 21 CGGGCTCTTG CGGGCTCTTG	LAVCIGLTVH VKSPLRESPV PPKVDPHSVK DGSHRCGATL PSHDYDI SLA AQVTLIDATT VSWGDBCAKP 1504.2 31 GTACCTCAGC CAAAGAGTTC	VVRYNOKKTY KSOVIKPSOQ IKKINKTESO IKKINTESO IKK	NYYSTLSFTT KHGYLAHNLL SYLMHCGSTR HCFTTYRIPA AVHRVCLPDA ITPRMLCAGS ALRDWITSKT 51 GGCGTCCGGC TCCAGAGCCA	120 180 240 300 360 420
50 55 60	1 NYRPDVVRAR DKLYAEFGRE ICRFESTEDP RSKTLGGER RHTASFGVTI SYEPOPDDVM RUCleic Aci Coding seque 1 GGCACGAGGC CCCCTGCTT	11 KRVCNEPWVI ASNIFTENSQ ETVDKIVQLV ETVDKIVQLV EVENTATORIA PVTGFGALKN DSCOPLVSSD 252 DNA sec dAccession ence: 71-1'	21 GLVIFISLIV RLESWYKNAF LHEKLQDAVG RITVHEKYKH DGYSONHLRQ RITVHEKYKH 21 #: NM_00: 71 21 GGGGCTCTTG CCGATTTCCG	LAVCIGLTVH VKSPLRESFV PPKVDPHSVK DGSHRGGATL PSHDYDI SLA AQVTLIDAT VSWGDBCAKP 1504.2 31 GTACCTCAGC CAAAGAGTTC	YVRYNOKKTY KSQVI KFSQQ IKKINKTETO INATWLVSAA ELSSPVPYTH ONEPQAYNDA NKPGVYTRVT 41 GGGAGGGCCA TACGAGGTGCA	NYYSTLSPTT KHGVLAHMLL SYLMFACGTT HCFTTYRIPA AVREVCLPDA LTPRHCADA LTPRHCADA ALRDWITSKT 51 GGCGTCCGGC TCCAGAGCCA AGACTATA	120 180 240 300 360 420
50 55	1 WYRPDUVRAR DKLVAEFGRE ICREMSTED RSKTLOGSLR RWTASFGVTI STEPOPUVM LEGKTDACOC GI Seq ID NO: Nucleic Aci Coding sequ 1 GGCACGAGGC COCCUTGCT GAGGGTCCTT GAGGGTCCTT GGCCTTGTC	11	21 GLUIFISLIV RLESHVKNAP LHEKLQNAP GENVRAP GENVRAP RIIVHEKYEM RIIVHEKYEM ARDIWYLAGI Quence a #: NM_003 771 21 GGGGCTCTTG CCGATTTCCG CCTCTGGACGT ACGTGCAATA	LAVCIGLTVE VKSPLRESFV PPKVDPHSVK DGSHRCGATL PSHDYDI SLA AQVTLIDAT VSWGDBCAKP 1504.2 31 GTACCTCAGC CAAAGAGTTC TACGCTGGTT TACGCTGGTT TACGCTGGTT TACGCTGGTT TACGCTGGTT TACGCTGCTGTT TACGCTGGTT TACGCTGGTT	YVRYNOKKTY KSOVI KFSOV INKINKTETO INATWLVSAN ELSEPVPTIM KNEPGVYTRVT 41 GCGAGCGCCA TACGAGCTGCA CCAGTTTCTG CCAGTTTCTG	NYYSTLSPTT KHGVLAHNLL SYLMHCGSTR HCFTTYRIPA AVHRVCLPDA AVHRVCLPDA AVHRVCLPDA AVHRVCLPDA FOR TOPMICAGS ALRDWITSKT 51 GGCGTCCGGC TCCAGAGCCA AGATCCTTCA GGTGGCAAGA TCATAAACTG	120 180 240 300 360 420 60 120 180 240 300
50 55 60	1 MYRPDUVRAR DKLYAEFGRE ICRFESTEDP SKYLJOSELR RHYASFGYL SYEPOPODVM LEGKTDACOC GI Seq ID NO: Nucleic AC Coding sequ 1 GCACGAGGC CCCCUTOCT GAGGGTCCT GAGGGTCCTT GAGGGTCCTT AGGGTTCTT AGGGTTCTT AGGGTTCTT AGGGTTCTT AGGGTTCTT	11	21 GUNIFISLIV RLESMYRNAF LIESKLQDAYG SIFMOASLOW RIIVBENYER DOVSOMILDO ARDIWYLAGI 1 %: NM_00: 771 GOGGCTCTTG CCGGATTCCC CCTCGGACT ACCGTAAAGA ACGTAAAGA	LAVCIGLTVH YKSPLRESFV PPKVDPHSVK DGSHRCGATL PSHDYDI SLA AQVTLIDAT VSWGDBCAKP 104.2 31 GTACCTCAGC CAAAGAGTTC GGATXCTGT CGATXCTGT ACAGTTCAT TCAGCTGGTT ACAGTTCAT TCAGCTGGTT ACAGTTCAT TCAGCTGAT TCAGCTGGTT TCAGCTGGTT TCAGCTGGTT TCAGCTGGTT TCAGCTGGTT TCAGCTGGTT TCAGCTGGTT TCAGCTGGTT TCAGCTGGTT TCAGCCTGGTT TCAGCCTGGT TCAGCTGGT TCAGCCTGGT TCAGCCTGGT TCAGCTGGT TCAGCT TCAGCTGGT TCAGCT TCAGCTGGT TCAGCTCGGT TCAGCT TC	YVRYMORKTY KSQVIKPSQQ IKKINKTETD INATMLVSAA ELSSPVPTTM ONEPQAYNDA NKPGVYTRVT 41 GCGAGCGCCA TACGAGGTGG TGTGCGTGCA CCAGGTTGCA CCAGGTTGCA TATTTATTATT	NYSTLSPTT KRGVLAHNLL SYLMRGGTT KRGVLAHNLL SYLMRGGTT LTPRMLCAGS ALRDWITSKT 51 GGCGTCCGGC TCCAGAGCCA AGATCTTCA AGGTGCAAGA TCATAAACTG TATTCTTTGT	120 180 240 300 360 420 60 120 180 240 300 360
50 55 60	1 MYRDBWURAR DLLYARRORE ICRPESTED PROKITOGORE RWITASTOVI I STEPOGROUM LEGKTDACOS GEOGROCIOCOTOGOT GEOGROCIOCOTOGOT GEOGROCIOCOTOGOT GEOGROCIA ACTIGAACAT TOGGGCAACAT TOGGCAACAT TOGGCAACAT TOGGCAACAT TOGGCAACAT TOGGCAACAT TOGGCAACAT TOGGGCAACAT TOGGCAACAT TOGGCAAC	II	21 COUNTISLIV RLESWONNA LIESKLODAUS SWPWOASLOM RITWIENTEN DOTONILLAN Quence 1 #: NW_002 771 21 COGGCTCTTG COGGCTCTTG COGGCTCTTG COGGCTCTTG COGGCTCTTG COGGCTCTTG COGGCTCTTG COGGCTCTTG COGGCGTATA ACCTCAGAGG TOGATATTCC	LAVCIGLTVH YKSPLRSESPU PKNOPHSVK DGSHRCGATL PSHDYDISLA AQVILIDATI VSWGDBCAKP 1504.2 31 GTACCTCAGC CAAAGAGTCTC TACGCTGGTT TACGCTGGTT TACACCTGGTT TACACCTGGTT TACACCTGGTT TACACCTGGTT TACACCTGGTT TACACCTGGTT TACACCTGGTT	YVRYMORKTY KSOUTKESOT INATHLYSAA ELSSPVPTTM ONEPQAYNDA NKPGVYTRVT 41 GGGAGGGCCA TACGAGGTGCA CCAGTTTCTG GAGGACACTA AAGGACACTA AAGGACACTA AAGGACACTA AAGGACACTA AAGGACACTA	NYSTLSPTT KHOULANNILL SYLMEWCOST HCFTTYKNPA AVERVCLPDA AVERVCLPDA AVERVCLPDA AVERVCLPDA SALRDWITSKT 51 GGCGTCCGGC TCCAGAGCCA AGATCTTCA GGTGGCAAGA TCATAACT TCATAACT TCATAACT TCATAACT TCATAACT TCATAACT TATTCTTTGT TATTCTTTGT	120 180 240 300 360 420 60 120 180 240 300
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50 55 60 65	1 NTRPDWVRAR DKLYARFORE ICRESTED REXTLOGSLR RWTASFOVI STED OF THE STED OF THE STED OF THE STED OF THE CODING SEQ ICCONTOCT GAGGATCCTT GAGGATCCTT GAGGATCCTT GAGGATCCTT GAGGATCCTT ACTTCAMACT TOTAMACTAT	11	21 GLWIFISLIV RLESWONNAF LIESKLOADUS SHFMOASLOM RITURENTIA DOTSONNILDO ARCHIVAGI COGGATTICCO CCTCCGACT ACCUTAAAGA TOGGATTICCT TOAATOTCCT TOATOTCCT TOA	LAVCIGITVH YESPLARSEN PENDPISUA OGRHEGATL PSHDYDISLA AQVILIDATI VSKGDECAKP 31 GTACCTCAGC CAAAGAGTTC GQAGTCATCT TAGCCTGGTT TAGCCTGGTT TAGCCTGGTT TCAACCTGGTT TCA	YVENHORKTY KSOVIKPSOO INKINESED INATVLUSAN ELSEVEVITH CASPOLITION NKROVITEVI 41 GCORGCOCA TACGROGIGE CAGGITTCTG TATTITLITE GARGACATTA AANGATAGC GAMGACATCT TATTITLITE GARGACATCT AANGACATCT CAGGACATCT TATTITLITE GARGACATCT AANGACATCT TATTITLITE CAGGACACATC TATTITLITE CAGGACACTC TATTIT	NYSTLSPTT KIGULAHMIL STUHPHOGTE RCFTTYRIPA AVENCLIPA TTPREGAS ALRUHITSKT 51 GGGGTCCGGC TCCANGGCCA AGATCATCT GGTGCCAGGA TCTATACTTTT TCAGGGGTG	120 180 240 300 360 420 60 120 180 240 300 420 480 540 600
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50 55 60 65 70	1 NTREDUVARA DIL VARAFORE I COPERTA DE LA CASA DEL CASA DE LA CA	11	21 CAUTIFISLIV RLESSYNONAF LIERLAGANONAF RESEARCH RES	LAVCIGITYM YISPIRASSY PSYNOPSING DSSINGOATL PSHOVDISIA AQVILIDAT VSWGDECAKP 31 GTACCTCAGC GAAAGAGTTC GAACTGTA ACAGTTTAA CAGTTTAA CAGTTAAACTGA CAGCAGCAG CAGCAGCAG CAGCAGCAG CAGCAGCAG CAGCAGCAGCAG CAGCAGCAGCAGCAG CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	YVENHORKTY KSOUTKESQO INKINKESTO	NYTSTLSPTT RISULAHMIL STUBHOSTE REPTTYMPA AVRENCEPD TYPHOLOGIS ALRIMITSKY 51 1000TCC00C COMMITSKY 67T0CAMGCC GGTGCCAMG TCAMGAACTG TATTCTTTC TATTCTTTC RATCAMACTG TATTCTTCAMGCCTC GGTGGCAMGACTC TCAMGAACTG TATTCTTCAMGCTC AGGGCGAACTG TCAMGAACTG TATTCTTCAMGCTC TCAMGAACTG TATTCTTCAMGACTG TCAMGAACTG TCAMGAACTG TCAMGAACTG TATTCTTCAMGACTTC TCAMGAACTG TCAMGAACTT TCAMGAACTG TCAMGAACTG TCAMGAACTT TCAMGAACT TCAMGAACTT TCAMGAACTT TCAMGAACTT TCAMGAACTT TCAMGAACTT TCAMGAAC	120 180 240 300 360 420 120 120 120 240 300 360 480 540 660 720 780
50 55 60 65	1	11	21 CUMIFISLIV RLESHVONAP LIESTAGONAL RESHVONAP LIESTAGONAL RETURNATION OF SHORE ARCHITECTURE RESHVONAP LIESTAGONAL RESHVONAP LIEST	LAVCIGITYM YKSPLASSPY PFRUPPISVA DGSHRCOATL PSHDYDISIA AQVILIDATI VSKGDECAM 31 GTACCICAG CAAAGAGTIC GAATGATGAT TAGGCTGTT TAGGCTGT TAGGCT TAG	YVENHORKTY KSQUIKPSQQ HIKKHKYEPT HATHLUSAA ELSSPUPYITH CHEPQANDA NKRGVYTRVT 41 GCGAGCGCCA TACGAGCTG TATGAGCTGC CAGTTTCTG TATTTATTC TATTTATTC TATTTATTC TATTTATTC TATTTATT	NYTSTLSPTT NGOVLAHMLL SYLHROCOTS HOPTIVARPA AVREVCLPDA ITPRICAGS ALROHITEKT 51 GCGCTCCGGC TCCAMGGCT TCCAMGGCT AGATCAAT TCAMAGCT	120 180 240 300 360 420 120 240 300 420 480 560 660 660 6720
50 55 60 65 70	1	11 REVOLUENT ASSISTED OF THE SECOND OF THE	21 GIMITELLY GIMITELLY ELESPYONAP ELESPYONAP ELESPYONAP ELESPYONAP ELESPYONAP ELESPYONAP ELESPYONAP ARCHYLAGI ELESPYONAP ELESPYONAP ARCHYLAGI ELESPYONAP ELES	LAVCIGITYM YKSPLASEN PSTROPHSW DGSHRCOATL PSHDVD1SLA AQVILIDAT VSWGDECAR 31	YVENHORKTY KSQUIKRSQQ INKINKTSTQ INKINTENTION INK	NYSTLSPTT RISCULANGLE STUDNICOS STUD	120 180 300 360 420 180 240 360 420 360 420 660 720 780 840 900 960
50 55 60 65 70	1 NYAPHVIRAR N	11 I I I I I I I I I	21 PUPISILY RESERVANCE OF THE PROPERTY OF THE	LAVCIGITYM YKSPLASSRY PSRVDPHSVA DGSHRCGATL PSRDVDHSVA SAGNICARD STACCTCAGC CAAAGAGT ACATCAGC CAAAGAGT ACATCAGC CAAAGAGT ACATCAGC CAAAGAGT ACATCAGC CAAAGAGT CAACCATCAGC CAACGAGT CAACCATCAGC CAACAGAGT CAACCATCAGC CAACAGAGT CAACAGAACT CAACAGAGT CAACAGAGT CAACAGAACT CAACAT CAACAGAACT CAACAGAACT CAACAGAACT CAACAGAACT CAACAGAACT CAACAGAACT CAACAGAACT CAACAT CAACAT CAACAT CAACAT CAACAT CAACAT CAACAT CAACACT CAACAT CAACAT CAACACT CAACAT CAACAT CAACAT CAACAT CAACAT	YNTHIORITY KSQUIKPSQQ INKINETSCI INKINKETSI	NYTSTLSPTT NIGULANUL STUDNOCH	120 180 300 360 420 120 180 300 360 424 480 660 660 780 80 900 900 900 900
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50 55 60 65 70 75	1 TAPPUVRAR DIAPATURAR DI	11 INCOMEDIUM INCOMEDI	21 CUTTIBLIY CUT	LAVCIGITYE YESPLEASEN PENDPHSY 1891/LASSEN PSHOPDISIA AND TLIDATI VSWGDECARP 31 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VYRTHORKTY KSOVI KRSOV KSOVI KRSOV KSOVI KRSOV KSOVI KRSOV KSOVI KRSOV KSOVI KRSOV KSOVI K	NYTSTLSPTT NIGOLABNIL STUBRECOTE STUBRECOTE OCCUPACION AVERGLAPA TEPRILCADO ALEBHITISKT S1 OCCUPACION COCCUPACION AVERGLAPA TOTOLOGICA AGAITATTO OTTOLOGICAGA TOTOLOGICAGA TOTOLOGICAGA ATOLOGICAGA ATOLOGICAGA ATOLOGICAGA ATOLOGICAGA ATOLOGICAGA ATOLOGICAGA ATOLOGICAGA TOTOLOGICAGA TOTOLOGIC	60 120 180 300 420 60 120 180 240 300 360 420 660 720 780 840 960 960 960 1020 1030
50 55 60 65 70 75	1 INTERDUVARA NATEROUVARA NATE	11 XEVCHERWIT XEVCHERW	21 ELESMYDNAP LIESKLODAVO STYDAN LIESKLODAVO RITVEIKTE SEMPORATO RITVEIKTE ARDINYLEGI RESURVEN RITVEIKTE RESURVEN RITVEIKT RESURVEN RESURVEN RITVEIKT RESURVEN RITVEIKT RESURVEN RITVEIKT RESURVEN RESURVEN RITVEIKT RESURVEN	LAVCIGITYME YASPLARSEN YASPLARSEN YASPLARSEN PSKYDPHSW SSW SSW SSW SSW SSW SSW SSW SSW SSW	YNTHIORITY KSOVI KIPSOO III KIKIHKITEN III COORGOOOCOO COORGOOOCOO COORGOOOCOO COORGOOOCO COORGOOO	NYTSTLSPTT SGOULAMELE	240 300 360 420 60 120 180 300 240 300 420 480 660 720 960 1020 960 1020 1080 1140 1200 1200 1200
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	CAGGRAGAAC	CATGGCACAG TTTTTTGGGA	GGGGGTTTGA	GAAGGCAGCG	GAAAGCACCA	GCTCCCGGAT	1680
	COMPONE CARD	Chammanana	TOTO CACTARE	TOROUGHAND.	CONTRACCATO	GGAGCAAGTT	1740 1800
5	ATTTATGTAA	CTTATTTCCC CTGGCTTTCA	TTTAGATTGT	AAGTTATGGA	CATGATTTGA	GATGTAGAAG	1860
	CCATTTTTTA	TTAAATAAAA	TGCTTATTTT	AGGCTCCGTC	CCCAAAAAAA	АААААААА	1920
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	RRDILFDYEQ	YEYHGTSSAM RHNHRNEDEE	VMFELAWNLS	KDINDMINNA	IVGL/IDQWVQ	DKITOMKYVT	240 300
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	TKNRRCKLLP	ASCLCTNLVI LVMAAPLSME	HGTVTVVGIP	PETDSSDRKN	PFGRAFEKAA	ESTSSRMLHIN	540
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30	1	11	21	31	41	51	
	GGCTGCGCTT	CCCTGGTCAG	GCACGGCACG	TCTGGCCGGC	CGCCAGGATG	CAGGCCCCGC	60
	ACARGGAGCA	CCTGTACAAG CTACGTGCAC	TTGCTGGTGA	TTGGCGACCT	GGGCGTGGGG	AAGACCAGTA	120 180
35	ACTIVACE	CANGGEGGEG	CACTGGGAGG	COGREGACTOT	GGTGGGGCCTG	CAGCTCTGGG	240
	ATATOGCAGG	TCAAGAAAGA TGTCTTCGAT	TTTGGAAACA GTCACCAGGC	TGACGAGGGT	TGAAGCAGTG	GAAGCTATGG	300 360
	A A A A MO A POP	GGACT CCAAG ATGTG ACCAG	TTALCTCTCC	CTARTGGCAA	ACCOGGTTTCA	GTGGTTTTGT	420 480
40	AGTTCTGCAA	GGAGCACGGT AGCCTCCAGA	TTCGTAGGAT	GGTTTGAAAC	ATCAGCAAAG	GAAAATATAA	540
	ACATTGATGA	AGCCTCCAGA TGAGCCGGAC	TGCCTGGTGA	AACACATACT	TGCAAATGAG	TGTGACCTAA	600
	GCTCTGGCTG	TGCCAAATCC AATTGTGCCT	TAGTAGGCAC	CTTTGCTGGT	GTCTGGTAGG	AATGACCTCA	720
45							780 840
43	GTTCTTTCTA	TGCTTTCCTC ACTTCTGTCA	ACCATCATCA	CAGTGTTTAC	AAACTTTTGA	AAATATTTAG	900
							960 1020
50	A A CTACCTOT	CAAGTCAAGG CTGATGGCCT	ACTRICCTOTIC	ACCUTAGCCCCT	GGTGTCTTTT	TCCAGATTTC	1080
30	GACCTCCATT	CTCGGCAGAC	CTAAGAGTTG	CCTCTGAGTT	AGCTCTTTGG	AATCGTGAAC	1200
	ACAGGTGTGC	TATATTGTCC	TTGTCCTAAC	TGTCACTTGC	CATGGCCTGA	ATGTTGGCTT	1260 1320
	CTCAAGCTGT	GGGGCTCCTC	TATACATGCT	ATACATGTAA	TATATATTAT	ATATATTTT	1380
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	LOLWDIAGOR	KLLVIGDLGV RFGNMTRVYY	REAMCAPIVE	DUTEPATFEA	VAKWINDLDS	KLSLPNGKPV	120
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	Seq ID NO:	256 DNA sec id Accession	guence n #: NM 0163	121			
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	1	11	21	31	41	51	
	GGFFCCGCCC	GCTGCCAGCC	CGGCCAGGCA	CCCCTGCAGC	ATGGCCTGGA	ACACCAACCT	60
75	CCGCTGGCGG	CTGCCGCTCA	CCTGCCTGCT	CCTGCAGGTG	ATTATGGTGA	TTCTCTTCGG	120
	GAACTTGAGC	OGCTACGACT GACATGGAGA	ACGAATTCTA	CTATCGCTAC	CCAAGCTTCC	AGGACGTGCA	240
	como secono	TTCGTGGGCT	TOTAL	CATCACTTC	CTGCAGCGCT	ACCGCTTCAG	300 360
80	GGGCTGGTTC	CACTTCTTAC	AAGACCGCTA	CATCGTCGTG	GGCGTGGAGA	ACCTCATCAA	420
	CGCTGACTTC	TGCGTGGCCT	CTGTCTGCGT	GGCCTTTGGG	GCAGTTCTGG	GTAAAGTCAG	480 540
	CATTCTCCTT	CTGCTCATCA AACCTGCTAA	AGGTGAAGGA	TGCAGGAGGC	TCCATGACCA	TCCACACATT	600
85						TAGAGCAGAG	720
	CCTOTOTOGATO	TACTGGCCCA	GCTTCAACTC	AGCCATATCC	TACCATGGGG	ACAGCCAGCA COGTGGCAAT	780 840
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	ATCCAGTGCC	/086443 CTGCACAAGA GTGGCCGTGG	AGGGCAAGCT	GGACATGGTG TGAGATGATG	CACATCCAGA	ATGCCACGCT ACGGTGCCCT	900 960
	CATCATCGGC	CGGCTGCACA	GCATCATCTC TCCAGGACAC	ATGTGGCATT	AACAATCTGC	ATGGCATTCC	1020 1080
5	TGGCATCATA	GGCGGCATCG GGGCTTGTCC	TGGGTGCTGT	GACAGOGGCC	TCCGCCAGCC	TTGAAGTCTA	1140
	ABGARCACAG	CGBAAGTTCC	AGATTTATGG	TCTCTTGGTG	ACCCTGGCCA	TGGCCCTGAT	1260 1320
	GAACTGCTTT	ATTGTGGGGC GAGGATGCGG	TCTACTGGGA	GATGCCTGAA	GGGAACAGCA	CIGICIACAT	1380
10	CCCACTACCC	CCCACCTTCA	CGGTACCCTT	GGTACCCTAG	GCTCCCAGGG	CAGGTGAGGA	1440 1500
	GCAGGCTCCA	CAGACTSTCC AAGCAGCACC	TGGGGCCCAG	AGGAGCTGGT	CAAGGTGCCT	CTAGGGATGC	1560 1620
15	CCTCCCCTTC	ATCCCAGGGG GGTTCTGGCT	GTCTGMCTGA	GAATGGAGAA	GGAGAAGCTA	CAAAGTGGGC	1680 1740
13	AGDDDDDACAG	GCTCAAAGTG	GGGCTGGGAC	CTGGTGGGTG	AACCTGAGCT	CTCCCAGGAG	1800
	AGCATCTCCT	TGCCAGTCAC ATGCTCCCTG	GGTCCCCCAG	ACCTCTCTGT	GTTGTGTGCG	TGGCAGCCTC	1920
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30	ARGUGURBAY	INTYCSLAAC	VLTSVAISSA	LHKKGKLDMV	HIONATLAGG	VAVGTAAEMM	300 360
	ONOT.PHYOUR	FVCGIISTLG GLVHSFDFQG	PRODUTARTO	GKFOTYGLLV	TLAMALMGGI	IVGLILRLPF	420
	NGQPSDENCF	EDAVYWEMPE	GNSTVYIPED	PTFKPSGPSV	PSVPMVSPLP	MASSVPLVP	
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45	GCATATATCC	ATCTGAAACC TGAGCTCATA	TTTACTCGAG	TGCAGAAATA	CGGACTCACC	TTGCTTGTAA	240 300
	TATACABOTO	TTCAGTTCAG ATGGCAGTTT	ASACTGGTTG	TAGTTATCTC	AAATATTGAA	AGTGGTGAGG	360 420
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							660 720
55	TAATTTTGAA	CAAAATTCCT ATGTGGTTTT TTTACATGGA	CCTGAAATCA	GGTCATCTAT	AGTTGATATG	TTTTATTCA	780 840
55	CCTTTATTTT	TTTGGTACCT	ATTTGACTTA	CCATGGAGTT	AACATCATGA	ATTTATTGCA	900 960
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••	AACAATGAAA	TATTGCTGTA TTCCAATTAT	TAGCTCCTTT	TGACCTTCAT	TTCATGTATA	GTTTTCCCTA	1200
	APREDIOTA C	TGTTTAATGT	TOTOTOTO	AGRACTOTTA	ARRATGTTTT	TTCATGTGTT	1320 1380
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75	QKAIQDEIRS	VIRQITATVT	FLPLLEVSCS	FDLLIYTDKD	LVVPEKWEES	GPQFITNSEE	180
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	CANUMATETG	COLOTARCAN					

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Seq ID NO: 261 Protein sequence

TARANTAGTA TOTOTTARAN ARRAMARAN ARRAMARAN ARR

50

55

80

85

Protein Accession #: NP_001202 60 21 41 MAAVKKEGGA LSEAMSLEGD ENELSKENVQ PLRQGRIMST LQGALAQESA CNNTLQQQKR AFEYEIRFYT GNDPLDVWDR YISWTEQNYP QOGKESMMST LLERAVEALQ GEKRYYSDPR 65 FLNLWLKLGR LCMEPLDMYS YLHNOGIGVS LAGFYISHAE EYEARENFRK ADAIFGEGIQ 180 OKAEPLERLO SOHROFOARV SROTLLALEK BEEBEVFESS VPORSTLAEL KSKOKKTARA 240 PIRVOGALK APSONGLON PFPOOMONIS RITUFDENAD RESTABLES TUTOPHIAPS PRAKENELOA GPHITGESIE HERGHITAEL IAVPAVLPS TPYVESTAQO PVMTFCKIEP SINHILSTEK PGKESIDPLQ RVQSHQQASE BKKEKMNYCK EKIYAGVGEF SPESIRAEVF 300 RKKLAEGERE BLITGAERRA EMOKOIEBME KALKHIOTTO (ESTGOOGE TMETKATTKI OIAGESKII OMIASSYCO YMCARETIA LEMIMORDHI SKOFSVYPSI FOFELLISEK MKSPFADPER VLAGREPLAV LATEBITISM EMVSDUCCE FIGIEZLEED AIIGFRAVT 70 480 540 600 ICPNPERTO FARABRYST PEHRIMSLED LPSDPERLE EEDLDVETSE DOOTACGTIY 660 SOTISTIKES PITESPEAT HESGREGGE SVASTSSIKC LOIPEKLELT NETSENFTQS 720 75 PWCSOYRROL LKSLPELSAS AELCIEDRPM PKLEIEKEIE LGNEDYCIKR EYLICEDYKL 780 PWVAPRNSAE LTVIKVSSQP VPWDFYINLK LKERLMEDFD HFCSCYQYQD GCIVWHQYIN 840 CPTLODILOH SEYITHEITV LIIYNLLTIV EMLHKAEIVH GDLSPRCLIL RNRIHDPYDC 900 NKNNOALKIV DESYSVDLEV OLDVETLSGE RIVQILEGOK ILANCSSPYQ VDLFGIADLA HILLPKEHLO VFWDGSPWKL SOMISELKDG ELWNKFFVRI LNANDEATVS VLGELAARMN

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CTACCATTGC TGTTCTACTT TTTGGTACAG GTATATTTTG ACGTCACTGA TATTTTTAT ACAGTGATAT ACTTACTCAT GGCCTTGTCT AACTTTTGTG AAGAACTATT TTATTCTAAA

ACREMENT ACASTGET ACCITETIAN TRANSCRAFT TETETETACT TITECCTETA 3480 CTTTTCCCAT TIGTARTIG TARANTETIC TCTTATGATC ACCATGTATT TIGTARATAA 3540

GVFDTTFQSH LNKALMKVGK LTSPGALLFQ
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PCT/US02/12476

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TGTTAACACT GCCCAGGAT ATGGAAGCT TTCTAATAGT CAGTCAGGG TCCAGTCTCA 10 540 600 ACTGARAGA GITTITCTG ATATARATGC ATCCCACRAG GATTATGATC TCAGCATTGT GALTECCCTT TITCCTGARA ARCTGTATGG CTTTCATARG GACTACATTG AGTGTGCCGR 720 AAAATTATAC GATGCCAAAG TGGAGGGAGT TGACTTTACG AATCATTTAG AAGACACTAG 780 15 ACGTARTATT ARTARGTOGG TTGARARTGA ARCACATGGC ARARTCAAGA ACGTGATTGG 840 TGAAGGTGGC ATAAGCTCAT CTGCTGTAAT GGTGCTGGTG AATGCTGTGT ACTTCAAAGG 900 CAAGTOGCAA TCAGCCTTCA CCAAGAGCGA AACCATAAAT TGCCATTTCA AATCTCCCAA 960 GTGCTCTGGG AAGGCAGTCG CCATGATGCA TCAGGAACGG AAGTTCAATT TGTCTGTTAT 1020 TGAGGACCCA TCAATGAAGA TTCTTGAGCT CAGATACAAT GGTGGCATAA ACATGTACGT 1080 20 TOTOCTOCOT GAGANTGACO TOTOTGANAT TGANANCANA CTGACCTTTC AGANTCTANT 1140 GGAATGGACC AATCCAAGGC GAATGACCTC TAAGTATGTT GAGGTATTTT TTCCTCAGTT CAAGATAGAG AAGATTATC AAATGAAACA ATATTTGGA GCCCTAGGGC TGAAAGATAT 1200 CTTTGATGAA TCCAAAGCAG ATCTCTCTGG GATTGCTTCG GGGGGTCGTC TGTATATATC 1320 AMSGATGATG CACAAATCTT ACATAGAGGT CACTGAGGAG GGCACCGAGG CTACTGCTGC 1380 25 CACAGGAAGT MATATTGTAG AMAAGCAACT CCCTCAGTCC ACGCTGTTTA GAGCTGACCA 1440 CCCAFTCCTA TITGITATCA GGAAGGATGA CATCATCTTA TICAGIGGCA AAGITTCTTG 1500 CCCTTGRAAR TCCRATTGGT TTCTGTTATA GCRGTCCCA CAACATCARA GRACCACCAC 1560 1620 CTAACATTOG TCAGCAGATG ACACTGGTGA CTTGACCCTT CCTAGACACC TGGTTGATTG 1680 30 TCCTGATCCC TGCTCTTAGC ATTCTACCAC CATGTGTCTC ACCCATTTCT AATTTCATTG 1740 TOTTTOTTOC CACGOTCATT TOTATCATTC TOCCOCATGA COOSTCTGGA AATTATGGAG 1800 1860 RGTGCTCAAC TGGTAAGGAG AACGTAGAAG TAGCCCTAGG GATCCTTTTT GAAACTCTAC AGTTATOGCA GATATTOTAG CTTCATTGTA AGCAATCTAG GAAATAAGCC CTGCTGCTTT 1920 CTACAAATAA CTCTGAAGGA TAAATTTTCT TTGTTGACCT ATGAAGATTT TAGAGTTTAC 1980 35 CITCATATGE TEGATITIAA ATCAGEGRAT AATCTAGATG GTAAAAAATG TGAAATTGGG 2040 ATTAGGGACC TACCAAAATA TITCATTAAT GCTTTCAATT GACAAATTIT GGCCTTTCTT 2100 TOATRAGACA ATATOFACAT GTTTTTTCAA ATATTAACA TOTTTAACT GTTATTAAC GTTTATACT GTATTAACA GATCATATT CATATCTG TGTAGTTTA AAGTTTTCC TCTATTATC 2220 AGAATRAAGA AATACAACAT ACCTGTAAA 40 Seq ID NO: 263 Protein sequ Protein Accession #: NP_003775 45 11 21 31 41 MASLAGANAE FOUNDEREND DECONORUPF SSLSLFAALA LVRLGAGDDS LSQIDKLLHV NTASGYCNES NEOSCLOSOL KRYPSDINAS HKDYDLSIVN GLFAEKVYGF HKDYIECAEK 120 LYDAKVERYD PTNHLEDTRR NINKWVENET HGKIKNVIGE GGISSSAVMV LVNAVYFKGK 100 50 MOSAFTKSET INCHFKSPKC SKRAVAMHQ ERKFNLSVIE DESMKILER YNGGIMMYU LPENDLSEIE NKLTFONLME WINFRRMISK YVEVFPPOFK IEKNYEMKQY LRALGLKDIF 240 300 DESKADLSGI ASSGRLYISR MMHKSYIEVT EEGTEATAAT GSNIVEKQLP QSTLFRADHP PLEATERDE THESERVACE 55 Seg ID NO: 264 DNA sequence Nucleic Acid Accession #: AB052906 Coding sequence: 74-814 50

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		ACGACCTACG					960
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85 Seq ID NO: 265 Protein sequence Protein Accession #: BAB61048.1

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20	AAATCCGAGC CCAGACGAAA GATTCCGGCC CTGTGTGTGC	AGATGTTGGA CTGCAACCTG TCACTGCAGA AGGATGGTCA ATGCACATGT ATCTTTAGAA	ATTATTOGCG GTGAAGTTAC GTGTGTTTTC	ACTGAAATTC CAGGAATGTT CATGAGGCAC	TTTGCCTTGA TTGGCTTAAC TAAAGCACAA TGCTTTTTAT	AGAAGAACTT CATTTCAGAA AGGACTTTGG GCATTTCCCT	360 420 480 540
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30	1	11	21	31	41	51	
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J	LPREGAPGKL	PKAPSPGSLA 272 DNA se	EASAGPAQIM				240
10	Mucleic Ac	id Accession	n #: Bos so				
	1 GGATACTGTG	11 TCACTCAAAG	21 TAATGGGAGG	31 GAGAGAGAAC	41 AGGGAGGGTA	51 GGGATGCTTT	60
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	GGAACTTGGA	CTTGGAGGCC	TCTCCACGCT	GTCCCACTGC	CCCTGGCCTA	GGCGGCAGCC	360
45	TGCCCTGTGG	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCGCTCTGGC	TCTGCTGAGC	AGCGTCGCAG	AGGCCTCCCT	420 480
75	CGCCGGCCAC	CTGCCGGGGG	GACGCACGGC	COGCTGGTGC	AGTGGAAGAG	CCCGGCGGCCC	540
	GCCGCCGCAG	CCTTCTCGGC GCGGCGCGGG	CCGCGCCCCC	GCCCCCTGCA	CCCCCATCTG	CTCTTCCCCG	600
		CTGCGCTCGC					720
50	CGACGAGCTG	GTGCGTTTCC	GCTTCTGCAG	CGGCTCCTGC	CGCCGCGCGC	GCTCTCCACA	780 840
	GCYCGTCAGC	CTGGCCAGCC CAGCCCTGCT	GCCGACCCAC	GCGCTACGAA	GCGGTCTCCT	TCATGGACGT	900
	CAACAGCACC	TGGAGAA CCG	TGGACCGCCT	CTCCGCCACC	GCCTGCGGCT	GCCTGGGCTG	960
55	AGGGCTOGCT	CCAGGGCTTT	GCAGACTGGA	CCCTTACCGG	TGGCTCTTCC	TGCCTGGGAC	1020
55	AGGCCCCTAC	AGTOCCACTA CGGTGGGTGA	TGGATATCAT	CCCCGAACAG	GTGAAGGGAC	AACTGACTAG	1140
	CAGCCCCAGA	GCCCTCACCC	TGCGGATCCC	AGCCTARAG	ACACCAGAGA	CCTCAGCTAT	1200
	CCCTCCTCTG	ATGAACACTA	CAGTGGCTGA	GGCATCAGCC	CCCCCCCAGG	CCCTGTAGGG	1320
60	ACAGCATTTG	AAGGACACAT CTCATGGGAG	ATTGCAGTTG	CTTGGTTGAA	AGTGCCTGTG	CTGGAACTGG	1380
	Seq ID NO:	275 Protein	sequence:				
65	1	11	21	31	41	51	
	ī	Ī	Ĭ .	Ī	Ĩ.	Ī	
	MELGLGGLST	LSHCPWPRRQ	PALWPTLAAL	ALLSSVAEAS	LGSAPRSPAP	REGPPPVLAS	60 120
70 .	RGCRLRSOLV	ARWCSGRARR PVRALGLGHR	SDELVREREC	SGSCRRARSP	HDLSLASLLG	AGALRPPPGS	180
	RPVSQPCCRP	TRYEAVSFMD	VNSTWRTVDR	LSATACGCLG			
	Sect TD NO:	276 DNA sec	mence				
75	Nucleic Ac:	ld Accession	1 #: NM 0570	91.1			
, ,		ience: 783-					
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	ACTGGCCGCT	GAGAGAAGAA	TCGGGTGGAG	CAGAGAGCAG	CTGCTGCAGG	GCAGACAGCC	60
80	GGACCCCCAA	ATCTGCACGT	ACCAGCAGTC	AGCCGCCCCA	CGCAGGGACC	GGCTTACCCC	120 180
	CGCGTGTCTA	COCTCACTCA CAAACTCAAC	TCCCGGTTTC	CGTGCCTCTC	CACCGCTCGA	GTTCTCTACT	180 240
	CTCCATATCC	GAGGGGGCCCC	TOCCAGCATO	TACCCCCCTC	CCAACCTCGG	GGGACCTAGC	300
85	CAAGCTAGGG	GGGACTGGAT GCGCTCCCAG	CCCCACCCYG	GGATCTGGTG	ACGCTGGGGC	TGGAATTTYIA	360 420
	CACCGGACGG	CTGCGGCGGC	GGGCAGGAGG	CTGCTGAGGG	ATGGAGTTGG	GCCCGGCCCC	480
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_	TARAGAGGC GCCCAGCACT TCAACAGGAG	ACTGCCAGGT GGTCCCCGGA GGTCGGGGAA	CCCGAGGGTG GTACAGTCCT AAGGTGCCTA CAGCTCAACA	GGGCATGCGC GAAGAACAAG ATGGCTGATG	TGTTTGAGCT GTGCAGGACC GGCGCTCCTG	TCGGGGGAGA CCGTGCTGCC GTGTTGATAG	600 660 720 780
5	AGATGGAACT AGCCTGCCCT CCCTGGGCTC	TGGACTTGGA GTGGCCCACC CGCGCCCGGC	GGCCTCTCCA CTGGCCGCTC AGCCCTGCCC GGGGGACGCA	CGCTGTCCCA TGGCTCTGCT CCCGCGAAGG CGGCCCGCTG	GAGCAGCOTC CCCCCCCCCT CTGCAGTGGA	CCTAGGCGGC GCAGAGGCCT GTCCTGGCGT AGAGCCCGGC	900 960 1020
10	COCGOGGGGG CGCGGGGGCTG GCTCCGACGA CACACGACCT	COGCGCGGGG COGCCTGGGC GCTGGTGCGT CAGCCTGGCC	CGGCCCGCGC CGGGCTGGGG TCGCAGCTGG TTCCGCTTCT AGCCTACTGG	GCCCGGGCAG TGCCGGTGCG GCAGCGGCTC GCGCCGGGGC	COGCOCTOGG COGCOCCGC CTGCCGCCGC CCTGCGACCG	GCAGCGGGGG CTGGGCCACC GCGCGCTCTC CCCCCGGGGCT	1080 1140 1200 1260 1320
15	ACGTCAACAG GCTGAGGGCT	CACCTGGAGA CGCTCCAGGG	TGCTGCCGAC ACCGTGGACC CTTTGCAGAC ACTAGCCAGC GTGATGGATA	GCCTCTCGC TGGACCCTTA GCCTCTGCC	CACCGCCTGC CCGGTGGCTC AGGGACGAAG	GCTGCCTGG TTCCTGCCTG	1380 1440 1500 1560 1620
20	CTAGGAGCC CTATGGAGCC GGACCCCTCC AGGGACAGCA	CAGAGCCCTC CTTCGGACCC TCTGATGAAC TTTGAAGGAC	ACCCTGCGGA ACTTCTCACA ACTACAGTGG ACATATTGCA GGAGCTGGCC	GACTOTGGCA CTGAGGCATC GTTGCTTGGT	CTGGCCAGGC	CTCGAACCTG	1680 1740 1800 1860
25	Protein Acc	277 Protein ession #: N	rP_003967.1 21 	31 	41 	51 	
30	PAGHLPGGRT	ARWCSGRARR PVRALGLGHR	PALWPTLAAL PPPQPSRPAP SDELVRFRFC VNSTWRTVDR	PPPAPPSALP SGSCRRARSP	ROGRAARAGG	PGSRARAAGA	60 120 180
35	Nucleic Aci	278 DNA sec id Accession ience: 1-714	1. #: NM_057				
40	TGGCCCACCC GCGCCCCGCA	TOGCCGCTCT GCCCTGCCCC	21 CCGAGGACAG CCCTGAGGCT GGCTCTGCTG CCGCGAAGGC	AGCAGCGTCG CCCCCGCCTG	TCTCCGCGCA CAGAGGCCTC TCCTGGCGTC	CCTGGGCTCC CCCCGCCGGC	60 120 180 240
45	CACCTGCOGG CAGCCTTCTC CGCGCGGGGGC CGCCTGCGCT CTGGTGCGTT	GGGGACGCAC GGCCCGCGCC GGGCTGGGG CGCAGCTGGT TCCGCTTCTG	GGCCGGCTGG CCCGGGGCAGC GCCGGTGCGC CAGCGGCTCC	TGCAGTGGAA GCACCCCCAT CGCGCTCGGG GCGCTCGGCC TGCCGCCGCG	GAGCCCGGCG CTGCTCTTCC CAGCGGGGGC TGGGCCACCG CGCGCTCTCC	GCCGCCGCCG CCGCGGGGGC GCGGGGCTGC CTCCGACGAG ACACGACCTC	300 360 420 480 540
50	AGCCAGCCCT ACCTGGAGAA GCTCCAGGGC CAGAGTCCCA	GCTGCCGACC CCGTGGACCG TTTGCAGACT CTAGCCAGCG	CGCCGGGGCC CACGCGCTAC CCTCTCGGCC GGACCCTTAC GCCTCAGCCA CATCCCCGAA	ACCICCTOCS CGGTGGCTCT GGGACGAAGG	GCTGCCTGGG TCCTGCCTGG CCTGAAAGCT	CIGAGGGCTC GACCCTCCCG GAGAGGCCCC	660 720 780 840
55	AGAGCCCTCA TTCGGACCCA CTGATGAACA TTGAAGGACA	CCCTGCGGAT CTTCTCACAG CTACAGTGGC	CCCAGCCTAA ACTCTGGCAC TGAGGCATCA TTGCTTGGTT	AAGACACCAG TGGCCAGGCC GCCCCCGCCC	AGACCTCAGC TCGAACCTGG AGGCCCTGTA	TATGGAGCCC GACCCCTCCT GGGACAGCAT	960 1020 1080 1140
60	Seq ID NO:	279 Protein cession #: 1	n sequence: NP_476501.1				
65	APRSPAPREG RAARAGGPGS	PPPVLASPAG RARAAGARGC	21 HLGALFLPEA HLPGGRTARW RLRSQLVPVR	CSGRARRPPP ALGLOHRSDE	QPSRPAPPPP LVRFRFCSGS	CRRARSPHDL	60 120 180
70	SEASLEGAGA Seq ID NO: Nucleic AC	280 DNA sec	SQPCCRPTRY quence n #: NM_051	EAVSFMDVNS	TWRTVDRLSA	TACGCLG	
75	1 CTGATGGGGG	11 CTCCTGGTGT	21 TGATAGAGAT	31 GGAACTTGGA	41 CTTGGAGGCC	51 TOTOCACGOT	60
80	GTGGCCCACC GTGGCCCACC CGCGCCCGGC CCACCTGCCG GCACCCTTCT	CTGGCCTA CTGGCCGCTC AGCCCTGCCC GGGGGACGCA CGGCCCGCGCGC	GGCGGCAGGC TGGCTCTGCT CCCGCGAAGG CGGCCCGCTG CCCCGCCGCC GCCCGGCAG	GAGCAGCGTC CCCCCCGCCT GTGCAGTGGA TGCACCCCCA	GCAGAGGCCT GTCCTGGCGT AGAGCCCGGC TCTGCTCTTC	AGCCTGCCCT CCCCGGCGGGGGGGGGGGGGGGGGGGGGG	120 180 240 300 360 420
85	CCGCCTGCGC GCTGGTGCGT CAGCCTGGCC	TOGCAGCTGG TTCCGCTTCT AGCCTACTGG	TGCCGGTGCG GCAGCGGCTC GCGCCGGGGC CCACGCGCTA	CTGCCGCCGC CCTGCGACCG	CTGGGCCACC GCGCGCTCTC CCCCCGGGCT	GCTCCGACGA CACACGACCT CCCGGCCCGT	480 540 600 660

5	CGCTCCAGGG GCAGAGTCCC CTACCGGTGG CAGAGCCCTC CTTCGGACCC TCTGATGAAC	/086443 ACCGTGGACC CTTTSCAGAC ACTAGCCAGC GTGATGGATA ACCCTGCGGA ACTACAGTGG ACTACAGTGG ACATATTGCA	TGGACCCTTA GGCCTCAGCC TCATCCCCGA TCCCAGCCTA GACTCTGGCA CTGAGGCATC	COGGTGGCTC AGGGACGAAG ACAGGTGAAG AAAGACACCA CTGGCCAGGC AGCCCCOGCC	TTCCTGCCTG GCCTCAAAGC GGACAACTGA GAGACCTCAG CTCGAACCTG CAGGCCCTGT	GGACCCTCCC TGAGAGGCCC CTAGCAGCCC CTATGGAGCC GGACCCCTCC AGGGACAGCA	720 780 840 900 960 1020 1080 1140
10	CTCACTCATG Seq ID NO:	GGAGCTGGCC 281 Protein	CC sequence;				
	Protein Acc	ession #: 1	IP_476431.1				
15	GPPPVLASPA SRARAAGARG	11 LSECPWPRRQ GHLPGGRTAR CRLRSQLVPV	WCSGRARRPP RALGLGRRSD	PQPSRPAPPP ELVRFRFCSG	PAPPSALPRG SCRRARSPHD	GRAARAGGPG	60 120 180
20		VSQPCCRPTR 282 DNA sec		STWRTVDRLS	ATACGCLG		
	Nucleic Act	d Accession	i i Eos seq	pence			
25	ATAGCAATTT	11 TGCCCTCTGT CCTTTGGTTT TATGAATGCT	TTAAGACTTC	TACATTGCTT	TTTCTTTTAT	TATCTGTGCT	60 120 180
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35	Seq ID NO: Nucleic Ac:	ATACCTACAT 283 DNA sei id Accession mence: 564-:	puence #: Eos se	TICARTATAT	ATGTATTTCT	TATT	
40		11	21	31	41	51	
40	CAAAGAGGTC	ATCATCTATC AAAAATTCAC	CCTTGTGCTT ATGTGTAGAC	TACGCAGACC AAATTAGGTC	CTACAATACA CCTTAAGATG	CTAGAGGCTT CCAGGCAAAC	60 120
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5 0	AAGGGCTGGC CCTCCCGGCC GCCTGGCGCG	CGTACTAAAC TAAGGGAGGC TCCACGCGTC CGCAGGGCCC CCAGATGTGG	AAGCTTGCAA CUGGGCGGAG GCCATGGCAA GCTGGCAAAG	ACAGCAGGCA GAAGCCAAGC CGCGGGGGTCT CGCGTCCCCG	CCTTCCTGCC TCTGCAGGCC GTGCTGGCCG CCGCGGCTCC	ACTGAGGAGG CTGACAAAGT GGATTGGCCG GCCAGTTTGA	480 540 600 660 720
	CCGGTTTCTC	TGCTGACTGC	AGACCCAGGT	CTCGGCCCTC	CTCGGACTCC	TGCTCAGTCC	780
55	CTATGACGGG CGCTGAGCTG AGTTTGACGA	CGCACGTGGG CAGCAATTCC GGACGACGGT TGCCCATGAT	CAGGGGCTGG ACCAGGTCGC GACGGGGAGG	AGGTGGTGCG TGTTGTCTCC ATGAGGAAGA	CTCGCCGTCG CCTTGGCCAC CGTGGATGAT	COGCCGCTGC CAGAGCTTCC GAGGAAGACG	840 900 960 1020
60	AGGGGTGCGC GCTTACCAGA AACGTGACCG AAGAAATGGA	CAGCACTCAG AAGCCGCCTG GCTGCAACTG AGAACGTGAA	GTTGAATCAG ACACCATGGG AAAGCTCTAG AAAAGAAAGA	AAAATAACCA AGGTGTGGTT AGGAATTAAA TAATTGCTGA	AGAAGAACAG TATTGGCAAA TCAACAACTA AGAAAAGCAC	AAACAGGTGC GAAAAAGAAG GAAAAAAGAA AAGGAATGGG	1080 1140 1200 1260
65	TTCAGANANA AGGANANAGC ATCANGANTG ANACANCAG ATCGTTCAN	GAATGAGCAA AGCAAAGGAA GTTAAAGAAA CAAGCTGAAA	AAAAGAAAG CTOGAGAAAG AAAAATGCTG TACAGGAGAA	AAGAGAACA AATACTTGCA AAGAATGTGA AAAGGAAATA TOCAGCTGCA	AAAAATTAAT AGAAAAAGCA GAGGAAGAAG GCAGAAAAAA AAGAGCTATG	AAAGAAAAT AAAGAAAAGA AGTTTCAAGA GTTATGCCAA	1320 1380 1440 1500 1560
70	GAAGAGTAAA AGCCAGGAGC AATAACATGC	ACAGGTTTTT AAACCAATTC AGACCTGTGA AATCTTTGCC TTTTATCTGG	TARGTCAGCC TTGGAACTCT AGCTATTTAA	ACACAAGTCA GTGCAGAATA TTTAAAAATC	TCATCTCTGG CAAAGATAGC AGAAATTGTT	TANTTCATAA GTATGTGGAA TTTTACTGCT	1620 1680 1740 1800 1860
75	CAGTCAATAA TGGAGTCCTT GTTGATCTTG	CTCAACACTT AGAGTTGAGG GCATGTTGTT TATTAAAAGT	AATGTGATTA AAGATATTTT TTGCAGAATA	TTGACAAATA CTGGATTTTG AGTGGCTGAA	GCAATITTIG GTTTTTATAA TATGTAAGAA	ACTITITATA ACTITITAAG TIGIGITIGI	1920 1980 2040
80	Seq ID NO: Protein Acc	284 Protei	Sos sequence				
	i i	11	21 	31	41	51 	
85	PRSRPSSDSC GEDEEDVDDE PWEVWFIGKE	LAGLARAGPA SVPMTGARGQ EDVDEDAHDS KEERDRLQLK EMEEKAAKEL	GLEVVRSPSP EAKVASLRGM ALEELNOOLE	PLPLSCSNST ELQGCASTQV KRKENEEREK	RSLLSPLGHQ ESENNQEEQK RKIIAEEKHK	SPOFDEDDGD QVRLPESRLT ENVOKKNEOK	60 120 180 240 300

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RRKRK

Seq ID NO: 285 DNA sequence
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Coding sequence: 1-1746

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CCAGGGAATA TCTTCGCCAA CCTCAATCGC CTCATGGCCA TCCAGCTGCA GAACAACCAG 1140 CTGGAGAACT TGCCCCTCGG CATCTTCGAT CACCTGGGGA AACTGTGTGA GCTGCGGCTG 1260 30 TATGACAATC CCTGGAGGTG TGACTCAGAC ATCCTTCCGC TCCGCAACTG GCTCCTGCTC 1320 AACCAGCCTA GGTTAGGGAC GGACACTGTA CCTGTGTGTT TCAGCCCAGC CAATGTCCGA 1380 GOCCAGTOCC TOATTATCAT CAATGTCAAC GTTGCTGTTC CAAGGGTCCA TGTCCCTGAG 1440 GTGCCTAGTT ACCCAGAAAC ACCATGGTAC CCAGACACAC CCAGTTACCC TGACACCACA 1500 TOTOTTOTT CTACCACTGA GCTAACCAGC CCTGTGGAAG ACTACACTGA TCTGACTACC 1560 35 ATTCAGGTCA CTGATGACCG CAGCGTTTGG GGCATGACCC AGGCCCAGAG GGGGCTGGCC 1620 ATTGCCGCCA TTGTAATTGG CATTGTCGCC CTGGCCTGCT CCCTGGCTGC CTGCGTCGGC 1680 TOTTGCTGCT GCAAGAAGAG GAGCCAAGCT GTCCTGATGC AGATGAAGGC ACCCAATGAG 1740 TOTTAAAGAG GCAGGCTGGA GCAGGCCTGG GGAATGATGG GACTGGAGGA CCTGGGAATT TEATETTTET GECTEGACCE CTOGGTCCAT GGAGCTTTCC CGTGATTGCT CTTTCTGGCC 1860 40 CTAGATAAAG GTGTGCCTAC CTCTTCCTGA CTTGCCTGAT TCTCCCGTAG AGAAGCAGGT 1920 COTOCOGGAC CITCCTACAA TEAGGARGAT AGATCEACT GGCCATOGCA AAAGCCTGG GGATTICGA TICATACCC TEGGCTTCCT TCGACAGGGC TCTTCCTCCA AATCCTCCCC 1980 2040 ACCURATION TO CARGARCAGO CITOCOTROG COCAGGODOC CITOCOGGOCT CIGITAGACIC ACTTAGTCCA CAGCCTGCTC ACTTCGTGGG AATAGTTCTC CGCTGAGATA GCCCCTCTCG 2160 45 CCTAAGTATT ATGTAAGTTG ATTTCCCTTC TTTTGTTTCT CTTGTTTGTG CTATGGCTTG 2220 ACCCAGGATG TOCCCTCAAA TGAAAGTTCT CCCCTTGATT TTCTGCTCCT GAAGGCAGGG 2280 TGAGTTCTCT CCTCAAAGAA GACTTCAAAC CATTTAACTG GTTTCTTAAG AGCCGTCAAT 2340 CAGGCTGGTT TTGGGGATGC TATGAAAGAG AGAAGGAAAA TCATGCCGCT CAGTTCCTGG AGACAGAAGA GCCGTCATCA GTGTCTCACT TGTGATTTTT ATCTGGAAAA GGAAGAAACA 2460 50 CCCCAGCACA GCAAGCTCAG CCTTTTAGAG AAGGATATIT CCAAACTGCA AACTTTGCTT 2520 TGAAAAGTTT AGCCCTTTAA GGAATGAAAT CATGTAGAAT TITGGACTTC TAAAAACATT 2580 ARANTCAGCT TATTARTACG GGATAGAGAA AGAANTCTGG TGCCT00000 TCCCTGTGTT CACCCCTAGA GTTTGTTTTA ARATTTTTAA TTGAAGCATG TGAAGTGTAC STGCAGAAAA 2640 2700 CTGGGAACAT GATAGTGTAT GGCTTGGTGG ATTTTCACAA ACTGAACATA CCTGTGTAAT 2760 55 CAGCATCTAG ACCCAGACCC AGAGCATCAC AAATATCCCC CATCCTGGGC TTTTCCCAGA 2820 GCAGATGGGG GCTTCTGAAG ATGGACTTAC CTGGGACCTG CCCCCCATGA GCCAGGACGG 2880 TCCCCCCACA GTCAGCCTGT GCAAAGGCCC CGTGGCCAGG GGTGGAGGAG AATATGTGGG 2940 TGTGGACAGG ATGGGAGACT GTGGCCTGAA CAGGAGATTT TATTATATCT GGAGACCCTG 3000 AGAGACCCTG AGACCTGGGG CACCATGGCT GGCCAGGTCA GAAGCATCCT GACTGCAGAG 60 3120 STOCSTSCAG CCACACCCTC TTCCCTGCCA GCAAGTTGTC TGCGGCTCAT CGGAGGCCCC TOCGCOTGGA GCCTTCTATG GACGTGATAT GCCTGTATCT GTTTTTAATT TTCATTCTTC 3180 ACTTAGGGGA AGTGAAATCG CTCAGAGATG AGATCCTTTA ATTGAAAACG AAGTGTAACG 3240 GAATCTAGTG TCTTTCTAAT GTGGTAAAAT TCTCCATCAA CATCACAGTC AGCTGGCAGC 3300 TGAACTTCAG AATCTCACTT ACAGCAGGGG ACACGGGGGT ACACGGATGG GTCACACTGG 3360 65 CTCTOGGGGC TCCCTGGAGC TCCTCCTGGG TGTGGTCTGG TTAGGAGTTG AGTTGTTTGC 3420 TOCAGGGTTA TTCTCCTCCT CGAGTCACAG TCACACGAAT ACCTGCCTTC TCTGGCTTTC 3480 CTGCTATACA CATATTCACA TGGGGCTCAA GAAGTTAGGC TCATGGCAAC GTGTGTCTTT CTCTGGACAA CTGGCCCAGT TTACAGTGAAA ATGGGAATTT ACGGGTCTCC ACGTCTGCCG AGGAAAGAAC TCTGGCTGAC TCCACGGGGA TCTGGAAATC GACGACGAAT CCGGATCGGC 2540 70 TCTTATTAGC TCCCCGCTCC ACAAGACACC TGTGCTTTGG AAATCCACCA CCAATCCCGA 3720 TOSSCTOTTA TERSCTCCCC GOTCCACAAS ACACCIGTGA TCTGGAAATC TACCACCAAT CCCGATCGGC TCTTATTAGC TCCCCGCTCC ACAAGACACC TGTGACATCC TCCAGGGCCA 3780 3840 CAGGAGCACG TGCTGACCAG TTTTCCCTTC CAGTTCCTGC ACAAAAAGTG TCCAGAGGGC 3900 TETTTECANA CACTAGTECA CTTTETAGET TTTCACCCTC TETCCCROSG ARTCTAGGAG 3960 75 AGATGAGGCC CGTCAGAGTC AAGAGATGTC ATCCCCCCAG GGTCTCCAAG GCATTTCCAC 4020 ACTATTGGTG GCACCTGGAG GACATGCACC AAGGCTTGCC AGAGCCAACA CGAAGTGAGC 4080 CCAGAGCATG GCACATGAGC ATCACCOGCT GATGGTOGCC TGCTGTGCCT GGTGCCAACA 4140 GGGGCATCOT GGCCDGTACC CCTCCAGACA GGAAGCATGG GTTTGCCCAC AGACCTGTCG 4260 GGTGCTCCTG TGAGTGGCCT CCAGATGTCT TTGTGCATAG GCACAAGTGG GCCAGGGCTG GAGGGAGGTG GGAAACCTCA TCATCCGGTG GGCCCTGCCA ATCTTAACCC AGAACCCTTA 80 4320 GGTATTCCTG GCAGTAGCCA TGACATTGGA GCACCTTCCT CTCCAGCCAG AGGCTGACCT 4390 GAGGGCCACT GTCCTCAGAT GACACCACCC AGGAGCACCC TAGGTGAGGG GTGAGGGCCC 4440 CCTTATGTGA ACCTCTTGCC TCTTCCTTTC TCCCATCAGA GTGGTTGGAT GGAGCCATTG 4500 GCCTCCTTT CTCAGCGGG CCCTTCAACC TCTCTGCACC ATGTTGTCTG GCTGAGGAGC 4560 85 TACTAGAAAA GCTGAGTGGA GTCTCCTTTC CAACAGGATG ATGCATTTGC TCAATTCTCA 4620 GGGCTGGAAT GAGCOGCTG GTCCCCCAGA AAGCTGGAAG GGGGTACAG GTTCAGTTTT CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG GTCGGAGTTA 4680 4740

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	CTCCTTCCGC	CCCAGGTTTC	TTCTTCTCTT	AAGGAGAGAT	TGTTCTCACC	AACCCCCTCC	5580
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	AGCCCTGGTG	GGCAGGGTTG	GGGGGTCTGT	CTTCTGCTGG	ATGCTGCTTG	TARTCCATTT	5760
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25	MDE VIIVE T.T.	VGCQAWGAGL	AVEGODSROT	CSPASOVECT	GARTVAVPTP	LPWNAMSLOT	60
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	GKNSLTHISP	LLSSNQLLQI RVFOHLGNLQ	VLRLYENRLT	DIPMGTFDGL	VNLOELALOO	NOIGLLSPGL	180 240
30	PHNNHNLORL	YLSNNHISQL NVFSNLRQLQ	PPSIFMOLPO	LNRLTLPGMS	LKELSLGIFG	PMPNLRELWL	300 360
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	YDNPWRCDSD VPSYPETPNY	ILPLRIWLLL PDTPSYPDTT	NOPRLGTDTV	PVCFSPANVR	GQSLIIINVN	GMTOAOSGLA	480 540
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	GAAATCTGGG	AGGAGCTGGG	TGTGATGGGG	GTGTATGATG	GGAGGGAGCA	CACTGTCTAT	720
55	CAGGTACCCG	GGAAACTGCT GCAGTAATCC	TGCGCGCTAT	GAGTTCCTGT	GGGGTCCAAG	GGCTCTGGCT	780 840
	GAAACCAGCT	ATGTGAAAGT CCCTGCGTGA	CCTGGAGCAT	GTGGTCAGGG	TCAATGCAAG	AGTTCGCATT	900
	GCCTACCCAT	CCCIGCGIGM	AGCAGC:11G	TIMOMOGNOO	Minanananan	CION	
60	Seq ID NO:	288 Protei	sequence:				
	Protein Acc	cession #: 1	_				
	1	11	21	31 	41	51. 	
65	MSSEQKSQHC	KPEEGVEAQE	EALGLYGADA	PTTEEQEAAV	SSSSPLVPGT	LEEVPAAESA	60 120
	LLRKYRAKEL	ALPTTISFTC VTKAEMLERV	IKNYKRCPPV	IPGKASESLK	MIFGIDVKEV	DPASNTYTLV	180
	TCLGLSYDGL	LGNNQIFPKT WVQENYLEYR	GLLIIVLGTI	AMEGDSASEE	BINEBLGVNG	VYDGREETVY	240 300
70	AYPSLREAAL	LEBEEGV	QAE GOSENICI	BEDWOEKNUN	DISTURBLE	***************************************	500
	Seq ID NO:	289 DNA sec	quence				
	Nucleic Ac	id Accession	1 #: NM_0023	162			
75	Courng sequ	dence: 40	.344				
	1 .	11	21	31	41	51	
	000000000	GCCCTGGTTG	GGTCYCCTCT	acres cocce	GOGOCATICOS	CONTROL CONTROL	60
80	GGCGACCTGA	AGCAGGCGCT	TCCCTGTGTG	GCCGAGTCGC	CAACGGTCCA	CCTCCACCTC	120
	CATCAGCGCG	GCAGCAGCAC ATAATATTGT	TGCAAAGAAA	GAAGACATAA TACACATGGA	ACCTGAGTGT CTGAGTTTGA	TAGAAAGCTA	180 240
	TTGACCAGAA	ATGTGCAGTC	TGTGTCTATT	ATTGACACAG	AATTAAAOGT	TAAAGACTCA	300
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	GTTCTACCTG	CAGCTGAATT TCCTCGATTA	CCATGGGCTT	TOGGACAGCT	TGGTATACGA	TGTGGAAGTC	480 540
	AAATCCCATC	TOUTGOATTA	*OTONIONCH	WOLL TWO LOLD	ACHONGAN		5.5

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	AGCAACCTCA	TCACCTGGAA	CCCGGTGCTG	CTGCTCCACG	GTCCTCCTGG	CACTGGAAAA	600
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10	CCTCGCCAGC	AGCTGCTGAC	CCTCCGAGAG	CTAGAGATGA	TTGGCTTCAT	TGAAAACAAC	1140
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	COGGTCCTGA	GAAAACTCCC	CTTTCTGGCT	CATGCGCTGT	ATGTCCAGGC	CCCCACCGTC	1260
	ACCATAGAGG	GGTTCCTCCA	GGCCCTGTCT	CTGGCAGTGG	ACAAGCAGTT	TGAAGAGAGA	1320
	ANGLAGOTTG	CAGCTTACAT	CHGATCCTGG	CCTTCCCCAT	CTGGTGCTTT	TCCCATGGAG	1380
15	AACACACAAC	CAGTAAGTGA	GGTTGCCCCCA	CACAGCCGTC	TCCCAGGGAA	TCCCTTCTGC	1440
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	GTTTYGTTCCC	AGCCCACCCC	CAGTGGATGG	GATGCATAAT	GCCAGCAAGT	TTTGTTTAAC	1680
20	AGCANARANG	GAAGATTAAT	GCAGGTGTTA	TAGAAGCCAG	AAGAGAAACT	CTCTCACCCT	1740
	ABACARCON	ATAATCATAG	CATTABABAT	CCACACATTA	CTCCAGGTGG	AAGGTGGCAA	1800
	THE CHEST CTC	ATATCAGCTC	CTTTCATTTL	CTCCAAAAAT	GTTTTCAAGA	CTATTTAATG	1860
	CATCTARARA	AGCCTATTTC	TACATTATAC	CAACTGAGAA	AAAAATGGTC	GGTAAAGTGT	1920
	mommon man	TAAATAATCA	ACL CATOCTC	CCPATACAC	CARARCTCCA	GACTCTGAGT	1980
25	COMPOGRAGOGA	AACACATGCT	COLCATOCCT	TOTALCOOK	TATOGGCCCC	CCTGCATTGC	2040
23	DOCCONTOURN	CTGCCCACGG	TTTTOTTTCT	CCAATAACCT	TATCACATTT	CTAATGAGGA	2100
	IGGOVIGITI	TATAATATAA	33773377707	TOTAL COLO	OPCTOPPTOP	CONTRACTO	2160
	TTCACATTAA	TTTATCTCAC	ACTANALANO.	ATATAATTA	333	0000011011	22.00
	MIGITITIGGE	TITALCICAC	MOTMANTINA	ATOTOMITAN	nnn		
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35	100000000000000000000000000000000000000	ALPCVAESPT	I THE THE PARTY OF	ORA PPROTNI	OVERT T NEUM	TURGRYTHTE	60
55	MDEMVGDERQ	QSVSIIDTEL	MULDOODIDI	el CTULLUTE	OTMEDGER	MILPROPERTY	120
	PUBPPLIKNV	EFHCLWDSLV	KANDOGLIDE	DICTIONALLE	DANIMENT TO	MADERAL FROD	180
	AANHWVLPAA	ALAQKLTIRL	ADAEAKSHPP	DIVMITEDES	DESIGNATION	MMEON TODAY	240
	PGTGKTSLCK	IDEVESTIAA	SSKIKIOQLI	ACADONOUS A	T O D O O C T V D V I	TOTE OF TANGEN	300
40	DDKDALVFVL	DRADIKQYIG	RNACRAGTED	SDAIRVVNAV	DIVIDUIARE	SNVVILLION	360
40	ITEKIDVAFV	LLLNDISRKS	PPSAAAIFKI	TESCHEBLMA	COLLIDATOR	TON CLASSON	420
			BOTROKATHK	PERFERENCE	OWNIALITOR	PÓVEDENVEN	420
	QFEERKKLAA	YI					
45		291 DNA se					
43		id Accessio		658.1			
	Coding seq	uence: 77-1	372				
	1	11	21	31	41	51	
F0	1	1	1	1	1	1	
50	GTCCCCGCAG	CGCCGTCGCG	CCCTCCTGCC	GCAGGCCACC	GAGGCCGCCG	CCGTCTAGCG	60
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	GAGCGACTCC	AAAGGCAGCA	ATGAACTTCA	TCAAGTTCCA	TCGAACTGTG	ACTOTOTAAA	180
	TOGAGGAACA	TGTGTGTCCA	ACAAGTACTT	CTCCAACATT	CACTGGTGCA	ACTGCCCAAA	240
	GAAATTCGGA	GGGCAGCACT	GTGAAATAGA	TAAGTCAAAA	ACCTGCTATG	AGGOGAATGG	300
55	TCACTTTTAC	CGAGGAAAGG	CCAGCACTGA	CACCATGGGC	CGGCCCTGCC	TGCCCTGGAA	360
		amagement of					420

CTCTGCCACT GTCCTTCAGC AAACGTACCA TGCCGACAGA TCTGATGCTC TTCAGCTGGG CCTGGGGAAA CATAATTACT GAGGAAACGG AGCGACCCT GGTGCTAGT GCAGGTGGGC CTAAAGCCGC TTGTCCAAGA GTGGATGGTG CATGACTGGC CAAAAGCAGG 420 ARAGCCCTCC TCTCCTCCAG AAGAATTAAA ATTTCAGTGT GGCCAAAAGA CTCTGAGGCC 600 CCGCTTTAAG ATTATTGGGG GAGAATTCAC CACCATCGAG AACCAGCCCT GGTTTGCGGC 660 CUSCITIANA ATATUGG GAGATICA CACATUMA ANCHECU GETTECOM-CATCARAGE GEOLOGGE GEGESCHOT CACATORIO TOTGEBAGGE GOTCARCAG CCCTOCCOG GTGATCAGC CORGACATO CTCATUAT TACCCARAGA AGGIGGACA CATOTICA CTGGGTGGC CAAGGCTRA CTCCARAGG CAAGAGAAA TAAGTICAA GGTGGBAAAC CTCATCATA ACAAGGACTA COCACAGG CAAGAGAA TAAGTICAA GGTGGBAAAC CTCATCATA ACAAGGACTA CAGGGCTGA ACGCTTGCTC ACCACAAGA 720 900 GOTGRADARO CTORATOTTA KAMAGRATA CHRONOTRA KANTITUTA KAMANANA CATTOCOTTO CTORAGATOC OTROCARGAS ASSOCIAGITA COCUMOCOLA COGGACTAT ACAGACORO TOCCTOCCT GRATOTATA CRATOCOLA TITOGCACA GOTGRAFAT CACTGCTT GRANANGAG ATTOTACCA CTATCTCTA COCGAGCAG TGANANGAC CATTOTTAGAS CTRATTICCO KOCUGAGTA TAMORGCCO CACTACTAGO GOTCTGAMOT 960 1020 1080 CACCACCANA ATGCTATGTG CTGCTGACCC CCNATGGMAA ACAGATTCCT GCCAGGGAGA 1200 CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCGGCGTA ACTTTGACTG GAATTGTGAG CTGGGGGCCT GGATGTGCCC TGAAGGACAA GCCAGGGGTC TACACGAGAG TCTCACACTT 1260 1320 CTTACCCTGG ATCCGCAGTC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC AGGGAGGAAA COGGCACCAC COGCTTTCTT GCTGGTTGTC ATTTTTGCAG TAGAGTCATC TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCCTGTGG 1500 CACCACCAGG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCTGGGT GCTGGCTGCC 1560 CAGACCCTCT GGCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT 1620 CHIGACTETT TO TOGACTGARG CCTGCROGRG TTANARAGG CROSCATO CCTGTGCATG GGCTCGRAGG GRAGGCAGC TCCCCCGRACG GTTGGGCATT TGTGRGGCCC ATGGTTGRGA 1680 AATGAATAAT TICCCAATTA GGAAGTGTAA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC 1800 ANTORATRAT TOCCAMETA COMMISSION CONCENTING THEORY OF THE ANTOROGOUS GEOGRACINGS ACCURACION CONTROLOGOUS GEOGRACINGS ACCURACIONAD THEORY OF THE ACCURATION CONTROLOGOUS GEOTESTAND THEORY OF THE ACCURATE STRUCTURATE THANGUET ANACONTORS THANGUET GEOTESTAND CONCENTRATE CONTROLOGOUS TOCTATION OF THE ACCURATE GALOROTTA TAGGICAL 1860 1920 1980 CIGGGGCCIC TIGGGICCCC CACGIGACAG TGCCIGGGAA TGTACTTATT CIGCAGCAIG ACCTGTGACC AGCACIGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT 2160 ATCCCTTCCT TTTAGCCTAG TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220 ACACTGAATA TITATATITC ACTATITITA TITATATITI TGTAATITIA AATAAAAGTG 2280

WO 02/086443 ATCAATAAAA TOTGATTTTT CIGA

ATCAATAAAA TGTGATTITT CIGA

Seq ID NO: 292 Protein sequence: Protein Accession #:NP_002649.1

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	HCEIDKSKTC	YEGNGHPYRG	KASTDTMGRP	CLPWNSATVL	QQTYHAHRSD	ALQLGLGKHN	120
10	YCRNPONRRR	PWCYVOVGLK	PLVOECMVHD	CADGKKPSSP	PERLKPOCGO	KTLRPRFKII	180
	GGEFTTIENO	PWFAAIYRRH	RGGSVTYVCG	GSLISPCWVI	SATHCFIDYP	KKEDYIVYLG	240
	REPLINENTOG	EMKFEVENLI	LHKDYSADTL	AHHNDIALLK	IRSKEGRCAQ	PSRTIQTICL	300
	PRMYNTHOPG	TECEITOFGK	RNSTDYLYPE	OLKMIVVKLI	SHRECOOPHY	YGSEVTTKML	360
		SCOGDSGGPL					420
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Seq ID NO: 293 DNA sequence Nucleic Acid Accession #: NM_001498 Coding sequence: 93..2006

20	Coding sequ	ience: 93	1006				
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	TCCTGCACAT	CTACCACGCC	GTCAAGGACC	GGCACAAGGA	CGTTCTCAAG	TGGGGGGATG	240
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35	CAAGAAATAT	CCGACATAGG	AGAGGAGAAA	AGGTTGTCAT	CAATGTACCA	ATATTTAAGG	720
	ACAAGAATAC	ACCATCTCCA	TTTATAGAAA	CATTTACTGA	GGATGATGAA	GCTTCAAGGG	780
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	TCCAGGTGAC	ATTCCAAGCC	TGCAGTATAT	CTGAGGCCAG	ATACCTTTAT	GATCAGTTGG	900
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40	TGTCAGACAT	TGATTGTCGC	TOGGGAGTGA	TTTCTGCATC	TGTAGATGAT	AGAACTCGGG	1020
	AGGAGGGAGG	ACTOGRACICCA	TTGAAGAACA	ATAACTATAG	GATCAGTAAA	TCCCGATATG	1080
	ACTUALTAGE	CAGCTATITA	TCTAAGTGTG	GTGAGAAATA	TAATGACATC	GACTTGACGA	1140
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	ATGTTGCTCA	TCTCTTTATT	AGAGACCCAC	TGACACTGTT	TGAAGAGAAA	ATACACCTGG	1260
45	ATGATGCTAA	TGAGTCTGAC	CATTTTGAGA	ATATTCAGTC	CACAAATTGG	CAGACAATGA	1320
	GATTTAAGCC	CCCTCCTCCA	AACTCAGACA	TTGGATGGAG	AGTAGAATTT	CGACCCATGG	1380
	AGGTGCAATT	AACAGACTTT	GAGAACTCTG	CCTATGTGGT	GTTTGTGGTA	CTGCTCACCA	1440
	GAGTGATCCT	TTCCTACAAA	TTGGATTTTC	TCATTCCACT	GTCAAAGGTT	GATGAGAACA	1500
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50	TTTGCAAAGG	TGGCAATGCA	GTGGTGGATG	GTTGTGGCAA	GGCCCAGAAC	AGCACGGAGC	1620
-	TCGCTGCAGA	GGAGTACACC	CTCATGAGCA	TAGACACCAT	CATCAATGGG	AAGGAAGGTG	1680
	TGTTTCCTGG	ACTGATCCCA	ATTCTGAACT	CTTACCTTGA	AAACATGGAA	GTGGATGTGG	1740
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55	ACAGTGTCAT	AACTGATGAA	ATGAATTATA	CCCTTATTTT	GAAGTGTAAC	CAAATTGCAA	1920
-	ATGAATTATG	TGAATGCCCA	GAGTTACTTG	GATCAGCATT	TAGGAAAGTA	AAATATAGTG	1980
	GAAGTARAAC	TGACTCATCC	AACTAGACAT	TCTACAGAAA	GAAAAATGCA	TTATTGACGA	2040
	ACTGGCTACA	GTACCATGCC	TCTCAGCCCG	TGTGTATAAT	ATGAAGACCA	AATGATAGAA	2100
	CTGTACTGTT	TTCTGGGCCA	GTGAGCCAGA	AATTGATTAA	GGCTTTCTTT	GGTAGGTAAA	2160
60	TOTAGAGTTT	ATACAGTGTA	CATGTACATA	GTAAAGTATT	TTTGATTAAC	AATGTATTTT	2220
	AATAACATAT	CTARAGTCAT	CATGAACTGG	CTTGTACATT	TITALATTCT	TACTCTGGAG	2280
	CARCCTACTG	TOTALGCAGE	TTTGTAAATG	TACTOGTAAT	TGTACAATAC	TTGCATTCCA	2340
	CACTTARART	GTTTACTGTA	AATTTTTTTTTT	CTTTTAAAGA	CTACCTGGGA	CCTGATTTAT	2400
	TGAAATTTTT	CTCTTTAAAA	ACATTTTCTC	TOGTTAATTT	TOCTTTGTCA	TTTCCTTTGT	2460
65	TGTCTACATT	AAATCACTTG	AATCCATTGA	AAGTGCTTCA	AGGGTAATCT	TGGGTTTCTA	2520
	GCACCTTATC	TATGATGTTT	CTTTTGCAAT	TGGAATAATC	ACTTGGTCAC	CTTGCCCCAA	2580
	GCTTTCCCCCT	CTGAATAAAT	ACCCATTGAA	CTCTGAAAAA	AAAAAAAAA	AAAA	

70 Seq ID NO: 294 Protein sequence: Protein Accession #: NP_001489

	1	11	21	31	41	51	
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	MGLLSCGSPL	SWEETKRHAD	HVRRHGILOF	LHIYHAVKOR	HKDVLKWGDE	VEYMLVSFDH	60
	ENKKVRLVLS	GEKVLETLOE	KGERTNPHHP	TLWRPEYGSY	MIEGTPCOPY	GGTMSEFNTV	120
	EANMRKRRKE	ATSILEENQA	LCTITSPPRL	GCPGFTLPEV	KPNPVEGGAS	KSLFFPDEAI	180
		RNIRHRRGEK					240
80	MGFGMGNCCL	QVTFQACSIS	EARYLYDQLA	TICPIVMALS	AASPFYRGYV	SDIDCRWGVI	300
	SASVDDRTRE	ERGLEPLKNIN	NYRISKSRYD	SIDSYLSKCG	EKYNDIDLTI	DKEIYEQLLQ	360
	BGIDHLLAQH	VAHLFIRDPL	TLFEEKIHLD	DANESDHFEN	IQSTNKQTMR	FKPPPPPNSDI	420
	GWRVEFRPME	VOLTDFENSA	YVVFVVLLTR	VILSYKLDFL	IPLSKVDENM	KVAQKRDAVL	480
	OGMFYFRKDI	CKGGNAVVDG	CGKAONSTEL	AAEEYTLMSI	DTIINGKEGV	FPGLIPILNS	540
85	YLENMEYDVD	TROSILNYLK	LIKKRASGEL	MIVARWMREF	IANHPOYKOD	SVITDEMNYS	600
	LILKUNQIAN	ELCECPELLG	SAFRKVKYSG	SKTDSSN			

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WO 02/086443 Seg ID NO: 295 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 247-816 5 31 41 51 AGTOTTORIC TORGGEAGGE ACCOUNTING TOGETACTIC COTTOCTOC ATCCCCCTTG GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120 CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180 10 GGGAGGCGC ACAACTICAC TGCCATTITG TGAGGIGCGG CCGTCTCTCC TCCAGCAAGG 240 GARACARTGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG ARACAGGAG CAGGAGACAG CCTTATTUCA GUCTCTGCCA TUTCCARAGA ARAGAAGCTT ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 420 480 ANDAGASSAN ANDAGATTE ACCURACIÓN FIGURITECE MARTIGATES CITUATIONS TECNOCIÓNS FAGABACTOS CASCANIOS CACCOSTOSOS ACGABACOTOS ACCAGORIT TECETOGRAS TEACOTRAGAS TECAGAGARA CAGCITETES TECCHARACOS ACCAGAGARA ACACCITETES TECCHARACOS ATRIANISTICAS ATARABACOST ANTATAGOTAS ACACACTOS ATRICOSTIGOS CUAMATATOS ARABACTETO CARATOCTO GAMOGRAFIO ANGGACITAC TECNOTICAGO E40 660 720 AGCGATTTT TIGANTCAT CATCAGGAA GCAGCAGAT GTATAGGAC AGACTTGTT AGCCACCTTA AGAGAAACT GAAACCTATG ATTTGGACA ACTTGTCCCT GGAGGATTAT CACACCCCAA ATGCATAATC TOTTATATG TTGTGGATA ACTTGTCCCT GGAGGATTAT 780 20 840 900 TTCTRCAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACOGA ATCAAATAGC CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTC TTTTTCCCAA AGCATTTTAT 960 1020 TIGARAGGAT ARCTIGIST TIGGITATIT TGTATICCCA CCIGIOCTGG TAGATATIAT
TRACCCATTA GGTARATACT ATTACAGTGG TGGTTTCTGC A 1080 25 Sec ID NO: 296 Protein sequence: Protein Accession #: Eos sequence 30 31 MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT GHAIPPSQLD SQIDDPTGFS KDRHMQKPGS NAPVGCNVTS SPSGDDLBCR ETASSPKSQR 120 BINADIKRKL VKELRCVGQK YBKIFEMLDG VQGPTAVRKR FFESIIKEAA RCMRRDFVKH 180 LXXXXLKRMI Sec ID NO: 297 DNA secruence Nucleic Acid Accession #: Eos sequence Coding sequence: 247-815 40 21 11 31 41 AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 45 GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 120 180 300 360 50 420 480 TTCRGCAAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAAGC CAACAAGAAA TTAATGCTGA TATAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 600 660 55 CAMAMATATG AAAAANTCTT OGAAATGCTT GAMOGAGTGC AAGGACCTAC TGCAGTCAGG AAACGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACC AGACTTTGTT AAGGACCTTA AGAAGAAACT GAAACGTATG ATTIGAGAT ACTIGAGAT CATGTTCCCT GGAGGATTAT 720 780 CACACCCCAA ATGCATAATC TCATTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900 TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAACTGGC 960 60 CTTCCRGAGG CTARGAAATT TCTGTTAGTA AAAGATGTTC TTTTTCCCAA AGGGTTTTAT TTGAAAGGGT AACTGTGTT TTGGTTAGTT GTGATTCCCA CCTGTGCTGG TAGATATTAT TAACCCATTA GGTAAATCTA TATTCAGTTG TGGTTTCTGC A 1020 Seq ID NO: 298 Protein sequence: 65 Protein Accession #: Eos sequence MIDKIEKVAV DPETVEKRPR ECDSPSYCKR ORMALLARKO GAGDSLIAGS AMSKEKKLMI 70 GHAIPPSQLD SQIDDFTGFS KDRHMQKFGS NAPVGGNVTS SFSGDDLECE ETASSPKSQQ EINADIKRKL VKELECVGOK YEKIFEMLEG VQGPTAVRKE FFESIIKEAA ROMERDFVKH 120 TAYKKY KRMT Seq ID NO: 299 DNA sequence 75 Mucleic Acid Accession #: Eos sequence Coding sequence: 247-815 80 AGTOTTOSSC TOGGGCAGGC ACCOUNTSSC TGGGTACTTC COTTCCCCC ATCCCCCTTG 120 CCTAGGGGGC ACATITCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG GOGAGGEGE ACAACTTCAC TOCCATTTIG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240 GAMACANTGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300

CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG AAACAAGGAG CAGGAGACAG CCTATTGCG AGCTCTGCG AGTTCCAAAGG AAAGGACTTA TGACAGGAGA TGCTATTCCA CCCAGCCAAT TGGATTCCA GATTGATGGA TTCACTGGTT

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10	TGAAAGGATA	TAAGAAATTT ACTTGTGTTT GTAAATACTA	TOGTTATTTT	GTATTCCCAC	TTTTCCCAAA	GCGTTTTATT AGATATTATT	1020 1080
15		300 Protein cession #: 1		31	41	51	
20	MTDKTEKVAV GHAIPPSQLD	DPETVFKRPR SQIDDFTGFS VKELRCVGQK	 BCDSPSYQKR KDRMMQKPGS	QRMALLARKQ NAPVGGNVTS	GAGDSLIAGS SFSGDDLECR	AMSKAKKIMT ETASSPKSQQ	60 120 180
25	Nucleic Ac	301 DNA sec id Accession sence: 247-8	#: Bos se	quence			
	1	11	21	31	41	51	
30	OGCCARACGG CCTAGGGGGC GGGAGGCGCC GARACRATGA	TGGGGCAGGC GATCGGTGCT ACATTTCCCA ACAACTTCAC CCGATAAAAC	TCTGGTGAGA CAACTCCCAG TGCCATTTTG AGAGAAGGTG	CGCCTCCCCA AGGGCAGGTT TGAGGTGCCG GCTGTAGATC	TGCACATCAC TCTAGAAAGT CCGTCTCTCC CTGAAACTGT	TCCCAGGTGC GCCACCAGTG TCCAGCAAGG GTTTAAACGT	60 120 180 240 300
35	AAACAAGGAG TGACAGGACA TCAGCAAAGA	GTGACAGTCC CAGGAGACAG TGCTATTCCA TGGGATGATG CTCTGGAGAT	CCTTATTGCA CCCAGCCAAT CAGAAACCTG	GGCTCTGCCA TGGATTCTCA GTAGCAATGC	TGTCCAAAGA GATTGATGAC ACCTGTGGGA	AAAGAGCTTA TTCACTGGTT GGAAATGTTA	360 420 480 540 600
40	AACAAGAAAT AATATGAAAA GATTTTTTGA ACCTTAAGAA	TAATGCTGAT AATCTTCGAA ATCCATCATC GAAACTGAAA ATAATCTCAT	ATAMATGTC ATGCTTGAAG AAGGAAGCAG CGTATGATTT	AAGTAGTGAA GAGTGCAAGG CAAGATGTAT GAGAATACTT	GGAAATCCGA ACCTACTGCA GAGACGAGAC GTCCCTGGAG	TGCCTTGGAC GTCAGGAAAC TTTGTTAAGC GATTATCACA	660 720 780 840 900
45	ACAATGGAGC CAGAGGCTAA AAGGATAACT	AGGATATTGC GAAATTTCTG TGTGTTTTGG AATACTATTA	TGAAGTCTCC TTAGTAAAAG TTATTTTGTA	TOGCATATGT ATGTTCTTTT TTCCCACCTG	TACCGAAAGCG	ACTGGCCTTC TTTTATTTGA	960 1020 1080
50	Seq ID NO: Protein Ac	302 Protein cession #: 1	os sequence				
55	1 HTDKTEKVAV GHAIPPSQLD EINADIKCQV KKKLKRMI	11 DPETVFKRPR SQIDDFTGFS VKEIRCLGQY	21 BCDSPSYQKR KDGMMQKPGS EKIFEMLEGV	31 QRMALLARKQ NAPVGGNVTS QGPTAVRKRP	41 GAGDSLIAGS NF9GDDLBCR FESIIKEAAR	51 AMSKEKKIMT GIASSPESQQ CMRRDFVKHL	60 120 180
60	Nucleic Ac:	303 DNA sec Ld Accession Lence: 247-8	ı #ı Eos se	quence			
65	GGCCAAACAG CCTAGGGGGC	11 TGGGACAGGC GATCGGTGCT ACATTTCCCA	TCTGGTGAGA CAACTCCCAG	CGTCTCCCCA AGOGCAGGTT	TGCACATCAC TCTAGAAAGT	TCCCAGATGC	60 120 180
70	GAAACAATGA CCCAGGGAAT AAACAAGGAG TGACAGGACA	ACAACTTCAC COGATAAAAC GTGACAGTCC CAGGAGACAG TGCTATTCCA	AGAGAAGGTG TTCGTATCAG CCTTATTGCA CCCAGCCAAT	GCTGTAGATC AAAAGGCAGA GGCTCTGCCA TGGATTCTCA	CTGAAACTGT GGATGGCCCT TGTCCAAAGC GATTGATGAC	GTTTAAACGT GTTGGCAAGG AAAGAGCTTA TTCACTGGTT	240 300 360 420 480
75	CCAGCAGTTT AACAAGAAAT AAAAATATGA AACGATTTTT	TAGGATGATG CTCTGGAGAT TAATGCTGAT AAAAATCTTC TGAATCCATC	GACCTAGAAT ATAAAACGTA GAAATGCTTG ATCAAGGAAG	GCAGAGAAAC AATTAGTGAA AAGGAGTGCA CAGCAAGATG	AGCCTCCTCT GGAACTCCGA AGGACCTACT TATGAGACGA	CCCAAAAGCC TGCGTTOGAC GCAGTCAGGA GACTTTGTTA	540 600 660 720 780
80	ACACCCCAAA TCTACAATGG TTCCAGAGGC TGAAAGGATA	GAAGAAACTG TGCATAATCT AGCAGGATAT TAAGAAATTT ACTTGTGTTT GTAAATACTA	CGTTAATGAT TGCTGAAGTC CTGTTAGTAA TGGTTATTTT	TGAGGAGAGA TCCTGGCATA AAGATGTTCT GTATTCCCAC	AAAGGATCAG TGTTACCGAA TTTTCCCAAA	ATTGCTGTTT TCAACTGGCC GCGTTTTATT	900 960 1020 1080
85	Seg ID NO:	304 Protein cession #: 1	sequence:				

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5	GHAIPPSQLD	DPETVFKRPR SQIDDFTGFS VKBLRCVGQK	KDRMMQKPGS	NAPVGGNVTS	SFSGDDLECR	ETASSPKSQQ	60 120 180
10	Nucleic Aci	305 DNA sec id Accession sence: 87-68	#: Eos seg	pence			
	1	l I	21 	31	41 	51	60
15	CCAGACTAGC	GCTAGCGCGA GAACAATACA	GECAGGATGG	CTAAAGGTGA	CCCCAAGAAA	CCAAAGGGCA	120
	AGATGTCCGC	TTATGCCTTC TGTCAATTTT	TTTGTGCAGA	CATGCAGAGA	AGAACATAAG CTCTGAGAGG	AAGAAAAACC TGGAAGACGA	180 240
	TGTCCGGGAA	AGAGAAATCT	AAATTTGATG	AAATGGCAAA	GGCAGATAAA	GTGCGCTATG	300 360
20	ATCGGGAAAAG	GCCACCGTCT	GGACCAGCTA GGATTCTTCC	TGTTCTGTTC	AGAATTCCGC	CCCAAGATCA	420
-	AATCCACAAA	CCCCGGCATC	TCTATTGGAG	ACCTGGCAAA	AAAGCTGGGT	GAGATGTGGA	480 540
	AGTATGAGAA	TGACAGTGAA GGATGTTGCT	GACTATAAGT	CGAAAGGAAA	GTTTGATGGT	GCAAAGGGTC	600
25	CTGCTAAAGT	TGCCCGGAAA	AAGGTGGAAG	AGGAAGATGA	AGAAGAGGAG	GAGGAAGAAG TTGTGAATAC	660 720
25	AGGAGGAGGA	GGAGGAGGAG GGAGCGCCGT	GATGAATAAA	CARACTETT	GAGAAGTGTC		720
	ATTAGGTTTA	ATTACAAAAT	TTGATCACGA	TCATATTGTA	GTCTCTCAAA	GTGCTCTAGA	840
	AATTGTCAGT	GGTTTACATG TATTTCCAAA	AAGTGGCCAT	GGGTGTCTGG	AGCACCCTGA	AACTGTATCA	900 960
30	CTGTGCACTT	TGCTGTTGGT	GTGACAAGGC	ATTTAAAGAT	GTTTCTGGCA	TTTTCTTTTT	1020
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55	CATGAGAATA	TTTTTTTTT	TAAGTGCGGT	AGTTTTTAAA	CTGTTTGTTT	TTARACANAC	1380
	TATAGAACTC	TARACACGAT	GCAAAGCAAA	GAGTCACTGC CTGTTATTTT	ATCAATGAAA	GTTCAAGAAC	1440 1500
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40	AGTCAATTTC	TGACTCACAG ATGTGGTAGC	CAGTGAACAA	ACCCCCACTC	CATTGTATTT	OGAGACTGGC	1620 1680
	TGAAGGAGAG	GGCTACTTGA	AGCTACTGTG	TGATTTTGTT	TGTGTCTGAG	TGGCATTCAG	1740
	ATGAAGTCTG	GAGGAGTTAG GTGATTAGGA	GAGAACGACA	TAGGCAAGGT	TCAGCAGCCT	TCCAAGGTAT	1860
45	CCTATTTTGT	GGGGCCAAAT	GCATTGCTAA	ACAGCAATTT	CAGAGTGTAT	GGTGTGTCAA	1920
	AAATTAAGGC	CTTATTGTTT	TTCTCTTTCA	CCCCTACCCC	CCGTGCTCCT	GGCACATATC	1980 2040
	AGTGAGGGTA	TGTGGGATGG	GGTGGTGGGG	TAGGGGACGG	TATCCTTTTT	TTGCTCCTAC	2100
50		CAAACACCCC AATGGAATCA	AAGGAAGATG	ATAGGCTCCA	TCTTGGGCCA	CCTGAGCTAT	2160 2220
50	GCCTGCTCAT	AAGTTTAGCT	CATTCACTGG	AAATGTAGAT	TGATGTTCAA	TGTTAAACTG	2280
	GAAGGAGCTT	GGGGAGATGG	TCAGTGGTTA	TATTAGTGGG	TAGTGTAACA	TTTTTATCCAG	2340 2400
	CTGATGTGTA	TATACATCAT	TACTGTCCGT	AGCAATGAAG	GATACAGTAC	TGTGTTGTGG	2460
5 5	GTGAGTGTTG	CTATTGCCCA	GCATTAATAT	TIGGGIGIGI	ATGTTTGAGG	CTATGAAACA	2520 2580
	GTTGAGAAAC	TTTTTTGTGCT	GGAGGCGGTG	TOCTCTCCGC	CCTGTCGGGT	CCTGGATGAG	2640
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70	CTACTCCCTC	TAACCACCTC	ACCCCATTCT	TGAATGACAT	TTTATCCTTC	GGAAAGAACA	3420 3480
	GTATTTGGGG	GTAGTGACTA ACGTTGGATG	CATTCATTTT	CIGTAATAAA	G	TGTCACOUNT	3480
75	Protein Acc	306 Protein cession #: 1	4P_005333.1				
	1	11	21	31 	41	51 	
80	DEMAKADKVR GDVAKKLGEM	GKMSAYAPFV YDREMKDYGP WNNLNDSEKQ EEEEEEEDE	AKGGKKKKDP	NAPKRPPSGF	FLFCSEFRPK	IKSTNPGISI	60 120 180
85	Nucleic Ac	307 DNA se id Accessio uence: 12	n #: NM_0223	842			

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	1	11	21	31	41	51	
		!	<u> </u>				60
5	ATGGGTACTA	GGAAAAAAGT	TCATGCATTT	GTCCGTGTCA	AACCCACCGA	TGACTTTGCT	120
,	CATGAAATGA	TCAGATACGG	AGATGACAAA	AGAAGCATIG	ATATTCACTT	AAAAAAAAAA	180
	ATTCGGAGAG	GAGTTGTCAA	TAACCAACAG	ACAGACTGGT	CGTTTAAGTT	GGATGGAGTT	240
	TTCACGATG	CCTCCCAGGA (CTIGGTTTAT	GAGACAGTIG (AAAGGATGT (AGTTICICAG	300
	CCCTCGATG	GCTATAATGG (CACCATCATG	TGTTATGGGC A	MGACGGGAGC :	IGGCAAGACA	360
10	ACACCATGA	TGGGGGCAAC TTAGGATGAT	GAGAATTAC .	AAGCACCIGG (MATCUICCU :	regreecere	420
10	AGCAGGTTT	TTACCATGAT (JSAAGAACGC	CCCACACATA	CATCACIGI (3CG1G111CC	480
	ACTTGGAAA	CACCAATGAC	SAGCCTGTTT	GATCTCCTGT	CACICIOCC (TATOTIONA	540
		TCACAAAGTCA					600
	LAGITICACC	TAGOCTCCCA	SOMO MOONI	AAAAACTCTT !	CONTRACTOR O	TOCATTTC	660
15	ACAGGATTA	TAGAGGCCCA	TOWNS TOWNS	TRATEGRADO :	AND CTACAT	CACTTOCADA	720
13	CONTOINCE	TGGATCTGGC	CCCOSCACAC	ACCOMMONGO A	CTCYCCCTC	rangagggaa	780
	TIANCITOS	AAGCCACCTA	TANCA ACA A A	TOCOTOTOTO !	POCTYGGAGCA (COCATCATT	840
	CCCTGRAGG	ACCAGAAGCG	CACCACATC	commerce :	CTCCAACCT (TACCCACTOCT	900
	TCALCCACT.	CGTTAGGGGG	AACTCCAAT	ATTOMORY OF S	CACADACAT (TATGGAGAA	960
20	CTCCCCCCC	TAGAAGAAAC	CTATCTTCA	CTCAGATTTG	CAGCAGGAT	PARCTACTO	1020
20	CCACTGAGC	CTGCCATCAA	GRARAGTAT	GATGCTGAGA (SAATGGTCAA	BAACCTOGAG	1080
	DATOLARDO	CACTACTCAA	CAGGAGCTG	GCTATCCATG	ACAGCCTGAC	CAACCGCACC	1140
	TTGTGACCT	ATGACCCCAT	GATGAAATC	CAGATTGCTG A	AGATCAACTC	CAGGTGCGG	1200
	GGTACCTGG	AGGGGACACT	GACGAGATC	GACATAATCA (CCTTAGACA	GATCAAGGAG	1260
25	TGTTCAACC	AGTTCCGGGT	GTTCTGAGC	CAACAGGAAC	AGGAAGTGGA	STOCACTITG	1320
	GCAGGAAGT	ACACCCTCAT	DGACAGGAAT	GACTTTGCAG	CATTTCTGC '	TATCCAGAAG	1380
	CGGGGCTTG	TGGATGTTGA	TGGCCACCTA	GTGGGTGAGC	TGAAGGACA	ADDITTORA	1440
	TCGGAGTCG	CCCCTTTCTC '	FACCAAACCT	GGGAAGAAAG (CAAGTCCAA (BAAGACATTC	1500
	AAGAGCCAC	TCAGGCCCGA (CACCCCACCC	TCCAAACCAG :	rGGCCTTTGA (GAGTTTAAG	1560
30	ATGAGCAAG	GTAGTGAGAT	CAACCGAATT	TTCAAAGAAA A	ACAAATCCAT	CTTGAATGAA	1620
	GGAGGAAAA	GGGCCAGCGA	BACCACACAG	CACATCAATG	CCATCAAGCG (GAGATTGAT	1680
	TGACCAAGG	AGGCCCTGAA	ITTCCAGAAG	TCACTACGGG A	NGAAGCAAGG	CAAGTACGAA	1740
	ACAAGGGGC	TGATGATCAT	CGATGAGGAA	GAATTCCTGC :	IGATOCTCAA	GCTCAAAGAC	1800
	TCAAGAAGC	AGTACCGCAG	OGAGTACCAG	GACCTGCGTG A	ACCTCAGGGC :	TGAGATCCAG	1860
35	ATTGCCAGC	ACCTAGTGGA :	PCAGTGTCGC	CACCGCCTGC '	CATGGAATT :	PGACATCTGG	1920
	ACAATGAGT	CCTTTGTCAT	CCCTGAGGAC	ATGCAGATGG	CACTGAAGOC .	AGGCGGCAGC	1980
	TCCGGCCAG	GCATGGTCCC '	TGTGAACAGG	ATTGTGTCTC '	IGGGAGAAGA	TGACCAGGAC	2040
	AATTCAGCC	AGCTGCAGCA	SAGGGTGCTT	CCTGAGGGCC	CTGATTCCAT	Creerrerae	2100
40		TCAAGATAGA	GCAGAAGCAT	AATTACTTGA	AAACCATGAT	3GGCCTGCAG	2160
40	AGGCACATA	GAAAATAG					
		308 Protei					
	Protein Ac	cession #: !	NP_071737				
45			21	31	41	51	
45	1	11	11	11	1	7*	
		VRVKPTDDFA		DOTOTIE EVO	TRRCTRRROO	TOWERS DOWN	60
	MSTRKKVHAP	ETVAKDVVSQ	REMIKYGODA	CHOCOTOLOGY	THE STREET	PUDCTI DDAT	120
	COMPRESENT	PTHAITVRVS	ALDGING III	DI LOTI DVVG	DOUTDMTIVE	NEOGVETEGL	180
50	QQVFRMISER	AFSLLPEGET	MULTINGOLD	PRESIDETAG	TTVI PAUCOT	LOPRIVITOR	240
50	THI UNI ACCE	RLGKSGSEGQ	VIVENTYINK	RIGHT-FOATT	ALCCOKROST	PEROCKLTHA	300
	I AD ST CONC.	MVLVTNIYGE	AMOURETLES	LEPASSMELV	TTEPAINERY	DARRHVIOLE	360
	VPI-ALT-YOUT	AIHDSLTNRT	BALADDANDEL	OLVEINSOAB	RYLEGILDRI	DIISLROIKE	420
	VPMOPPUUT.	QQEQEVESTL	PRIVITATION	DPAAISATOK	AGLVDVDGHL	VGRPEGONFG	480
55	LOVADROTKE	GKKAKSKKTF	KEPLEPOTPE	SKPVAFREPK	NEGGSEINRI	PKENKSILNE	540
	BEKRASETTY	HINAIKREID	VIXEALNEON	SLREKOGKYR	NKGLMI I DEE	EFLLILKLKD	600
	I KKOABBEAU	DLRDLRAEIQ	VCOHLVDOCE	HRLLMEPDIW	YNESFVIPED	MOMALKPGGS	660
	IRPGMVPVNR	IVSLGEDDQD	KPSOLOORVL	PEGPDSISFY	NAKVKIEQKH	NYLKTMMGLQ	720
	QAHRK					_	
60	~						
	Seq ID NO:	309 DNA se	quence				
		id Accessio		uster			
15	1	11	21	31	41	51	

65	1	11	21	31	41	51 	
05	THEFTHE	AUTTTTTTAA	TGCCTGCTGT	CATGCTCTGT	CTACCAGGGT	GAATTTCCAA	60
			TAGCCAAAAC				120
	CACATTGAAG	ACCARAGGAA	AGAGTGAAGA	AGTGTAGTTG	GGTCATTGTG	AATGGATGTT	180
	TAGATTGTCA	AGAAAAGTGG	GCCAGAGGCC	CCACCTCACA	CTAGGACGGC	AATTGCCTCT	240
70			TGGGTCTTAT				300
	TAATGAACCC	TCAGCCTCCA	GCTTCTCTTC	TTCGGGGATTC	TTCTTAGGGC	CTCCTTTTTC	360
			TGAATTTCTT				420
			ATTCACTTTA				480
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13							

Seq ID NO: 310 DNA sequence Nucleic Acid Accession #: NM_018622.2 Coding sequence: 1-1140

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	GATAGCATAA	GACCACAAAA	AGAAGGAGAC	TTCAGAAAGG	AGATTAACAA	GTGGTGGAAT	480
	AACCTAAGTG	ATGGCCAGCG	GACTGTGACA	GGTATTATAG	CTGCAAATGT	CCTTGTATTC	540
-	TGTTTATGGA	GAGTACCTTC	TCTGCAGCGG	ACAATGATCA	GATATTTCAC	ATCGAATCCA	600
5			TCCAATGTTG				660
	CACATGGCAG	CAAATATGTA	TGTTTTGTGG	AGCITCTCTT	CCAGCATAGT	GAACATTCTG	720
	GGTCAAGAGC	AGTTCATGGC	AGTGTACCTA	TCTGCAGGTG	TTATTTCCAA	TTTTGTCAGT	780
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4.0			CTGCACTAAG				900
10			AGCAGGGAAT				960
			GAAATTTTTT				1020
			TTACGGTCAT				1080
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Seq ID NO: 311 Protein sequence: Protein Accession #: NP_061092.2

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			PPVERTVFYP				120
			DSIRPQKEGD				180
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25	COEOFMAVYL	SAGVISNEVS	YLGKVATGRY	GPSLGASGAI	MTVLAAVCTK	IPECRLAIIF	300
	LPMFTFTAGN	ALKAIIAMDT	AGMILGWKFF	DHAAHLGGAL	PGIWYVTYGH	ELIWKNREPL	360
	VKIWHEIRTN	GPKKGGGSK					

30 Seq ID NO: 312 DNA sequence Nucleic Acid Accession #: NM_000625 Coding sequence: 195..3656

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		GAAGAACATC					180
	GTAAAGCCAT	AGAGATGGCC	TGTCCTTGGA	AATTTCTGTT	CAAGACCAAA	TTCCACCAGT	240
40		TGGGGAAAAA					300
	CCAGTCCAGT	GACACAGGAT	GACCTTCAGT	ATCACAACCT	CAGCAAGCAG	CAGAATGAGT	360
	CCCCGCAGCC	CCTCGTGGAG	ACGGGAAAGA	AGTICTOCAGA	ATCTCTGGTC	AAGCTGGATG	420
	CAACCCCATT	GTCCTCCCCA	CGGCATGTGA	GGATCAAAAA	CTGGGGCAGC	GGGATGACTT	480
	TCCAAGACAC	ACTTCACCAT	AAGGCCAAAG	GGATTTTAAC	TTGCAGGTCC	AAATCTTGCC	540
45	TGGGGT CCAT	TATGACTCCC	AAAAGTTTGA	CCAGAGGACC	CAGGGACAAG	CCTACCCCTC	600
	CAGATGAGCT	TCTACCTCAA	GCTATCGAAT	TTGT CAACCA	ATATTACGGC	TCCCTCAAAG	660
	AGGCAAAAAT	AGAGGAACAT	CTGGCCAGGG	TGGAAGCGGT	AACAAAGGAG	ATAGAAACAA	720
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		CTGCATTGGG					840
50	GCTGTTCCAC	TGCCCGGGAA	ATGTTTGAAC	ACATCIGCAG	ACACGTGOGT	TACTOCACCA	900
	ACANTGGCAA	CATCAGGTCG	GCCATCACCG	TGTTCCCCCA	GCGGAGTGAT	GGCAAGCACG	960
		GTGGAATGCT					1020
		GGACCCTGCC					1080
		OGGCCGCTTC					1140
55		CGAAATCCCCA					1200
		TCGGGAACTG					1260
		GGGCGGCCTG					1320
		AGTCCGGGAC					1380
		GGGCCTGGAA					1440
60		CATTGCTGTG					1500
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0.0		GGAGATCCAC					3000
		GCACCACGGC					3060
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PCT/US02/12476

3720 3780

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Seq ID NO: 313 Protein sequence: Protein Accession #: NP 000616

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31

41

51

Seq ID NO: 314 DNA sequence Nucleic Acid Accession #: XM 087254

21

Coding sequence: 47..2332 11

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CTTGTTTGCC TOTALACTAT TATTTTCTTG CTAAATGTAAC ATTTGTCCTT CTCAMGGATT
AAGCTATTA AGACTATTAA GCTAAATAT AATTTCAAA AACAGTCCTT CTTTAACTTA 2960 4080 30 GATATTICAT ACCTIGATIT AGGARGATCI GITATTCIGG ANGTACTARA AAGAATAATA CAACGTACAA TGTCIGCATI CACTAATTCA TGITCCAGAA GAGGAAATAA TGAAGATATA 4140 4200 CTCAGTAGAG TACTAGGTGG GAGGATATGG AAATTTGCTC ATAAAATCTC TTATAAAACG 4260 TOCATATAAC AAAATGACAC CCAGTAGGCC TGCATTACAT TTACATGACC GTGTTTATTT 4320 GCCATCAAAT AAACTGAGTA CTGACACCAG ACAAAGACTC CAAAGTCATA AAATAGCCTA 4380 35 TGACCAACTG CAGCAAGACA GGAGGTCAGC TCGCCTATAA TGGTGCTTAA AGTGTGATTG 4440 ATGUARTITE CUGTACUCAC CATTUGARGE TAGUTARGEA GRACUTURET TUTTURARAN 4500 AMSTANATOG CHACCACTAG TGTGCTCATC CIGAACTGTT ACTCCAAATC CACTCCGTTT 4560 THANGCAAN ATTATCTTGT GATTTTAAGA AANGAGTTTT CTATTTATTT AAGAAAGTA CAATGCAGTC TGCAAGCTIT CAGTAGTTIT CTAGTGCTAT ATTCATCCTG TAAAACTCTT 4690 CANTOCAGE GROADCTT CONTACTITE CONTROLLAR ATTRACTUR PARACECTE ACRACITACA CAGRANATCA ARGGARAGE TOCCCTITICS RYATTICTIT HARATETITE CITIOGRAMS TATGATGITE ATANTHARE TROCCTIANT TOCCARAGE REAGCARANT GCTANATACS TRATTOCTAN TOATGGTCH CHARTCHATT TOCCTCCCTT TOCCTOSTCT GROGOCTETA ROCCTGARGA TROTGGCARG CACCAGTCA CHITCOCARA TROCCCCTCA 40 4740 4800 4860 GCTGCTTTAA GTGACTCAGC ACCCTGGCTC AGCTTCAGCA GGGGTAGGCT CACCCTGGGC
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	AA	AAAAATTOTA	O-MOCKACK!	THEFT	AUGUNANCE		
	AA.						
60	0 TD 170-	317 Dunk +4					
00		317 Protei					
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	1	11	21	31	41	51	

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70	LAAPPPVYYP GCTGARPANP	PAYMEDAAAA AASPGPCRVF SAYAAAYAGP ALGACYNPGG	GLVPERPLSP DGAYPQGAGS	ELGPAPSGPG AIFAAAGRLA	GSCAFASAGA GPASPPAGGS	PATTTGYQPA	240 300 360

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~ -	GCAAGACGGA	TATGCATGCA	ATCARAATCA	GGGCCGCTGC	TACAATGGCG	AGTGCAAGAC	2040
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			AAGGCACTGA				2160
			ATGATGTGTT				2220
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	ACAAATTCAA	GCCCTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AAGTCTGTTC	2460
	GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CICCATTIGI	GATTTCACCT	GGGCAGGGAC	2520
	AGATTGCAGT	ATCCGGGATC	CAGTTAGGAA	CCTTCACCCC	CCCAAGGATG	AAGGACCCAA	2580
25	GGGTCCTAGT	GCCACCAATC	TCATAATAGG	CTCCATCGCT	GGTGCCATCC	TGGTAGCAGC	2640
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	ATTCTGGGTA	TGACATACTC	GCAGCAGTGT	TACTGGAACT	ATTAAGTTTG	TARACARAAC	2820
	CTTTGGGTGG	TAATGACTAC	GGAGCTAAAG	TTOOGGTGAC	AAGGATGGGG	TAAAAGAAAA	2880
40	CTGTCTCTTT	TOGAAATAAT	GTCAAAGAAC	ACCTITCACC	ACCTGTCAGT	AAACGGGGGA	2940
40	GGGGGCAAAA	GACCATGCTA	TAAAAAGAAC	TGTTCCAGAA	TOTTTTTT	TUCUTAATGG	3000
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Seq ID NO: 325 Protein sequence: Protein Accession #: NP_003803

45 MKPPGSSSRQ PPLAGCSLAG ASCGPQRGPA GSVPASAPAR TPPCRLLLVL LLLPPLAASS RPRANCAAAP SAPHNIRTAE KNIGVLADED NTLOONSSEN ISYSNAMOKE ITLPSRLIYY 50 INQUSESPYH VLDTKARHQQ KHNKAVHLAQ ASFQIEAFGS KFILDLIAN GLLSSDYVEI 180 HYENGKPOYS KOGEHCYYHG SIRGVKDSKV ALSTCNGLNG MPEDDTPVYM IEPLELVHDE 240 KSTORPHIIQ KTLAGQYSKQ MKNLTMERGD QWPFLSBLQW LKRRKRAVNP SRGIFEENKY LELMIVNDHK TYKKHRSSHA HTNNFAKSVV NLVDSIYKEQ LWTRVVLVAV ETWTEKDQID 300 360 ITTNPVOMLE EPSKYRORIK CHADAVHLIS RVTFHYKRSS LSYFGGVCSR TRGVGVNEYG 55 LPMAVAQVLS QSLAQNIGIQ WEPSSRKPKC DCTESWGGCI MEETGVSHSR KFSKCSILEY 480 RDFLORGGGA CLEMRFIKLF EPIECGNGYV BAGEBCDOGF HVBCYGLOCK KCSLSNGAHC SDGPCCNNTS CLEOPRGYBC RDAVNBCDIT EYCTGDSOQC PPNLHKQDGY ACNONQGRCY 540 600 MGECKTRONG COYINGTKAA GSDKFCYEKL NTEGTEKGNC GKDGDRWIGC SKHDVFCGFL LCTNLTRAFR IGGLGGEIIP TSFYNGGRVI DCSGAHVVLD DDTDVGYVED GTPCGFSHMC 660 60 LDRKCLQIQA LNMSSCPLDS KGKVCSGHGV CSNEATCICD FTWAGTDCSI RDPVRNLHPP 780 KDEGPKGPSA TNLIIGSIAG AILVAAIVLG GTGWGFKWVK KRRFDPTQQG PI

Seq ID NO: 326 DNA sequence Nucleic Acid Accession #: AK074418.1 Coding sequence: 244-1515

21 41 CTITICICCAA GACGGCCGGC CATGCTCTCC TCCTCTGCCA GTCTCCTCCA CCACTCTCTA 70 ACCIGAGAGE CIGIGGAACC IGCCCGTCTC CCCTCCTCCA TCAGACACAC CIGCCTAGGA 120 AACAGATGGA AAAAGTGAGG GACCGGTGAG TGACTTGCTG CTAAAGTTTA TACCAGATGC 100 AAATGACAGA GCTGGAGTTC TGCTGTGCCT GGAAAGGACC TCGGAAGTCT TCTAAGGAGA 240 AARTGACAGA GCTCGAGTTC TGCTGTGCT GGAAAGGACC TGCGARAGTCT TCTAAGGAGA GCTGCTGCGT TATACAGAGA GCCTTGCAGT GGAACTGCA TGCTGAATT CAAAGGAGA GACTTTACCA GCTTGCGGGA TCACTGCCTG AGCATGGGC GGAGGTTTAA GGATGAGACA TCCCCCGCGA CAAATCTTC CATAG 300 75 420 480 ATARGCAGAT TIGACATCCA ACARGGAGGC GCAGCIGACT GCTGGTTCCT GGCAGCACTG 540 GGATCCTTGA CTCAGAACCC ACAGTACAGG CAGAAGATCC TGATGGTCCA AAGCTTTTCA 600 CACCACTATG CTGGCATTIT COGTTTCCGG TTCTGGCAAT GTGGCCAGTG GGTGGAAGTG 660 80 GTGATTGATG ACCGCCTACC TGTCCAGGGA GATAAATGCC TCTTTGTGCG TCCTCGCCAC 720 CAAAACCANG AGTTCTGGCC CTGCCTGCTG GAGAAGGCCT ATGCCAAGCT GCTCGGATCC 780 TATTCCCATC TGCACTATGG CTTCCTCGAG GATGCCCTGG TGGACCTCAC AGGAGGCGTG 840 ATCACCAACA TCCATCTGCA CTCTTCCCCT GTGGACCTGG TGAAGGCAGT GAAGACAGCG 900 ACCAAGGCAG GCTCCCTGAT AACCTGTGCC ACTCCAAGTG GGCCAACAGA TACAGCACAG 960 85 ACCHROSCAS GETCCTORT MACTITOCA ECTRACITE TOACTOGGE TRACKGRATT CAATACOGAA GEGCCTGGE GAGICTCCAT GCCTACACTE TGACTGGGC TGAGCAGATT CAATACOGAA GEGCCTGGGA RAAATTATC TCCCTGTGGA ACCCCTGGGG CTGGGGCGAG 1020 1000

ACCGRATGGA GAGGGCGCTG GAGTGATGGG TCTCAGGAGT GGGAGGAAAC CTGTGATCCG

WO 02/086443 CGRAAAGCC AGCTACATAA GAAACGGGAA GATGGCGAGT TTTGGATGTC GTGTCAAGAT 1200 TTCCAACAGA AATTCATCGC CATGTTTATA TGTAGCGAAA TTCCAATTAC CCTGGACCAT 1260 GGAAACACAC TCCACGAAGG ATGCTCCCAA ATAATGTTTA GGAAGCAAGT GATTCTAGGA 1320 AACACTGCAG GAGGACCTCG GAATGATGCT CAATTCAACT TCTCTGTGCA AGAGCCAATG 1380 GAAGGCACCA ATGITGTCGT GTGCGTCACA GTTGCTGTCA CACCATCAAA TTTGAAAGCA 1440 GRAGATSCAA AATTTOCACT CGAITTCCAA GTGATTCTGG CTGGCTCACA GAACACTGT CCAAAGCCCA AATAATAAAT TCGGCGGCAA CTTGACCATA ACTIMCCATA TGGGCCTGG GAACTMIGTT GTGGTTGGCA GAGCAGGGG AAAATCAGCG GAGTTCTTGC TCGGAATTGT 1500 1560 GARCHARTT GTGTTCCCA CAGCACCGA ANATCAGCG GAGTTCTTC TCUGANTCT 120 CCTGANANTC CAGGACATG ACAGCACCT GAGGACATG CAGCACCA GAGTAGAGG 1680 AGGCCTTCA GAACATGGT CCCAACAAG CATTTCAAC AGATAGCTC AGCAGTATG 1740 GTACTAGCA CCCAGGGGCC TTACGTGGA TTGGAGAAAG GGGACTGG GGAGGACACA 1800 CCCCACAGG CCCTTACTGG GATGCAGGA GAGGAGTGA CTTGATGGAC TATTTTACCT 1860 10 CCCCCCCC AGTCCTCCC GGGGGACTTC AAGCTGGAAAT GCAGAGCTTA GAAAGGAGTG 1980 15 GGATAATTAT GGGGTGTGAG GTGCATTGCC CTCTAAATCT TTAAACAAGC AATTGGCAGT 2040 ACCCCGTGAA ACCTTTCCTT CTCCTACTCG GCCACCTCCC ACCAACCTGG CATCGTTCCT 2100 ACCCCGGGAG ACCTITECTT CTCCTACTCG GCAAGCACC ACCACCTGG CATGATCATTS
CCCCGGGAGCT AGCCACCTTC AGAAAGCACA TACAGCATCC TTGCTGCCAA ACCACCTATS
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Seq ID NO: 327 Protein sequence: Protein Accession #: BAB85075.1

25 1 2 31 41 51

MAYYORREVE TELLEPHON PETILERICA MERTERIET PAROSIQOK LIGERILANY
THEREGOLPO GENERILADI SEPTIOGOSA ROCHERIA SILVENENS 100
30 OKASTERRE MOCONIVOV IDRELIPHOS KOLFWERIN MERTERIE MERITARIA SILVENENS 100
MERICARIA, TYPURAZIO YRREMETI SIMBOWNINGT BRIGHERIS GENERICTUR 100
KROLINERIO GENERICOTO PORTIVATICA SILVENTINO SILVENTINO 100
KROLINERIO GENERICOTO CHIPATRICI SILVENTINO THILBRIGHO DENERICOTO MERICATION 100
KRI. TAGGERINA DIVIVIOLITY ANTERNILAZI DARFILORY ILAGGERICO 400

KRI.

Seq ID NO: 328 DNA sequence Nucleic Acid Accession #: BC017490.1

Nucleic Acid Accession #: BC017490. Coding sequence: 74-2788

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	CCTAGGCACA	GAGGGGCCCC	TGGAGGAAGA	AGAGGATGGA	GAGGAGCTCA	TTGGAGATGG	300
	CATGGAAAGG	GACTACCGCG	CCATCCCAGA	GCTGGACGCC	TATGAGGCCG	AGGGACTGGC	360
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	GTATGACAGC	GATGAGGAGG	ACGAGGAGCG	CCCTGCCCGC	AAGCGCCGCC	AGGTGGAGCG	540
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	TCTCAAAGGC	CACTCTGTGC	GCGAGTGGGT	GAGCATGGCG	GGCCCCCGGC	TGGAGATCCA	660
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	CTTGGCAGCC	AGGGAGCACG	TGCTGGCCTA	CTTCCTGCCT	GAGGCACCGG	CGGAGCTGCT	840
	GCAGATCTTT	GATGAGGCTG	CCCTGGAGGT	CGTACTGGCC	ATGTACCCCA	AGTACGACCG	900
	CATCACCAAC	CACATCCATG	TCCGCATCTC	CCACCTGCCT	CTGGTGGAGG	AGCTGCGCTC	960
	GCTGAGGCAG	CIGCATCIGA	ACCAGCTGAT	CCGCACCAGT	GGGGTGGTGA	CCAGCTGCAC	1020
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	GATCTTTGCC	AGCATTGCTC	CTTCCATCTA	TOGTCATGAA	GACATCANGA	GAGGCCTGGC	1560
		TTCGGAGGGG					1620
70	TATCAACGTG	CTCTTGTGCG	GAGACCCTGG	CACAGCGAAG	TCGCAGTTTC	TCAAGTATAT	1680
	TGAGAAAGTG	TOCAGOOGAG	CCATCTTCAC	CACTGGCCAG	GGGGCGTCGG	CTGTGGGCCT	1740
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	CTTTGACATC	CIGIGIGIGG	TGAGGGACAC	CGTGGACCCA	GTCCAGGACG	AGATGCTGGC	2100
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00	GGCCAATGGC	AGCGCTGCTG	AGCCCGCCAT	GCCCAACACG	TATGGCGTGG	AGCCCCTGCC	2220
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	CCACGCGCGC	ATCCATCTGC	GGGACTATGT	GATUSAAGAC	GACGTCAACA	TGGCCATCCG	2460
85	CGTGATGCTG	GAGAGCTTCA	TAGACACACA	GAAGTTCAGC	GTCATGCGCA	GUATGCGCAA	2520
	GACTTTTGCC	CGCTACCTTT	CATTCCGGCG	TGACAACAAT	GAGCTGTTGC	TCTTCATACT	2580
	GAAGCAGTTA	GTGGCAGAGC	AGGTGACATA	TCAGCGCAAC	CGCTTTGGGG	CCCAGCAGGA	2640
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		TTTTATGACA					276
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_	TGAACTCGGG	GTACTAGGGT	CAGGGCTTAT	AGCAGGATGT	CTGGCTGCAC	CTGGCATGAC	294
5	TGTTTGTTTC	TCCAAGCCTG	CTTTGTGCTT	CTCACCTTTG	CCTCCCATCC	CITGCCAGTG	300
	TGTCTTACTT	GGTTGCTGAA	CATCTTGCCA	CCTCCGAGTG	CTTTGTCTCC	ACTCAGTACC	306
	TTGGATCAGA	GCTGCTGAGT	TCAGGATGCC	TGCGTGTGGT	TTAGGTGTTA	GCCTTCTTAC	312
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10	TCTGTGCCCC	TGTGGTGGAA	GAGGGCACGA	CAGTGCCAGC	GCAGCGTTCT	GGGCTCCTCA	330
	GTCGCAGGGG	TGGGATGTGA	GTCATGCGGA	TTATCCACTC	GCCACAGTTA	TCAGCTGCCA	336
	TTGCTCCCTG	TCTGTTTCCC	CACTCTCTTA	TTTGTGCATT	CGGTTTGGTT	TCTGTAGTTT	342
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15 Seq ID NO: 329 Protein sequence: Protein Accession #: AAH17490.1

20	GPLERREDGE DREAGRGL/GR	11 ASSPAQRERG ELIGDSMERD MREGLLYDSD	YRAIPELDAY BEDEERPARK	EARGLALDDE RRQVERATED	DVEBLTASQR GEEDEEMIES	EAAERANRQR IENLEDLKGH	60 120 180
25	EHVLAYFLPE HINQLIRTSG PEVMMEETIY NYDGSINTAN	PRLEIHHRFK APAELLQIFD VVTSCTGVLP QNYQRIRIQE GFPVFATVIL	EAALEVVLAM QLSMVKYNCH SPGKVAAGRL ANHVAKKONK	YPKYDRITNH KCNFVLGPFC PRSKDAILLA VAVGELTDED	IHVRISHLPL QSQNQEVKPG DLVDSCKPGD VKMITSLSKD	VEELRSLRQL SCPECQSAGP BIELTGIYHN QQIGEKIFAS	240 300 360 420 480
30	SRAIFTTGQG HEAMEQQSIS CVVRDTVDPV KKYIIYAKER	IKRGLALALF ASAVGLTAYV ISKAGIVTSL QDENLARFVV VHPKLNQMDQ VNMAIRVMLE	QRHPVSREWT QARCTVIAAA GSHVRHHPSN DKVAKMYSDL	LEAGALVLAD NPIGGRYDPS KEEEGLANGS RKESMATGSI	RGVCLIDEFD LTFSENVDLT AAEPAMPNTY PITVRHIESM	KMNDQDRTSI EPIISRFDIL GVEPLPQEVL IRMAEAHARI	540 600 660 720 780 840
35		FGAQQDTIEV					900

Seq ID NO: 330 DNA sequence Nucleic Acid Accession #: M17254 Coding sequence: 257-1645

40							
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		GAACCAAGGG					240
		AAGGACATGA					300
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		CACATGCCAC					660
		ACCCTATGGA					720
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	TCATTATGTG	GGGGCTTTGT	TCTCCACAGG	GTCAGGTAAG	AGATGGCCTT	CTTGGCTGCC	2700

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AGGORGE GRITTIGGET AGGORGECT CAGITITICET TEMETOGOG
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AGGARGATARA AGGARGATA CAMITORNE CHORANTE TITITICOCOC TITITANIA 220
TACANATORA AGGITACHA TOTALAGATO CAGAMUTAC GRAMATURA GRAMAT 5

10 Seq ID NO: 331 Protein sequence Protein Accession #: AAA52398 Protein Accession #:

MOTOYPERA HIKEALSVYS EDGELFECKY GTERLAKTEM TASSSEDTED TERMESRAVED 60 (MOLOGRAM VITINEELENS DIELENS ANALONA VESSTETTEM TERMESRAVED 60 (MOLOGRAM VITINEELENS DIELENS ANALONA VESSTETTEM TERMESRAVED 60 (MOLOGRAM VITINEELENS DIELENS ANALONA VESSTETTEM TERMESRAVED 60 (MOLOGRAM VITINEELEN 15 20

Seq ID NO: 332 DNA sequence 25 Nucleic Acid Accession #: NM_000020 Coding sequence: 283-1794

	couring sect	Adica, Ada-					
	1	11	21	31	41	51	
	î	11	ī*	ĭ-	i	Ī -	
30	100222000	TTATTAGGAG	CONCERCATOR	NOCTODOCCA.	GGCAGGAAGA	CCCNGGAATA	60
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	TCTGAGCAGG	GCGACACGAT	GTTGGGGGAC	CTCCTGGACA	GTGACTGCAC	CACAGGGAGI	900
45	GGCTCAGGGC	TCCCCTTCCT	GGTGCAGAGG	ACAGTUGCAC	GGCAGGTTGC	CTTGGTGGAG	
45	TGTGTGGGAA	AAGGCCGCTA	TGGCGAAGTG	TGGCGGGGCT	TGTGGCACGG	TGAGAGTGTG	960 1020
	GCCGTCAAGA	TOTTCTCCTC	GAGGGATGAA	CAGTCCTGGT	TCCGGGAGAC	TGAGATCTAT	
	AACACAGTAT	TGCTCAGACA	CGACAACATC	CTAGGCTTCA	TOGCOTCAGA	CATGACCTCC	1080
	CGCAACTCGA	GCACGCAGCT	GTGGCTCATC	ACGCACTACC	ACGAGCACGG	CICCCICIAC	1140
=0	GACTTTCTGC	AGAGACAGAC	GCTGGAGCCC	CATCTGGCTC	TGAGGCTAGC	TGTGTCCGCG	1200
50	GCATGCGGCC	TOGCGCACCT	GCACGTGGAG	ATCTTCGGTA	CACAGGGCAA	ACCAGCCATT	1260
	GCCCACCGCG	ACTTCAAGAG	CCGCAATGTG	CTGGTCAAGA	GCAACCTGCA	GTGTTGCATC	1320
	GCCGACCTGG	GCCTGGCTGT	GATGCACTCA	CAGGGCAGCG	ATTACCTGGA	CATCGGCAAC	1380
		TGGGCACCAA					1440
		TTGAGTCCTA					1500
55	GAGATTGCCC	GCCGGACCAT	CGTGAATGGC	ATCGTGGAGG	ACTATAGACC	ACCCTTCTAT	1560
	GATGTGGTGC	CCAATGACCC	CAGCTTTGAG	GACATGAAGA	AGGTGGTGTG	TGTGGATCAG	1620
	CAGACCCCCA	CCATCCCTAA	CCGGCTGGCT	GCAGACCCCGG	TCCTCTCAGG	CCTAGCTCAG	1680
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	AAGACACTAC	AAAAAATTAG	CAACAGTOCA	GAGAAGCCTA	AAGTGATTCA	ATAGCCCAGG	1800
60	AGCACCTGAT	TOCTTTCTGC	CTGCAGGGGG	CTGGGGGGGGT	GGGGGGCAGT	GGATGGTGCC	1860
	CTATCTGGGT	AGAGGTAGTG	TGAGTGTGGT	GTGTGCTGGG	GATGGGCAGC	TGCGCCTGCC	1920
	TRETTERROCCE	CCAGCCCACC	CAGCCAAAAA	TACAGCTGGG	CTGAAACCTG	ATCCCCTGCT	1980
	GTCTGGCCTG	CTCAAAGCGG	CAGGCTCCCT	GACGCCTGGC	TCTCTCCCCA	CCCCTATGGC	2040
	CAGCATGGTG	CACCCCCTAC	CACTCCCGGG	ACAGGATGCA	AAAGAGGCTC	CAGAGTCAGA	2100
65	GTGCCAAGCC	AGGGAATCCC	ACTCCCAGAC	TCAGAGCCCG	GGCCTGCACT	TTGCCCCCTG	2160
	COCTTGATCA	ACCCCACTGC	COCACCAGAG	CTGCCAGGGT	GGCACAGGGC	CCTGTCCAGC	2220
	CCCTGGCACA	CACTTOCCTG	CCAGGCCTCA	GCCTCTAGCA	TAAGCTCCAG	AGAGCCAGGG	2280
	CCCATCACTT	TOTOTOTOTO	CATTTGTATC	TCAGCTCCAT	GATGCCTTGG	GCTTTCTGTC	2340
	TOCTOBACAS	GAGTGCAGCT	TOTTCAATCT	CAGCTGCCTG	AGAGAGCTGG	GGCCTGACTT	2400
70	ACTROGGCAT	TARATOCTAR	GAGGTCCTAC	TGAGGTGTGG	CAGGATCACA	GGCCAGTGGA	2460
, ,	ANAROGOCAG	GTCAGATGGG	CARGGCCCAG	GACTTTCAGA	TTAACTGAGA	GGATATCGAG	2520
	CCCAACCATC	GCACCOCCAA	COTTON	TOTCARGAGA	CCCAGGCCTG	ACCCCGGATG	2580
	TETROCECCAT	GTGACAAAAG	CACCCCTCTC	TCACCACCTT	TACTAL CALL	TTTTCCTTCT	2640
	TITIGOTO CAT	GACACGGAGT	TECCCOCACA	TTCTCCLGGC	TAGROTOCAR	TOTOCATCATC	2700
75	CONCOMONO	ORCACOGAG1	CCTCCCCCCC	TOTALATORT	CTCTTCCCTC	AGACTCCCGA	2760
15	CONGCIONCE	TTACAGGCAC	ATTOCCAGGI	COCHOCOGO	THENTON	TTACTACAAA	2820
	GTAGCTGGGA	CCATGCTGGC	AIGCCACCAI	CTCTGGCTAA	TCACCTCACC	TOTTOTACCT	2880
	LAGGGITTCA	CCCAAAGTGC	CAIGCIGGII	CICGARCICC	ATOCOCCOTO	COCYCCACCA	2940
	ACCTCAGCCT	TCTACATATT	TGGGGTTACA	OGIGIGAGCC	ATCGCGCCTG	GCCAGGACCT	3000
80	TIGITTCTTA	GACACTTCAG	GGANGA TTIG	S.CCIGATGT	CCTTTGMGGC	TOTAL STRUCT	3060
00	CTAGTTCTCT	GACACTTCAG	CUTATATUAC	AGCIAACTIC	CLASSICICA	TCIAITCCTT	3120
	ATGCTCCAGC	CCCTGGCAAT	TIGUCTUAAG	AIGGGGGTTT	GRAAATAACT	LIACUTUACT	3120
	CAAGGAGTGT	CTGGAGCACC	TUUTAGTUTA	ASTUTGUARG	CTGCAGTTCT	TUCCTAAAAC	
	CATGCCAGTG	GCCACCCTTG	GGCTCAGACA	GCTCTGGGCC	TTTTGACCAC	AAGCCAGCCC	3240
0.5	CTCGCCCTCT	CTGTGGCATA	GTCTTCTCTG	CCCCAGGACT	GCAGGGCGGC	TTOUTCCAAG	3300
85	GCTTCCAAGG	CTCANAAGAA	ATTTGGCTCC	ATCCAAGAAG	GCTCCAGCTC	CCCTACTGGC	3360
	CCCTGGCTTC	AGGCCCACAC	CCCTGGGCCA	GGSCCAGAGA	GIGIGICICA	GGAGAATTCA	3420
	ATGGGCTCTA	GAGAGACACA	CAGAAAGTTT	GGGCATTTGG	GAAATTTTCA	AGGICIGTATG	3480

	WO 02/	GTATGGHGCA	GGTTGTCCTG	GTCCYKGGGT	GCAGGGAAGT	GOGCTGCAGG	3540
5	GACAAGGACA GCAGTGAAGA GCATCTTATG CATTGTGCAA TGGATGGGCT AATCCACCCA	GGAGGGGAGC GCCCAAGGT AAGCTCTCCC TGTGTCTTCC GGCTCGGAAG AGGTTCCCAG GCCCACGAAT	TGGGAAGACC CGCTCCTGCT ACCATCCTCA AGAACCAGGA ATCATTAGGG CATCTCCCTC	TGGCCTTAGT GTAATGACCC TGGTGGCACT AGTGAAACTG CAGAGTTTGC TTTGAAGGAT	CGTCCTCAGC AGAGTAGCCT TTTCTAGGCC GGTGAAAACA ACGTCCTCTG TTTWATTTCT	CTAGGGCAGG CCCCAGGCCG TGTCTCCCAG GAAAGCTCAA GTTCACTGGG ACTGGGTTTT	3660 3660 3720 3780 3840 3900 3960
10	TGGAAAATCC GAGAAGGGG ATGCTTCTGT AGACGCTGTT	CCTGCTGAGA CTAAGAGAAG CCCAATGGCC CTGAGTGCAG TGTGGGAGCA CCTGAAAAAA	GCCTGGGGGA AGGGAGTGAA GAAGGTGTTC CTGGGCTCAT	MAGGAAKTGG GGAGGTGGCG	AGTGACAGGG TTGCTGAGAG	CAGTCTGCAC	4020 4080 4140 4200 4260
15		333 Proteir		11			
20	RHPQEHRGCG	11 LMLLMALVTQ NLHRELCRGR ALVALGVLGL	PTEFVNHYCC WHVRRROEKO	RGLHSELGES	SLILKASEQG	DTMLGDLLDS	60 120 180
25	DCTTGSGSGL RETEIYNTVL RLAVSAACGL YLDIGNNPRV YRPPFYDVVP	PFLVCRTVAR LRHDNILGFI AHLHVEIFGT GTKRYMAPEV NDPSFEDMKK	QVALVECVOK ASDMTSRNSS QGKPAIAHRD LDEQIRTDCF VVCVDQOTPT	GRYGEVWRGL TQLWLITHYH FKSRNVLVKS ESYKWTDIWA	WHGESVAVKI EHGSLYDFLQ NLQCCIADLG FGLVLWEIAR	FSSRDEQSWF RQTLEPHLAL LAVMHSQGSD RTIVNGIVED	240 300 360 420 480
30	TALRIKKTLQ	KISNSPEKPK	VIQ				
35	Nucleic Aci	334 DNA sec id Accession mence: 108-) #: X74 0041	.26.1			
	100000m000	11 CGTGCCGGCC CTGCCAGAGC	TACCOCCAGO	CCCCTTCTGG	CCCCSSSSSTC	CCTGCCCTTC	60 120
40	ACATCGAAGA AAGTGAAGTT AAGAACGTTC	TTTGCCAGAG GCAGAGACAA TGGAGAGGAT	AAGGAAAAC CAAGTGTCTA CCTCTAGTAA	TGAAAATGGA AATGTTCTGA AGGGAATTCC	AGRAGACAAG AGRAGACAAG	AACTATATTG AACCCCTTTA	180 240 300 360
45	ACANTTATGG	TGTTTTAGTT AGGAGACTTT TCTTTGCTCA AAATAAGAAC AAGTTTTGTC	ATTACTTGAG	AAACCAACAT ATATAGATAG TTTTTTTAAGA CATGACACTT	GCTTTTTANG GGTTATGTAT GAGCAGAGAG CTTTCAGTAT	GAAGGAAGAA AAAAGCATAT TATCAGATGT ATTGCTTGAT	420 480 540 600
50	Seq ID NO: Protein Acc		NP_0041				
	1	11	21	31	41	51	
55	MPALHIEDLP KNPFKEKG9C	AIS	ÖLRKEVKLQR	QQVSKCSEEI	KNYIEERSGE	DPLVKGIPED	60
60	Nucleic Ac	336 DNA se id Accessio uence: 555-	n #: NM_005 1940				
65	CAAGCTCTGC TTCCCACCTT	11 ACAACCTCTC TAACTGAATC GCTTGTGGGT TCACAAAGAA	TCATCCTAAT AAATCTCTTC	TGCAGGATCA TGCGGAATCT AGCTGGACTG	CATTGCAAAG CAGAAAGTAA GGTCTTGACC	AGTTCCATCC CCTGGAATTT	60 120 180 240
70	AAGAAATTOT GACAATTOTG GAATAATAAA AAAGAAAACT	TARAGACAAT CATATCGTCT AACCCATACT ACTACAACTT	GTCAAATATG AATAATAAAA AGCCTATAGA GACAAGACTG	ATCCAAGAGA ACCCATACTA AAACAATATT CTGCAAACTT	AAATGTGATT GCCTATAGAA TGAAAGATTG CAATTGGTCA	TGAGTCTGGA AACAATATTT CTACCACTAA CCACAACTTG AGCATATTTC	300 360 420 480 540
75	ATTTGGGCTT TTATGATTCT TTACTAGAAA CCATTCAACA	TGTTACAGCA TGTTACAGCA TARAATCATG AGCAGAAGGC	AAAAAGTGTA GAATTAGAAG ACAGCTCAAT GTTTACTGCA	AGAGTOCTGA ATGAATGTTA ACAGAACCTG	GGACTCAATT CCAAAAGATT GGATGGATGG	CAGTTGGGAG ATGCAAGACC CTCTGCTGGA	600 660 720 780 840
80	ATCCATCAGA CAAGCAACAG AGACTGCACT	AAAAGTTACA AACATGGACA AAATTTGTTT	AAGATCTGTG AATTATACCC TACCTGACCA	ACCANGATEG AGTGTANTGT TANTTGGACA	TAACACCCAC CGGATTGTCT	GAGAAAGTGA ATTGCATCAC	900 960 1020 1080
85	TACACAAAAA CTGCAGTGGC AGTTCATTCA	CARCARCCAG TOTALCCAG	TCATTTGTTT GCCTTAGTAG ATGGGCTGTA	GTAACTCTGT CCACAAATCC ATTACTTTTG TTGCAGAGAA	TGTAACAATC TGTTAGTTGC GATGCTCTGT GCAACATTTA	ATTCACCTCA AAAGTGTCCC GAAGGCATTT ATGTGGTATT	1140 1200 1260 1320 1380

	WO 02/						
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	GCCCAATTTG	TGCTGCTTTA	CTGGTGAATC	TTTTTTTTTTT	GTTAAATATT	GTACGCGTTC	1560
	CATCACCAA	TATCTTGGTG	ACACACCAAG CCATTGCTTG	CCATTGAATT	TOTOTTGATT	CCATGGGGAC	1620
5	CTGRAGGRAR	GATTGCAGAG	GAGGTATATG	ACTACATCAT	GCACATCCTT	ATGCACTTCC	1680
-	AGGGTCTTTT	GGTCTCTACC	ATTTTCTGCT	TCTTTAATGG	AGAGGTTCAA	GCAATTCTGA	1740
	GAAGAAACTG	GAATCAATAC	AAAATCCAAT	TTGGAAACAG	CTTTTCCAAC	TCAGAAGCTC	1800
	TTCGTAGTGC	GTCTTACACA	GTGTCAACAA	TCAGTGATGG	TCCAGGTTAT	AGTCATGACT	1860
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10	CAGAAAATTT	ATATAATTGA	AAATAGAAGG TGACTCTGTA	ATGGTTGTCT	TTCAATATTA	TGCTTCTCCT	2040
	AACTCAAGGA	TRANCARCAC	CCTTCACATG	ANATTROTAG			2100
	ATCCACCTCT	ATGTGGGAAA	AAAGAAATCC	TGGTTTGTAA	TGTTTGTCAG	TARATACTCC	2160
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	ANTAGAGTOT	GGAATGCT					
30	Sec ID NO.	337 protein	n semience				
50	Protein Acc	ession #:	NP_0057	86.1			
	1	11	21	31	41	51	
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35	MEKKCTLYFL	VLLPFFMILV	TABLEESPED	SIQLCVTRNK	INTAQYECYO	KIMQDPIQQA	60
	EGVYCHRTWD	GHLCWNDVAA	GTESHOLCPD	YFQDFDPSEK	ALKICDODON	WFRHPASNRT	120
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40	IVVAVFAEKQ	HENWYYFEGW	KVTHQABSNL	ATAKSBITAD	NUMBER	T.T DWPD DOWN	360
40	ABBUNDALAR	TIMHEOGIAN	STI FCFFNGE	VOATLERNWN	OYKIOFGNSF	SNSEALRSAS	420
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				HVDDRESODI			
45	Seq ID NO: Nucleic Ac	338 DNA se	quence n #: NM_001	795			
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45 50	Seq ID NO: Nucleic Ac: Coding seq	338 DNA seld Accession mence: 25-2	quence n #: NM_001 379 21 GAAGATGCAG	795 31 AGGCTCATGA	41 TGCTCCTCGC	CACATCGGGC	60
-	Seq ID NO: Nucleic Ac: Coding sequents 1 GCACGATCTG GCCTGCCTGG	338 DNA set Id Accession sence: 25-2	quence n #: NM_001' 379 21 GAAGATGCAG	795 31 AGGCTCATGA GTGGCAGCAG	41 TGCTCCTCGC CAGGTGCTAA	CACATOGGGC CCCTGCCCAA	120
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50	Seq ID NO: Nucleic Act Coding seq 1 GCACGATCTG GCCTGCCTGG CGGGACACCC CAGATGCACA	338 DNA se Ld Accession dence: 25-2 11 TTCCTCCTGG GCCTGCTGGC ACAGCCTGCT TTGATGAAGA GTCGCAAGAA	quence n #: EM_001' 379 21 GARGATGCAG AGTGGCAGCA GCCACCAC GARAARACAC TGCCAAGTAC	31 AGGCTCATGA GTGCAGCAG CGGCGCAAA TCACTTCOCC	41 TGCTCCTCGC CAGGTGCTAA AGAGAGATTG GAGAATATGT	CACATCOGGC CCCTGCCCAA GATTTOGAAC CAAGATCAAG GGGCAAGGTC	120 180 240 300
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50	Seq ID NO: Nucleic Ac: Coding sequil GCACGATCTG GCCTGCTGG CGGGACACCC CAGATGCACA TCCAGGGTGA ATTCCAGGGTGA	338 DNA set de Accession mence: 25-2 11 TTCCTCCTGG GCCTGCTGCT ACAGCCTGCT TTGATGAAGA GTCGCAAGAAA ATGCAGAGAA ATGCAGAGAAAAGACCTCAC	quence n #: NM_001' 379 21 GAAGATGCAGCA GCCCACCCAC GAAAAACACC TGCCAAGTAC AGGAGACTG TGCTTCATT TGCTTCATTCA	31 AGSCTCATGA GTGGCAGCAG CGGCGCAAA TCACTTCCCC CTGCTCAAAG TTCGCCATTG GTGGACAAGG	41 TGCTCCTCGC CAGGTGCTAA AGAGAGATTG ATCATGTAGG GAGAATATGT ACACTGGTA ACACTGGTA ACACTGGTA	CACATCOGGC CCCTGCCCAA GATTTGGAAC CAAGATCAAG GGGCAAGGTC CCOGGAGAAT AAACCTGGAG TGTGTTCACG	120 180 240 300
50	Seq ID NO: Nucleic Ac: Coding sequing sequing GCACGATCTG GCCTGCCTGG CGGGACACCC CAGATCACA TCMAGGTGA TTCCGGGTCG ATCTTCAGAT ACTCCTTCCA	338 DNA set di Accessio: sence: 25-2 11 TTCCTCCTGG GCTGCTGCT ACAGCTGCT TTGATGAAGA GTGCCAGGAA ATGCAGAGAAC ACCACCTCAC GCTTCACCAT TCAATGCGTC	quence n #: NM_001 379 21 GARGATGCAG AGTGGCAGCA GCCCACCAC GCCAACCAC GCCAACTAC TGCCTAGTAC TGCTGTCAT CAAAGTTCAT CATACTTCAT GTGCTGTAGT	31 AGGCTCATGA GTGCAGCAG CGGCGCCAAA TCACTTCGCC CTGCTCAAAG GTGGACAAGG GACTGGACATG TCGCCGGCTG	41 TOCTCCTOSC CAGGTGCTAA AGNGAGATTO ATCATGTAGG GAGAATATGT AGAGCTGGA ACACTGGCC TOGGGACCTC	CACATCOGGC CCCTGCCCDA. GATTTOGAAC CAAGATCAAG GGGCAAGGTC CCOGGGAGAAT AAACCTGGG TGTGTTCACG AGTCATCTCT	120 180 240 300 360 420 480 540
50	Seq ID NO: Nucleic Act Coding sequitions 1 GCACGATCTG GCCTGCCTGG GCGGACACCC CAGATCACAC TCCCGGGTGG ACTCTCCAGGT ACTCCTCCA CATCGGTTGT TGCAGGCAG	338 DNA set di Accessionence: 25-2 11 TTCCTCTGG GCCTGCTGG ACAGCTGCT TTGATGAAGA GTCGCAAGAA ATGCAGAGAC ACCACCTCAC GCTTCACCAT TCAATGCGTC TGGATGCAGA	quence n #: NM_001 379 21 GARGATGCAG AGTGGCAGCA GCCAACCAC TGCCAAGTAC AGGAGACATC TGCTTCATT CAAAGTTCAT CGTGCCTCAG GGACCACCAC GGACCACCAC GGACCACCAC TGCTGAT	31 AGGCTCATGA GTGGCAGCAG GGGGCCAAA TCACTTCCCC CTGCTCAAAG TTCGCCATTG GTGGCAAGG GACGTGAACG GACGTGAACG GTGGGCAAGG	41 TOCTCCTOSC CAGGTGCTAA AGAAGATTIG ACAGGCTGGA ACACTGGCC TOGGGACCTC ACGCCTCTGT	CACATCOGGC CCCTGCCCAA GATTTOGAAC CAAGATCAAG GGGCAAGGTC CCOGGAGAAT AAACCTGGAG TGTGTTCAG AGTCATCTCT CATGTACCAA	120 180 240 300 360 420 480 540 600
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50	Seg ID NO: Nucleic Act Coding segui 	338 DNA seld Accessionence: 25-2 11 TTCCTCCTOG GCCTGCTGGC ACAGCTGCT TTGATGASAGA ATGCAGAGAC ACCACCTCAC GCTTCACCAT TCAATGCCTC TCAATGCCTC TCAATGCCTC TCAATGCCAGA ACCACCTCAC GCTTCACCAT TCAATGCCAGA ACCACGAGAA ACCACCACACA ACCACGAGAA ACCACCACACA ACCACGAGAA ACCACCACACA ACCACGAGAA ACCACCACACA ACCACCACACA ACCACCACACA ACCACC	quence n #: NM_001' 379 21	31 1 ASSCTCATOA GTOGCAGCAG GTOGCACAAA TCACTTCOCC GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAG GTOGCAAAATCCG GTOGCAAAATCCG GTATAAATCCG	41 	CACATCOGGC CCCTGCCCAA GATTTOGAAC CAAGATCAAG GGGCAAGGTC CCOGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCTCT CATGTACCAA CACAATAACG GCGAGAATGCC	120 180 240 300 360 420 480 540 600 660 720
50	Seq ID NO: Nucleic Ac: Coding sequipment of the control of the con	338 DNA sed Accession sence: 25-2 11 TTCCTCCTGG GCCTGCTGGC ACAGCCTGCT TGATGAAGA ATGCAGAGAC ACCCTCAC TCAATGCCTC TGGATGCAGA GGAAGAGAA ACGAGGAAGAAA ACGAGAGAAA GGAAAGAGTA ACGAGAGAGAAAGGTA ACGAAGAGAAAGGGAAGGG	quence n #: NM_001: 379 21 GAAGATGCAG GCCACCCAC GAAAAACACC TGCTGTCATT TGCTGTGTTCATT TGAAGTTCAT CGTGCCTGAG CGACCCAC TTTTGCCTGAG GCACCCACT TTTTGCCATC GCAGCCAGG GGGCAGGCCAGG	31 	41 	CACATOGGC CCCTGCCCAA GATTTGGAAC CAAGATCAAG GGGCAAGGTC CCGGGAGAAT AAACCTGGAG TGTGTTCAAG AGTCATCTCT CATGTACCAA CACAATAACG GCGAGAATGCC AGACATCAAT	120 180 240 300 360 420 480 540 600 660 720 780
50	Seq ID NO: Nucleic Ac: Coding seq Genciarting Genciarting Genciarting Genciarting Articognic Articognic Articognic Articognic Articognic Giacagona Articognic Giacagona Articognic Giacagona Articognic Giacagona Articognic	338 DNA seld Accessionence: 25-2 11 1 TTCCTCCTGG GCCTGCTGTGTGAGGAAAAAAAAAAAAAA	quence n #: EM_001' 379 21	31 	41 	CACATOGGC CCCTGCCCAA GATTTOGAAC CAAGATCAAG GGGCAAGGTC CCGGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCCTA CACATAAACG GCGAGATGCC AGGAATGCCAA AGACACCGGT	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	Seq ID NO: Nucleic Ac: Coding sequence Goacgators Goacgators Goaggacaccc CAGATGACA TOMAGGTGA ATTCAGGGTG ATTCAGGGTG ATCTAGGGTG ATCTAGGACACACA CAGCACACAC CAGCACACTCC GACAACTTCC GACAACTTCC GTGGGCACC	338 DNA set di Accessionalence: 25-2 11 TTCCTCCTGG GCCTGCTGGC ACAGCTGGC TTGATGAAGA ATGCAAGAG ATGCAAGAG ATGCAAGAG ATGCAAGAG ATGCAAGAG ATGCAAGAGAG GCTTCACCAT TCAATGCGTC TGGATGCAGA GGAAGAGTA ACCGAAGAGAA GGAAGAGTA ACCGAAGAGAA CCTGTTGAC CCTTGTTCAC CTGTTGGAC CTGTTGGAC CTGTTGGAC	quence n #: NM_001' 379 21 GAAGATGCAGA GCCCACCAC GCAGCCAC TGCCAGTAC TGCTOTCATT CGTGCCTGAG GAACACGC GGAGCCAG GGAGCAG GGAGCAG GGAGCAG TTTTTGCATC GCAGCCAG GGAGCAG TTTTTTGCATC TTTTTGCATC TTTTTGCATC TGCAGCAGC TGCTGAGCAG TTTTTTTTTT	31 AGGCTCATGA GTGGCAGCAG GGGGCCAAA TCACTTCGCC CTGCTCAAAG TCGTCGACATG GACGTGAAAGG TCGTCGGCTG GTGGGAGACC GATAATTCTG TATGAGATGG ACCTGGTGG TACAGATTG ACCGTGCTGG TACACATTG GAGGACCCAG	41 TGCTCCTCGC CAGGTGCTAA AGAGAGATTG ACACTGGGC TGGGGACTGGA ACACTGGGC TGGGGACTCTG ACACCTCTGT TGGTGGAGGC TCACCTCTGC TCACCTCTGC TCACCTCTGCA TCACCTCTGCA	CACATCOGGC CCCTGCCCAA GATTTGCAAC CAGGATCAAG GGCAAGGTC CCOGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCTCT CATGTACCAA CACAATAACG GCGAGATGCC AGACATCAAT AGACACCCGT GAACCCGGATGAACACGAACACCGGAACACCCGGT GAACCGGGATGAACACGAACACCGGAACACCCGGT	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	Seq ID NO: Nucleic Ac: Coding seq: GCACGATCTG GCACGATCTG GCACGATCACA TOAMGCGTGA ATTCCGGGTG ATTCTCAGAGT ACTCCTTCCA ATCGGTTGT GTGACAGCA ATCCTGAGAG ACCGTAGAGCA ACCGTAGAGC AAAAGCTTGC GAGACTTCC GTGGCACCT ACTGCTGACACT ACTGCTACACT ACTGCTACACT ACTGCTACACT ACTGCTACACT ACTGCTACACT ACTGCTACT ACTGCTACACT ACTGCTACT ACTGCTAC	338 DNA seid Accessionerce: 25-2 11 1 TECRECTOS GCCTGCTGGC ACAGCTGCT TGATGAAGA ATGCCAAGAA ATGCAAGAA ACGCTCAC TCAATGCCTGCT TGGATGCAGGAAGGGAATGCCTGGATGCAGGAGGGGGGACTC CTTGTGTGGGGGGACTC CTTGTGTGGGGGACTC CTTGTGGGGGACTC CTTGTGGGGGACTC CTTGTGGGGGACTC CTTGTGGGGACTC CTTGTGGGGGACTC CTTGTGGGGGACTC CTTGTTGGGGACTC CTTTTTGGGGACTC CTTTTTTGGGGACTC CTTTTTTTGGGCACATTTTTTTTTT	quence n #: NM_001* 379 21 GARGATGCAGCA GCCCACCAC GCGAGCAGCA TGCGMGTAC TGCTGTGAT TGCTGTGAT TGTGCTGAG GSACCACC TTTTGCCACG GGGGACGACG GCCAGCACG TGCGAGCACG TGCGAGCACG TGCGAGCACG TGCGAGCACG TGCGAGCACG TGCGAGCACG TGCGAGCACG	31 AGGCTCATGA GTGGCAGCAG GTGGCAGCAG GTGGCATGG GTGGCATGG GTGGGCATGG GACCTGAACG GACCTGAACG GACGTGAACG GAGGAGACC GATAATTCTG ACGGTGCTGGTG ACGGTGCTG ACGGTGCTGC ACGGTGCTG ACGGTG	41 TOCTCOTOSC CAGGTSCTAA AGAGACATTOS ATCATOTTAGS GAGACATGGC TOGGGACCTC ACCCTCTGT GACCTATTAT TOGTGGAAGC TCGTCCTGCA ATCAGCCTCCA ATCAGCCTCCA ATCAGCCTTCA	CACATOGGC CCCTGCCCAA GATTTOGAAC CAAGATCAAG GGCAAGGTC CCGGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCTCAC ACCAATAACG GCGAGATGAC AGACATCATA AGACACCGGT GAACCGGATG GACAACCCGT GAACACCGGATG	120 180 240 300 360 420 480 540 600 720 780 840 900
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	TCTGACGTGG	ATTACGACTT	CCTTAACGAC	TGGGGACCCA	GGTTTAAGAT	GCTGGCTGAG	2340
	CTGTACGGCT	CGGACCCCCG	GGAGGAGCTG	CTGTATTAGG	CGGCCGAGGT	CACTCTGGGC	2400
	CTGGGGACCC	AAACCCCCTG GACTCCCCAG	CAGCCCAGGC	CAGTCAGACT	CCAGGCACCA	ACCTCATCAG	2460 2520
5	CCTTGGGATA	GCAAACTCCA	GGTTCCTGAA	ATATCCAGGA	ATATATGTCA		2580
	TTCTCAAATG	CTGGCAAATC	CAGGCTGGTG	TTCTGTCTGG	GCTCAGACAT	CCACATAACC	2640
	CTGTCACCCA	CAGACCGCCG	TCTAACTCAA		TGGCTCCCCA AGGGTCCCTG		2700 2760
		GAGGTCCTGG	TGCTTATCTG	CCTGGAGGCA	AAGGCCTGGA	CAGCTTGACT	2820
10			AGCCCATTCC	CANGGGAGAC	TGACCATCAT	GOCCTCTCTC	2880
	GGGAGCCCTA	GCCCTGCTCC	AACTCCATAC	TCCACTCCAA	GTGCCCCACC	ACTCCCCAAC	2940
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	CCTAAATAAA	GAAAAATCTT	TAGCCTGGGC	AACAAAAAA	niomerem.		
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		339 Protein	sequence	06			
	Protein Acc		NP_0017				
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33		SGACLGLLAV	1	NORDELICE I B	THRROKEDWI	MANAGETTAPPY	60
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	VIVDKDTGEN	LETPSSFTIK	VHDVNDNNPV	FTHRLFNASV	PESSAVGTSV	ISVTAVDADD	180
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	DYQDAFTIET	NPAHNEGIIK IFQQPFYHFQ	PMKPLDYEYI	QQYSFIVEAT	ARHSIGYSIR	PPAGNICACIVI	420
		KELDREVYPW	YNI.TVEAKEL	DSTGTPTGKE	SIVQVKIEVL	DENDNAPEFA	480
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	VVAILLCILT	ITVITLLIFL	RRRLRKOARA	HCKSVPEIHE	QLVTYDEEGG	GEMDTTSYDV	660 720
	SVLNSVRRGG	AKPPRPALDA YGYEGSESIA	RPSLYAQVQK	PPRHAPGARG	GPGEMAAMIE NDNGPPFKMI	ARTAGROPPE	720
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	GTGCTGCAGG	CGGCCAACGA	GAGGAACCTC	TOCACGOGGC	AGGGTATGGA	CCTGTCTGCC	960
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		CCTCCAGCAA	GAATGCCAGC	TGCTACTTTG	ACATOGAGTG CCAAGAAGAA	GUGTGAUCGG	1140 1200
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PCT/US02/12476

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TCTGCTTTCA GGAAAGCCC TCTTCCCAGC CAAGGAAGGA GTCTATGGGC CCCCGGGCC 65 1500 1560 TOGAGACTGA TCCTGAGCCC GCTCCTTGG GCTCCAGTTC TGCACACTTG ACAAACAAT 1620
GGGTGAAAGT CGGGGACTGT GATCTGCGG ACAGACCAG GGGTGCCTTG CTGCGGGAGT 1680 CCCTCTTGG CTCTAGTGAT GCATAG 70 Seq ID NO: 343 Protein sequence Protein Accession #: FGENESH predicted 75 MGKDFMTKTP KAPATKAKID KUDLIKLKSF CTAKETIIRV NSOPTOWOKT FAIYPSDKGV IARIYKELEQ IYKKKEPTET LETHFLSEPK GNCWPLGPRG DSWQLGGPSG ARABGEGGGT GLGKPAVEGG DRAPDTALRP RAGGIQVGSS SACGASENEA GVRPVPPLAG ALARAGRRRT 180 PHCRPCWLLG LGGLLQPAPR YHEAAGGRGG LHPARWGAQH RACGRRAARC ARAPAGRPRA 240 80 RRGLQRPAVL GRTGAQAFPL HPGERAFAGF LLAVLRPRES KRRIAAVGGG APTLHERAEM RGTPGHEKNGE ARSKEMECH LEANNSYLCKY GEVLUCEAFR PGAASNLSYR APPQLHEAAL DESPENTEVS ALCRGQLPIS VTCIADEIGA RHOKKSGOVI. CPCFGRYLEA GECAELPHICL 300 360 420 DDLGGFACEC ATGFELGEDG RSCVTSGEGO PTLGGTGVPT RRPPATATSP VPQRTWPIRV 480 DEKLGETPLV PEQDNSVTSI PEIPRWGSQS TWSTLQMSLQ AESKATITPS GSVISKFNST 540

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WO 02/086443 Seq ID NO: 344 ENA sequence Nucleic Acid Accession #: HM_012072 Coding sequence: 149-2107

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35		345 Protein	sequence	0.4			
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50							
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	CAGCTGGGCT	ACCCGCAGCA ACGACGTGAG	CCCCGGGCCTC	AATGCGCACG TACAACTCCA	GCGCAGCGCA TGACCAGCTC	GCAGACCTAC	600 660
	CAGCTGGGCT ATGCACCGCT ATGAACGGCT	ACCCGCAGCA ACGACGTGAG CGCCCACCTA	CCCGGGCCTC CGCCCTGCAG CAGCATGTCC	AATGCGCACG TACAACTCCA TACTCGCAGC	GCGCAGCGCA TGACCAGCTC AGGGCACCCC	TGGCATGGCT	660 720
70	CAGCTGGGCT ATGCACCGCT ATGAACGGCT	ACCCGCAGCA ACGACGTGAG CGCCCACCTA	CCCGGGCCTC CGCCCTGCAG CAGCATGTCC	AATGCGCACG TACAACTCCA TACTCGCAGC	GCGCAGCGCA TGACCAGCTC AGGGCACCCC	TGGCATGGCT	660 720 780
70	CAGCTGGGCT ATGCACCGCT ATGACCGCT CTTGGCTCCA TCTTCCTCCC	ACCCGCAGCA ACGACGTGAG CGCCCACCTA TGGGTTCGGT ACTCCAGGGC	CCCGGGCCTC CGCCCTGCAG CAGCATGTCC GGTCAAGTCC GCCCTGCCAG	AATGCGCACG TACAACTCCA TACTCGCAGC GAGGCCAGCT GCCGGGGACC	GCGCAGCGCA TGACCAGCTC AGGGCACCCC CCAGCCCCCC TCCGGGACAT	TGTGGTTACC GATCAGCATG	720 780 840
70	CAGCTGGGCT ATGCACGGCT ATGAACGGCT CTTGGCTCCA TCTTCCTCCC TATCTCCCCG	ACCCGCAGCA ACGACGTGAG CGCCCACCTA TGGGTTCGGT ACTCCAGGGC GCGCCGAGGT	CCCGGGCCTC CGCCCTGCAG CAGCATGTCC GGTCAAGTCC GCCCTGCCAG GCCGGAACCC GCCTGCCAG	AATGOGCACG TACAACTCCA TACTOGCAGC GAGGCCAGCT GCCGGGGCCCCA GCCGCCCCCA	GCGCAGCGCA TGACCAGCTC AGGGCACCCC CCAGCCCCCC TCCGGGACAT GCAGACTTCA GCACACTGCC	TGGCATGGCT TGTGGTTACC GATCAGCATG CATGTCCCAG CCTCTCACAC	660 720 780
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	CAGCTGGGCT ATGCACCGCT ATGCACCGCT CTTGGCTCCA TCTTCCTCCC TATCTCCCGG CACTACCAGA ATGTGAGGGC TGGGAGGGGT	ACCCGCAGCA ACGACGTGAG CGCCCACCTA TGGGTTCGGT ACTCCAGGGC GCGCCGAGGT	CCCGGGCCTC CGCCTGCAG CAGCATGTCC GGTCAAGTCC GCCTGCCAG GCCGGAACCC GCCCGGCACCG ACTGGAGGGG ACTGGAGGGG	AATGOGCACG TACAACTCCA TACTOGCAGC GAGGCCAGCT GCCGGGGGACC GCCGCCCCCA GCCATTAACG GGAGAAATTT	GCGCAGCGCA TGACCAGCTC AGGGCACCCC CCAGCCCCCC TCCGGGACAT GCAGACTTCA GCACACTGCC TCAAAGAAAA	TGTGGTTACC GATCAGCATG CATGTCCCAG CCTCTCACAC ACGAGGGAAA	660 720 780 840 900 960
70 75	CAGCTGGGCT ATGCACGGCT ATGCACGGCT CTTGGCTCCA TCTTCCTCCC TATCTCCCGG CACTACCAGA ATGTGAGGGC	ACCCGCAGCA ACGACGTGAG CGCCCACCTA TGGGTTCGGT ACTCCAGGGC GCGCCGAGGT GCGGCCCGGT CGGACAGCGA	CCCGGGCCTC CGCCTGCAG CAGCATGTCC GGTCAAGTCC GCCTGCCAG GCCGGAACCC GCCCGGCACCG ACTGGAGGGG ACTGGAGGGG	AATGOGCACG TACAACTCCA TACTOGCAGC GAGGCCAGCT GCCGGGGGACC GCCGCCCCCA GCCATTAACG GGAGAAATTT	GCGCAGCGCA TGACCAGCTC AGGGCACCCC CCAGCCCCCC TCCGGGACAT GCAGACTTCA GCACACTGCC TCAAAGAAAA	TGTGGTTACC GATCAGCATG CATGTCCCAG CCTCTCACAC ACGAGGGAAA	720 780 840 900 960 1020
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75 80	CAGTOGACT ATGAACGCT ATGAACGCT ATGACGCT ATGACGCT CTTGGCTCCA TCTTCTCCC TATCTCCCG TGCAGGGGC TGGGAGGGGT TGGAGGGC TGGGAGGGGT AAAAA Seq ID NO: Protein Aci	ACCGCACCA ACGACTGAA ACGACTGAA ACGACTGAG CGCCACCTA TGGCTTCGGT GGGCCCGGT GGGCCCGGT CGGACAGCGA GCRAAGAGG 347 Protein cession #: 11 TELKPPGPQQ INSEISKRIG LPGGLIARGG	COCGGGCCTC GGCCTGCAG CAGCATGTCC GGTCAAGTCC GGTCAAGTCC GCCCGGCACG ACTCGAGCGA ACTCGAGCGA ACTCGAGCGA CAA8343 1 Sequence CAA8343 21 TSGGGGGNST AGMKLSETE SSMASGVGVG	AATGGGACG TACACTGGAGC GAGGCAGC GCGGGCGCCA GCGGCCCCA ACACGCAGC GCATTAACG GGAAAATT ACAGCATGGA 31 AAAAGGRQKK KRFFIDEAK KGGAGWKN KRFFIDEAK GGGAWN	GCGCAGGGCA TGACCAGGTA AGGGCACCCCC CCAGCCCCCC TCCGGGACATCA GCACACTGCC TCAAAGAAAA GAAAACCCCG 41 SPDRVKRPMN LRALHIMKSHH LRALHIMKSHH LRALHIMKSHH LRALHIMKSHH LRALHIMKSHH LRALHIMKSHH LRALHIMKSHH MDSTAHRHICH	TGGGATGAGT TGTGGTTACC GATCAGCATG CATGTCOCAG CCTCTCACAC ACCAGGGAAA TACGCTCAAA 51 AFMVWSRGQR DYKYRPERET SNGSYSMMQD	660 720 780 840 900 960 1020 1080
75	CAGETOSACT ATGAACOGCT ATGAACOGCT CTTGGCTCCA TCTTCCCTCC TATCTCACGGA ATGTCACGGG ATGTCAGGGGGT AAAAA Seq ID NO: Protein Ac: 1 HSARMYNNME RUMAGERFKM KTLMKKDKYR	ACCGCAGCA ACGCGCACCTA ACGACGTGAA GCCCCACCTA TGGGTTCGGT ACTCCAGGGC GCGCACAGCGGA GCAAAAGAGC 347 Proteir cession #: 11 1 TELKPPGPQQ HNSEISKRLG LPGGLAPGQ AMHGAAOMOP	CCCGGGCCTC CGCCTGCAG CAGCATGTCC GGTCAAGTCC GGTCAAGTCC GCCGGCACCG ACTGCAGGG ACTGCAGGG ACTGCAGGG ACTGCAGGG ACTGCAGGG TAAGAA 1 Sequence CAA8343 21 TSGGCGGNST AGWKLLSETE NSMASGVGVG MERYDVSALQ MERYDVSALQ MERYDVSALQ MERYDVSALQ	AATGGCACC TACTCGCAGC TACTCGCAGC GAGGCAGCAGC GCGGCCCCCA GCGAGAAATT ACAGCATGGA 31 AAAAAGGQQKA KRFFIDEAKK AGLAGAGWAGG	GCGCMGGGCA TGACCAGCTC AGGGCACCCC CCAGCCCCCC TCCGGGACAT GCAGACTTCA GCACATCGC TCAAAGAAAA GAAAACCCGG 41 	TGGGATGACT TGTGGTTACC GATCACCATG CATGTCCAG CCTCTCACAC ACGAGGGAAA TACGCTCAAA 51 AFMVWSRSQR DYKYEPERET SNGSYSHNQD TSQQQTDGMA	660 720 780 840 900 960 1020 1080
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75 80	CAGETOGACT ATGAACGCT ATGAACGCT ATGAACGCT CTTGGCTCCA TCTTCCTCCC TATCTCCCG TATCTACCAGA ATGTGAGGGC TGGGAGGGGT AAAAA Seq ID NO: Protein Ac: HSARHYRBME RKUAGENFKM KTLMKKDKYT QLGYFQHFGL LGSMGSVVKS	ACCGCAGCA ACGCGCACCTA ACGACGTGAA GCCCCACCTA TGGGTTCGGT ACTCCAGGGC GCGCACAGCGGA GCAAAAGAGC 347 Proteir cession #: 11 1 TELKPPGPQQ HNSEISKRLG LPGGLAPGQ AMHGAAOMOP	COCGGGCCTC GGCCTGCAG CAGCATGTCC GGTCAAGTCC GGTCAAGTCC GCCCGGCACG ACTGGAGCGC CAA8341 1 Sequence CAA8341 1 TSGGCGGNST AGMCLLSETE NSMASGVGVG MERTUVSALQ SSSISSRAPQ	AATGGCACC TACTCGCAGC TACTCGCAGC GAGGCAGCAGC GCGGCCCCCA GCGAGAAATT ACAGCATGGA 31 AAAAAGGQQKA KRFFIDEAKK AGLAGAGWAGG	GCGCMGGGCA TGACCAGCTC AGGGCACCCC CCAGCCCCCC TCCGGGACAT GCAGACTTCA GCACATCGC TCAAAGAAAA GAAAACCCGG 41 	TGGGATGACT TGTGGTTACC GATCACCATG CATGTCCAG CCTCTCACAC ACGAGGGAAA TACGCTCAAA 51 AFMVWSRSQR DYKYEPERET SNGSYSHNQD TSQQQTDGMA	660 720 780 840 900 960 1020 1080

WO 02/086443 Sec ID NO: 348 DNA secuence Nucleotide Accession #: NM 002638 Coding sequence: 120-473 21 CRATACAGCT AAGGAATTAT CCCTTGTAAA TACCACAGAC CCGCCCTGGA GCCAGGCCAA GCTGGACTGC ATAMAGATTG GTATGGCCTT AGCTCTTAGC CAMACACCTT CCTGACACCA 120 10 TGAGOGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGAGG CTGGTTCTAG 180 AGGCAGCTOT CACGGGAGTT COTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCCAT
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TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGGGC 420 15 480 COGTOCTTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540 TOCTGOCCTT CCCCTTCCCA CACTGTCCAT TCTTCCTCCC ATTCAGGATG CCCACGGCTG GAGCTGCCTC TCTCATCCAC TTTCCAATAA A 20 Seq ID NO: 349 Protein sequence: Protein Accession #: NP_002629 21 25 MRASSFLIVV VFLIAGTLVL BAAVIGVPVK GQDTVKGRVP PNGQDPVKGQ VSVKGQDKVK ACEPYKOPYS TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCCEGSCG MACFYPQ Seq ID NO: 350 DNA sequence 30 Nucleic Acid Accession #: NM_007183 Coding sequence: 75-2468 11 21 31 35 GAATTCCGGA CAGCACGTGA AGATAGTTGG GTTTGGAGGC GGCCGCCAGG CCCAGGCCCG GTGGACCTGC CGCCATGCAG GACGGTAACT TCCTGCTGTC GGCCCTGCAG CCTGAGGCCG 120 GOGRACOTO COTOGOGOTO COTTORACO TGCAGTGGA COGCOGGGG GCGAGGGGG GGGAGGCGA GCGGCTGCGG GCAGCOGGG TCCAGGAGCA GGTCCGCGC CGCCTCTTGC 180 AGCTGGGACA GCAGCCGCGG CACAACGGGG CCGCTGAGCC CGAGCCTGAG GCCGAGACTG 300 40 CCACAGGCAC ATCCAGGGG CAGTACCACA COCTGCAGGC TGGCTTCAGC TCTCGGTCTC
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85 Seq ID NO: 351 Protein sequence Protein Accession #: NP_009114.1

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10	FLRNLSSASQ EMPPSALORL	ATROKMRECH EGRGRRDLAG	APPGEVVGCF	TPOSERLEEL	PLANDALTFA	EVSKDPKGLE	480 540 600 660	
15	LDRVRTADHH	QLRSLTGLIR ASPIAARDLL	NERNARNKU YFDGLRKLI F	EMSTKVVSHL	IEKLPGSVGE	LEGERILNPL KSPPAEVLVN LANLWQYNKL	720 780	
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20	Coding sequ	id Accession Lence: 1-65	1					
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30	AAGAAGAATC TTCCTCTGGC GCTCTCGCCC	TTCAGTACTA TTCAGTACTA TTGCTAGGAA CACCAGAAGT	OCA CAGGAAA	GCCAAAGTA GACCCTAACT CCAGCTTTGG	ACTACAACTT TGGAATTTGT CAGCACAGTA	TGAAAAGCCC TGCCATGCCT TGAGCACGAC	420 480 540 600	
35		353 Protei						
40	1	11	21	31	41	51		
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50	1	11	21 	31 	41 	51 		
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70	CAGAGAATAA TGTCCTCCAG CATCAATCCT	CTCAGAATAT CACCATAGAG TTACCACTCT	AGGCGCTAGA ACCAAATAAT AAGTGTATTT	GCCCATTCCT TTCATATTCA CTTCCCCTTA	CTTTCTCCAC AGCTTCAGAA CTCTCACACC	CACACACCCC	1020 1080 1140 1200 1260	
75	ACTITITATI TAAATTATGI	TAATTAAATG TTTAAACACA CDDAATDDAT	TATTTAATTA TGCCTTAAAT	TTGTTTAATT AATGTTTAAG	AAATTTAACT TATTAACTTA	AGCCATTCAC GTARAGAACT CTGGTTTCTA CAACGATATA TAGGGTAATG	1320 1380 1440 1500 1560	
80	CCGTAGGAAA	AATAAAACTT 355 Protei	CACATTTAAA	AAAAA				
	Protein Ac		NM_002	820		61		

MORRIVOQMS VAVFILSYAV PSCORSVEGI SRRIKRAVSE HQLLHDKORS IQDLERRFFL 60 HELTAELHTA EIRATSEVSP NSKESENIKN HEVREGSDDE GRYLTQGTMR VETTKEQPLK 120

WO 02/086443 TPGKKKKKKP GKRKEQEKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTTSL ELDSR

Seq ID NO: 356 DNA sequence Nucleic Acid Accession #: NM_017522 Coding sequence: 1-2100

	1	11	21	31	41	51 I	
	Amongoomag	CCGAGCCGGG	Commission	CTTCTGGGGG	TOCTOCTOCT	acracracra	60
10	ATGGGGCCTCC	TGCGGCTCCA	OCATOTTOOO	accectacee	CTGATCCGCT	activacacac	120
10	CIGCIGCIGC	CCAAGGAGTG	CCALCITOCA	CAATTYYCAGT	OCCOGRACCIA	COCCTCCATC	180
	CAMGGGCCGG	GGAGATGCGA	CONNANGGAC	CACTICCAGI	ACCACACOCA	CCACCACCAC	240
	TOOCCOOK NOT	AGACCTGTGC	ACA CACTOCAC	CONCLUCIO CONCUE	ACCACAGGGGA	CONGGREGAT	300
		AGTGTGACGG					360
15	ACTITICATE OCA	AGCAGGTGTG	TO CONGRESS CAR	ANGCTONGCT	GTGGACCCAC	CAGCCACAGG	420
10	MC11GCACCA	CCTCGTGGCG	CECTOCHORO	CACRACCACT	CCCACCCTCC	AGCOGATICAG	480
	COCCCCTOTIC	CTACCTCACT	CIGCACCTOC	COTOGOGACO	AGTTOCAGTG	TOCOGRATOGG	540
	ACA TOTOTO	TTGCAATCAA	GCACTGCAAC	CAGGAGCAGG	ACTICTOCAGA	TOGGGAGTGAT	600
	Chacerocer	GCCTACAGGG	CCTCAACGAG	TYSTCTYSCACA	ACANTOGOGG	CTGCTCACAC	660
20	TWO CLOSEL	ACCTCAAGAT	SCCCHTTOOA A	TOTO TOTO TOTO	CACCACCCTT	CONGCOCCO	720
20	ATCTOCACTG	CTTGTGGCGA	COMMISSION	TOCKLOTOCC	CAGATGCCTC	CACCCAGATC	780
	DOMOCROTA A DR	ACAAGGGCTA	CHILDWIGHG	CACTOCTACC	CTCCCTCCCA	CATCCACCTA	840
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25	ACGAGIGGGG	CACTAGATGT	CCV & CALLOCOC	ACCARTOCCA	TOTACTGGTG	TOLOCTOTOC	1020
20	MA COCCEA A CA	TCTATAGCGC	CTACATCCAC	AACCCCCACTC	ACCCCALAGA	CCCCCACCTC	1080
	OTTO TOTAL	AGCAGTTGCA	CTCTCCACAC	agormagena	TOGACTOGGT	CCACAAGCAC	1140
	ATTORNES	CTGACTCGGG	CANTARCACC	ATCTCACTOG	CCACACTTGA	TOGTOGCCCC	1200
	OCT COCT CAC	TCTTCAGCCG	TANCOTCACE	GRACCCCCCCC	CCATCISCTOT	TGACCCCCTG	1260
30	CORCOCTTCA	TGTATTGGTC	TOACTOOGG	GACCAGGCCA	AGATTGAGAA	ATCTGGGCTC	1320
50	AACCCTCTCCC	ACCEGCAAAC	ACTOCTOTO	CACAATATTC	AATGGCCCAA	COGRATCACC	1380
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00	AACCCACATG	ACATTGTCAT	CTTCCATGAG	CTGRAGCAGC	CAAGAGCTCC	AGATGCCTGT	1680
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		CTCCCAAGTA					1800
		GCTACCGAGA					1860
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	ACATCCAAAG	GATGTGAGAG	TTTTTCTATG	TATAATGITT	TATACACTTT	TTAACTGGTT	2340
	GCACTACCCA	TGAGGAATTC	GTGGAATGGC	TACTGCTGAC	TAACATGATG	CACATAACCA	2400
	AATGGGGGCC	AATGGCACAG	TACCTTACTC	ATCATTTAAA	AACTATATTT	ACAGAAGATG	2460
50	TTTGGTTGCT	GGGGGGCTTT	TTTAGGTTTT	GGGCATTTGT	TTTTTGTAAA	TAAGATGATT	2520
	ATGCTTTGTG	GCTATCCATC	AACATAAGT				

Seq ID NO: 357 Protein sequence Protein Accession #: NP_059992

55 31 21 | 41 51 MGLPEPGPLR LLALLLLLL LLLLRLQHLA AAAADPLLGG QGPAKECEKD QFQCRNERCI PSYWRODEDD DOLDHSDEDD CPKKTCADSD PTCDMGHCIH ERWKCDGESE CPDGSDESEA 60 TCTKQVCPAE KLSCGPTSHK CVPASHRCDG EKDCEGGADE AGCATSLGTC RGDEFQCGDG 180 TCVLAIKHON QEQDOPDGSD EAGCLQGINE CLHNNGGOSH ICTDLKIGFE CTCPAGFQLL 240 TOTALISMS GEOGRESSES BACKGERSES CLERROCES (TOTALISMS CTEMBRICA)

TABLES PER SETTING CONTROLLER EVALUATION TRAININGS STATISMS STAT 300 420 65 480 540 600

70 YRKTTEEEDE DELHIGRTAG IGHVYPARVA LSLEDDGLP

Seq ID NO: 358 DNA sequence Nucleic Acid Accession #: M27826

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80	CGTTGCCTTC	TTTTCAAGGG	CCTGTTTCCC	TIGCCCCCAT	AACTGTTGTG	GGTATTGACG	240
	GCCAAGCTTC	ARRACCCCTG	AAAACTCCCC	CACTCTGGTG	CCAACTTGGA	CAACACTCTT	300
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	TAACCAAATT	ATCTGCTTCC	CTGACTATTC	CTGGAGTACA	GCTACATCTC	ATTGCTGCCC	420
	TTCTTCCCAA	TCCAAAGCCT	CCTTTGTGTC	CTCTAACATC	CCCACAATAT	CAGCCCTTAC	480
85	CACAAGACCT	CCCTTCAGCT	TAATCTCTCC	CACTCTAGGT	TCCCACGCCG	CCCCTAATCC	540
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	ACATCCAGAT	GGCCTCTGAG	AACTGAAGAT	CCACAAAAGA	AGTAAAAACA	GCCTTAACTG	780			
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5		CCCTTAAGAA					900 960			
,	CCCAAATCCT	ATAAAACAGC	CCCACCCCTA	TCTTCCTTCA	CIGACICICI	TTTCGGACTC	1020			
	AGCCACCGGC	ACCCAGGTGA	ARTAAACAGC	TTTATTGCTC	AC					
	Seg ID NO:	359 Protein	secuence							
10	Protein Accession #: AAA65999									
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	I	1	1	1	1	1				
15	PKKHLTNFKS	DLFGLATEDW	RCPIASEVPW	LWCOLGORSE	MHSELVIPTC	DIDTGATHST	60 120			
	TKLSASLTIP	GVQLHLIAAL	LPNPKPPLCP	LTSPQYQPLP	QDLPSA	I DI DIIGIIII				
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25	TGTGTAGCAA	ACATCOCTGG	CGATACCTTG	GANAGGACGA	AGTTGGTCTG	CAGTCGCAAT	120			
	TTCGTGGGTT	GAGTTCACAG GAAACGGTGG	TTGTGAGTGC	GGGGCTCGGA	GATGGAGCCG	TOGTOCTCTA	180 240			
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20	TTCACAATTC	TCCAGAGGGA	ATATCAAAAA	CAACGGGATT	TTGCACAAAC	AGAAAGAATT	360			
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	CAAAAAAAGG	AATTCAGTCT	TTCCTTTTAT	CTATATATAA	TGAGCATGGT	ATTCAGCAAA	540			
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35	TAGCARTCAG	COTOGAGAAG	AAAACTGTGA	CAATGATTGT	TGATTGTAAG	AAGAAAACCA	720			
	CGAMACCACT	TGATAGAAGT	GAGAGAGCAA	TTGTTGATAC	CAATGGAATC	ACGGTTTTTG	780			
	GAACAAGGAT	TTTGGATGAA GGCAGCATAT	GAAGTTTTTG	AGGGGGACAT	TCAGCAGTTT	GACTOTTCAG	840 900			
40	CACCCAAGGC	TGCTCAAGCT	CAGGAACCTC	AGATAGATGA	GTATGCACCA	GAGGATATAA	960			
40	TCGAATATGA	CTATGAGTAT	GGGGAAGCAG	AGTATAAAGA	GOCTGAAAGT	GTAACAGAGG	1020 1080			
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50	CAGGACCTGC	AGGTATTATG	GGTCCTCCAG	GTCTACAAGG	COCCACTGGA	CCCCCTGGTG	1560			
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00		TGTAGATGGC AGGTCAACAA					2220 2280			
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	GTGCTGATGG	GCCTCCTGGT TGGTCCACAA	CATCCTGGGA	AAGAAGGCCA	GTCTGGAGAA	AAGGGGGCTC	2400 2460			
65	CAGATGGTGT	CAGAGGTCTC	AAGGGATCTA	AAGGTGAAAA	GGGTGAAGAT	GGTTTTCCAG	2520			
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70	GAAGACAAGG	TOCARAGGGT	TCCACTGGAT	TCCCTGGGTT	TCCAGGTGCC	AATGGAGAGA	2760			
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	GTGGCGATGG	CCCTCCTGGC	CCTCCAGGTG	AAAGAGGTCC	TCAAGGACCT	CAGGGTCCAG	2940			
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40							

Seq ID NO: 361 Protein sequence Protein Accession #: NP_001845

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	70	GLKGDPGSKG	EKGHPGLICL	IGPPGEQGEK	GDRGLPGTQG	SPGAKGDGGI	PGPAGPLGPP	1500
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		PVCFLG						

80 Seq ID NO: 362 DNA sequence Nucleic Acid Accession #: NM_003107 Coding sequence: 351-1775

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		/086443					
	TCTCTCTTTA	CCCACCTCCG	CCCCTGCGAG	GAGTTGAGGG	OCCAGTTCGG	COGCCGCGCG	300
	CONTENTED	GAGGGTGTGA	GOYCGOGTGG	GOGCOCGCCG	AGCCGAGGCC	ATGGTGCAGC	360
	AAACCAACAA	TGCCGAGAAC	ACGGAAGCGC	TGCTGGCCGG	CGAGAGCTCG	GACTCGGGCG	420
5	CCGGCCTCGA	GCTGGGAATC	GCCTCCTCCC	CCACGCCCGG	CTCCACCGCC	TCCACGGGGG	480
	GCAAGGCCGA	CGACCOGAGC	TGGTGCAAGA	CCCCGAGTGG	GCACATCAAG	CGACCCATGA	540
	ACCOCTTCAT	GGTGTGGTCG	CAGATCGAGC	GGCGCAAGAT	CATGGAGCAG	TCGCCCGACA	600
	TGCACAACGC	CGAGATCTCC	AAGCGGCTGG	GCAAACGCTG	GAAGCTGCTC	AAAGACAGCG GCTGACTACC	660 720
10	ACAAGATCCC	GTACCGGCCC	ACCARCAGO	TONNETCOOR	CARCICCARC	TCCACCTCCT	780
10	COGACTACAA	CTCCTCCAAG	COGGGGGGGG	AGGGAGACAA	GGTYYGGTTGGC	AGTGGGGGGG	840
	GOGGCCATGG	GGGCGGCGGC	GGCGGCGGGA	GCAGCAACGC	GGGGGGAGGA	GGCGGCGGTG	900
	CGAGTGGCGG	CGGCGCCAAC	TOCARACOGG	CGCAGAAAAA	GAGCTGCGGC	TCCAAAGTGG	960
						GCAGGCGGCG	
15						CAGGCGGGGG	
						AAGGCGCGGA	1140
	CTCCCAGCGC	CTCGGCCGCG	GCCTCCTCGG	CAGCCTCGGC	CTCCGCAGOG	CTCGCGGGCCC	1260
	COGGCKAGCK	CCTGGGGGGAG	anonnousen	CCCCCCCCCC	CCCGGGGGGG	CCCCTGGGCC	
20	TOTACGAGGA	GGAGGGCGCG	GGCTGCTCGC	CCGACGCGCC	CAGCCTGAGC	GGCCGCAGCA	1380
	GOGOCGCCTC	GTCCCCCGCC	GCCGGCCGCT	CGCCCGCCGA	CCACCGCGGC	TACGCCAGCC	1440
	TGCGCGCCGC	CTCGCCCGCC	CCGTCCAGCG	CGCCCTCGCA	CGCGTCCTCC	TCGGCCTCGT	1500
	CCCACTCCTC	CTCTTCCTCC	TCCTCGGGCT	CCTCGTCCTC	CGACGACGAG		1560
25	ACCTGCTCGA	CCTGAACCCC	AGCTCAAACT	TTGAGAGCAT	GTCCCTGGGC	AGCTTCAGTT	1620
23						GGCTCGCACT	1680 1740
	TOGAGTTCCC	GGACTACTGC	ACGCCCGAGG	1GNGCGNGAT	GRICIOGGA	GACTGGCTCG	1800
	AGTOCAGCAT	AGGAGAGGAG	DEGGGGGGG	TOPPRESSO	DAGGEROOGE	ĞACAGACGAA	1860
	CAGTTTAAAG	AGAAAAGGGA	AAAAAGAAAG	ARARAGTARG	CAGGGCTCGT	TOGOCOGOGT	
30	TCTCGTCGTC	GGATCAAGGA	GCGCGGCGGC	GTTTTGGACC	CGCGCTCCCA	TCCCCCCACCT	1980
	TCCCGGGCCG	GGGACCCACT	CTGCCCAGCC	GGAGGGACGC	GGAGGAGGAA	GAGGGTAGAC	2040
		TGTGATTGTT					2100
	TTCGAGTTTG	CTCCCCTTTG	CTTGAAGAGA	CCCCCTCCCC	CTTCCAACGA	GCTTCCGGAC	2160
35	TTGTCTGCAC	CCCCAGCAAG	AAGGCGAGTT	AUTTITICTAG	AGACTTGAAG	GAGTCTCCCC AAGGAGGGGA	2220 2280
55	CHICCHOCAL	CACCACCTIC	CCCCTTTTTT	TRANCOCTE	ATGRAGACAC	AAGGCTCCGG	2340
	GGTGACGAAT	TTGGCCGATG	GCAGATGTTT	TGGGGGAACG	CCGGGACTGA	GAGACTCCAC	2400
	GCAGGCGAAT	TOCOGTTTGG	GGCCTTTTTT	TCCTCCCTCT	TTTCCCCCTTG	CCCCCTCTGC	2460
	AGCCGGAGGA	GGAGATGTTG	AGGGGAGGAG	CCCACCCACT	GTGACCGGCG	CTAGGAAATG	2520
40	ACCCGAGAAC	CCCGTTGGAA	GCGCAGCAGC	GGGAGCTAGG	GGCGGGGGGG	GAGGAGGACA	2580
	CGAACTGGAA	GGGGGTTCAC	GGTCAAACTG	AAATGGATTT	GCACGTTGGG	GAGCTGGCGG	2640 2700
	CGGCGGCTGC	TGGGCCTCCG	CCTTCTTTTC	TACGTGAAAT	CAGTGAGGTG	AGACTTCCCA	
	GACCCCGGGAG	TTCGGAAAAA	GAGGAGACTG	ANALOGO	TACAGGGGCA	GTCAGTGGAG	2760
45	GGCGMG1001	TICGGRAAAA	ADDODUGIONOGI	AUGUNGGG			
	Seg ID NO:	363 Protein	sequence				
		cession #:	NP_0030	198			
		11	21	31	41	51	
50	1	11	11.	11	i.	ĭ	
-	MUCOTINIAEN	TEALLAGESS	DSGAGLELGI	ASSPIRGSTA	STGGKADDPS	WCKTPSGHIK	60
	RPMNAFMVWS	OIERRKIMEO	SPDMHNAEIS	KRLGKRWKLL	KDSDKIPFIR	EAERLRLKHM	120
	ADYPDYKYRP	RKKVKSGNAN	SSSSAAASSK	PGEKGDKVGG	SGGGGHGGGG	GGGSSNAGGG	180
55	GGGASGGGAN	SKPAQKKSCG	SKVAGGAGGG	VSKPHAKLIL	AGGGGGKAA	AAAAASFAAE	240
22	QAGAAALLPL	GAAADHHSLY	Kartpsasas	assaasasaa	LAAPGKHLAE	KKVKRVYLFG	300
	GLGTSSSPVG	GVGAGADPSD	PLGLYEEEGA	GCSPDAPSLS	GRSSAASSPA	AGRSPADHRG SSNFESMSLG	360 420
		DLDFNFEPGS					420
	DISSSSALDR	PUPPERFGS	CONFERENCE	** PASEUT SC	PHPPOPTONE	****	
60							
, -	Seq ID NO:	364 DNA se	quence				
	Nucleic Ac	id Accession	n #: U10860				
	Coding seq	dence:	123-220	14			

	couring sequence:		123-2204				
65	1	11 	21	31 	41	51 	
	TGCCGGCTGC	TCCTCGACCA	GGCCTCCTTC	TCAACCTCAG	CCCGCGGGGGCGC	CGACCCTTCC	60
	GGCACCCTCC	CGCCCCGTCT	CGTACTGTCG	CCGTCACCGC	CGCGGCTCCG	GCCCTGGCCC	120
	CGATGGCTCT	GTGCAACGGA	GACTCCAAGC	TGGAGAATGC	TGGAGGAGAC	CTTAAGGATG	180
70	GOCACCACCA	CTATGAAGGA	GCTGTTGTCA	TTCTGGATGC	TGGTGCTCAG	TACGGGAAAG	240
	TCATAGACCG	AAGAGTGAGG	GAACTGTTCG	TGCAGTCTGA	AATTITCCCC	TTOGARACAC	300
	CAGCATTIGC	TATARAGGAA	CAAGGATTCC	GTGCTATTAT	CATCTCTGGA	GGACCTAATT	360
	CTGTGTATGC	TGAAGATGCT	COCTGGTTTG	ATCCAGCAAT	ATTCACTATT	GGCAAGCCTG	420
	TTCTTGGAAT	TIGCTATGGT	ATGCAGATGA	TGAATAAGGT	ATTTGGAGGT	ACTGTGCACA	480
75	AAAAAAGTGT	CAGAGAAGAT	GGAGTTTTCA	ACATTAGTGT	GGATAATACA	TGTTCATTAT	540
	TCAGGGGCCT	TCAGAAGGAA	GAAGTTGTTT	TGCTTACACA	TGGAGATAGT	GTAGACAAAG	600
	TAGCTGATGG	ATTCAAGGTT	GTGGCACGTT	CTGGAAACAT	AGTAGCAGGC	ATAGCAAATG	660
	AATCTAAAAA	GTTATATGGA	GCACAGTTCC	ACCCTGAAGT	TGGCCTTACA	GAAAATGGAA	720
		GAAGAATTTC					780
80	AGAACAGAGA	ACTTGAGTGT	ATTOGAGAGA	TCAAAGAGAG	AGTAGGCACG	TCAAAAGTTT	840
	TOGTTTTACT	CAGTGGTGGA	GTAGACTCAA	CAGTTTGTAC	AGCTTTGCTA	AATCGTGCTT	900
	TGAACCAAGA	ACAAGTCATT	GCTGTGCACA	TTGATAATGG	CTTTATGAGA	AAACGAGAAA	960
	GCCAGTCTGT	TGAAGAGGCC	CTCAAAAAGC	TTGGAATTCA	GGTCAAAGTG	ATAAATGCTG	1020
	CTCATTCTTT	CTACAATGGA	ACARCMACCC	TACCAATATC	AGATGAAGAT	AGAACCCCAC	1080
85		TAGCAAAACG					1140
	TTGGGGATAC	TTTTGTTAAC					1200
	AGGAGGTTTT	CCTTGCCCAA	GGTACTTTAC	GGCCTGATCT	AATTGAAAGT	GCATCCCTTG	1260

WO 02/086443 TTGCAAGTGG CAAGCTGAA CTCATCAAAA COCATCACAA TGACACAGAG CTCATCAGAA 1320 AGTTGAGAGA GGAGGAAAA GTAATAGAAC CTCTGAARGA TTTTCATAAA GATCAAAGTGA 1340 AGATTTTGGG CAGGAAACTT GGACTCGGG AGAGATTAAT TTCCAGGCAT CCATTCCAG 1440 GTCCTOGCCT GGCAATCAGA GTAATATGTG CTGAAGAACC TTATATTTGT AAGGACTTTC 1500 5 CIGAAACCAA CAATATITIG AAAATAGTAG CIGATITITC TGCAAGTGTT AAAAAGCCAC 1560 ATACCCTATT ACAGAGAGTC AAAGCCTGCA CAACAGAAGA GGATCAGGAG AAGCTGATGC 1620 AMATTACON TOTOCATTCA CTGAATGCCT TOTTGCTGCC AATTACAGT GTAGGTGTGC AGGGTGACTG TCGTCTCCTAC AGTTACGTGT GTGGAATCTC CAGTAAAGAT GAACCTGACT 1740 GGGATCACT TAITITICTG GCTAGGCTTA TACCTCGCAT GTGTCACAAC GTTAACAGAC TTGTTTATTA TAITITIGGCCA CCAGATTAAGA GACCTCCTAC AGANGTTACT COACHTTCT TGACAACAGA GTGGCCAGT ACCTTATCAC AGACCATT TGAGGCCACTA AACCTATTT TGAGGCCACTA AACCTATTT TGAGGCCACTA AACCTATTT TGAGGCCACTA AACCTATTCTCA 1800 10 1860 1920 OGGAGICIGG GIATGCIGGG AAAATCAGCC AGAIGCOGGI GATTITGACA CCATTACAIT 1980 TTGATCGGGA CCCACTTCAA AAGCAGCCTT CATGCCAGAG ATCTGTGGTT ATTCGAACCT TTATTACTAG TGACTTCATG ACTOGTATRC CTGCAACACC TGGCAATGAG ATCCCTGTAG 2100 15 AGGTGGTATT AAAGATGGTC ACTGAGATTA AGAAGATTCC TGGTATTTCT CGAATTATGT 2160 ATGACTTAAC ATCAAAGCCC CCAGGAACTA CTGAGTGGGA GTAATAAACT TC Sea ID NO: 365 Protein sequence Protein Accession #: AAA60331 20 21 MALCINGDSKL ENAGGDLEDG HHHYEGAVVI LDAGAQYGKV IDRRVRELFV QSEIFPLETP AFAIKEOGPR AIIISGGPNS VYAEDAPNPD PAIFTIGKPV LGICYGMQMM NKVFGGTVHK 120 25 KSVREDGVFN ISVDNTCSLF RGLOKEEVVL LTHGDSVDKV ADGFKVVARS GNIVAGIANE 100 SKKLYGAQFE PEVGLTENGK VILKNFLYDI AGCSGTFTVQ NRELECIREI KERVGTSKVL 240 VLLSGGVDST VCTALLNRAL NOBQVIAVEI DNGFMRRES OSVEEALKKL GIOVKVIMAA HSFINGTITL PISDEDRIPR KRISKILMNI TSPEEKRKII GDTFVKIANE VIGEMNLKPE EVFLAGGTLR POLIESASLV ASGKAELIKT HENDTELIKK LREEGKVIEP LKOPHKDEVR 30 ILGREIGLPE ELVSRIPPPG PGLAIRVICA EEPYICKDFP ETINILKIVA DFSASVKKPE TLLQRVKACT TEEDQEKLNQ ITSLHSLNAF LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW 480 540 ESLIFLARLI PRMCHIVIRV VYIFGPPVKE PPTDVTPTFL TTGVLSTLRQ ADFEARNILR ESGYAGNISO MPVILTPLHF DEDPLOKOPS CORSVVIRTF ITSDFMTGIP ATPGNEIPVE VVLKNYTEIK KIPGISRIMY DLTSKPPGTT EME 35 Seq ID NO: 366 DNA sequence Nucleic Acid Accession #: NM_004219 46-654 Coding sequence: 40 41 GCGGCCTCAG ATGAATGCGG CTGTTAAGAC CTGCAATAAT CCAGAATGGC TACTCTGATC TATOTTGATA AGGAAAATOG AGAACCAGGC ACCCGTGTGG TTGCTAAGGA TGGGCTGAAG 120 45 CTGGGGTCTG GACCTTCAAT CAAAGCCTTA GATGGGAGAT CTCAAGTTTC AACACCACGT 180 TTTGGCARAA CGTTCGATGC CCCACCNGCC TTACCTAAAG CTACTAGAAA GGCTTTGGGA 240 ACTOTCAACA GAGCTACAGA AAAGTCTGTA AAGACCAAGG GACCCCTCAA ACAAAAACAG CCAAGCTTTT CTGCCAAAAA GATGACTGAG AAGACTGTTA AAGCAAAAAG CTCTGTTCCT GCCTCAGATG ATGCCTATCC AGAAATAGAA AAATTCTTTC CCTTCAATCC TCTAGACITT 420 50 GAGAGTTTTG ACCTGCCTGA AGAGCACCAG ATTGCGCACC TCCCCTTGAG TGGAGTGCCT CTCATGATCC TTGACGAGGA GAGAGAGCTT GAAAAGCTGT TTCAGCTGGG CCCCCCTTCA 400 540 CCTGTGAAGA TGCCCTCTCC ACCATGOGAA TCCAATCTGT TGCAGTCTCC TTCAAGCATT 600 CTGTCGACCC TGGATGTTGA ATTGCCACCT GTTTGCTGTG ACATAGATAT TTAAATTTCT TAGTGCTTCA GAGTTTGTGT GTATTTGTAT TAATAAAGCA TTCTTCAACA GAAAAAAAAA 55 Seq ID NO: 367 Protein sequence 60 MATLIYVDKE NGEPOTRVVA KDGLKLGSGP SIKALDGRSQ VSTPRFGKTF DAPPALPKAT RKALGTVNRA TEKSVKTKGP LKOKOPSPSA KKMTEKTVKA KSSVPASDDA YPEIEKFFFF NPLDFESDL PEBHOLAHLP LSGVPLMILD EERELEKLFO LGPPSPVKNP SPPNESNLLO 65 SPSSILSTLD VELPPVCCDI DI Seq ID NO: 368 DNA sequence Nucleic Acid Accession #: NM_000597 70 Coding sequence: 118-1104 41 51 ATTENDEGEN AGGRAGGAGG AAGAAGCIGA GGAGGCGGCT COCGCTOGCA GGGCCGTGCA 75 CCTGCCCGCC CGCCCGCTCG CTCGCTCGCC CGCCGCGCCG CGCTGCCGAC CGCCAGCATG 120 CTGCCGAGAG TGGGCTGCCC CGCGCTGCCG CTGCCGCCGC CGCCGCTGCT GCCGCTGCTC 180 CCGCTGCTGC TGCTGCTACT GGGCGCGAGT GGCGGCGGCG GCGGGGCGCG CGCGGAGGTG 240 CTGTTCCGCT GCCCGCCCTG CACACCCGAG CGCCTGGCCG CCTGCGGGGCC CCCGCCGGTT GCGCCGCCCG CCGCGGTGGC CGCAGTGGCC GGAGGCGCCC GCATGCCATG CGCGGAGCTC 360 80 GTCCGGGAGC CGGGCTGCGG CTGCTGCTCG GTGTGCGCCC GGCTGGAGGG CGAGGCGTGC 420 GGCGTCTACA CCCCGCGCTG CGGCCAGGGG CTGCGCTGCT ATCCCCACCC GGGCTCCGAG 480 CTGCCCCTGC AGCCGCTGGT CATGGCCGAG GGCACTTGTG AGAAGCGCCG GGACGCCGAG 540 TATGGCGCCA GCCCGGAGCA GGTTGCAGAC AATGGCGATG ACCACTCAGA AGGAGGCCTG 600 GTGGAGAACC ACGTGGACAG CACCATGAAC ATGTTGGGCG GOGGAGGCAG TGCTGGCCGG 660 85 AAGCCCCTCA AGTCGGGTAT GAAGGAGCTG GCCGTGTTCC GOGAGAAGGT CACTGAGCAG 720

CACCGGCAGA TGGGCAAGGG TGGCAAGCAT CACCTTGGCC TGGAGGAGCC CAAGAAGCTG

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5	TOCACCATGC CCCAACTGTG CAGGGTGGGG ACCATCCGGG GTGCACACCC GCCCTCTCC TTCCAGTTCT CCCGGCCTCT CCCGGCCTCT	### JOS ### JO	CCTGTACAAC TGTGAACCCC GTGTCATCTC GTAGACCGCA AGAAAACGGA TTTATATTTG CTGCAGATGC	CTCAAACAGT AACACCGGGA TTCTACAATG GCCAGCCGGT GAGTGCTTGG GAAAGAGACC CACACCTGCT	GCAAGATGTC AGCTGATCCA AGCAGCAGGA GCCTGGGGGC GTGGTGGGTG AGCACCGAGC CCTTCTTGCT	TOTGAACEGG GGGAGCDCCC GGCTTGCEGG CCTGCCCCCC CTGGAGGATT TCGGCACCTC TTCCCCGGGG	900 960 1020 1080 1140 1200 1260 1320 1380
10	TTTATTTTTG	AACCCCTGTG 369 Protein	TCCCTTTTGC	ATAAGATTAA	AGGAAGGAAA	AGT	1380
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15	1	11	21	31	41	51	
20	VAPPAAVAAV ELPLQALVMG RKPLKSGMKE ISTMRLPDER	PLPPPPLLPL AGGARMPCAE EGTCEKRRDA LAVFREKVTE GPLEHLYSLH LPYNEQQEAC	LVREFGCGCC EYGASPEQVA QHRQMGKGGK IPNCDKHGLY	SVCARLEGEA DNGDDHSEGG HHLGLEEPKK	CGVYTPRCGQ LVENHVDSTM LRPPPARTPC	GLRCYPHPGS NMLGGGGSAG OOELDOVLER	60 120 180 240 300
25	Nucleic Ac:	370 DNA seid Accession lence: 6-44	n #: NM_0042	64			
	1 .	11	21	31	41	51	
30	TTTGTAATGC AGACAGCAAT CAGCACTGAT	GGATCGGCTC CATTGGAGTA TAACAAAGAC TGCACGAACA AGCTGCTTTA	TTGCAGCAAT CAGCCAGCTA GCAAAAGACA	GTGGTCCTCC ACCCTACAGA TTGATGTTTT	TGCCTCTTTC AGAGTATGCC GATAGATTCC	AATAATATTC CAGCTTTTTG TTACCCAGTG	60 120 180 240 300
35	AAGCTGCTAC AAAGCGCACT AGTCTCTTCC	ATGTGTGGAG TGCTGATATT AGACTCATAG GAATTCTGCA TGACACATTA	GATGTTGTTT GCACAGTCAC CATCAGTGGA	ATCGAGGAGA AGCTGAAGAC TACCATGTGG	CATGCTTCTG AAGAAGTGGT CTGAGAAAAG	GAGAAGATAC ACCCATAGCC AACTGTTTGA	360 420 480 540
40	GATAAGCTTA GAGTGAAATT	TARATCATGA ATTAAGGCAT TGACATAATT	TTGAATCAGC GTAATACATT	TTTAAAGCAT AATGAACATA	CATACCATCA	ACATATGTAA	660 720 780
45	Seq ID NO:	371 Protein	n sequence				
	Protein Acc	ession #:	NP_0042	:55			
50	1 MADRLTQLQD LIARTAKDID	11 AVNSLADQFC VLIDSLPSEE KTRSGTHSQS	21 NAIGVLQQCG STAALOAASL	31 PPASFMNIOT	41 AINKDQPANF ATCVEDVVYR	51 TEEYAQLFAA GDMLLEKIQS	60 120
50 55	1 MADRLTQLQD LIARTAKDID ALADIAQSQL Seq ID NO: Nucleic Ac:	11 AVNSLADOFC VLIDSLPSEE	21 HAIGVLOOCG STAALQAASL LPDS quence n #: AJ27105	31 PPASFIRMIQT YKLEBENHEA	AINKDQPANP	TEEYAQLFAA	
	1 MADRITGLOD LIARTAKDID ALADIAGSQL Seq ID NO: Nucleic Ac: Coding sequ 1 ATGGAGAATC CTGCCCTTOG	11 AVNSLADGFC VLIDSLPSEE KTRSGTHSQS 372 DNA seid Accessionence: 1-11	21 HAIGWLOCGS STAALQAASL LPDS q:ence n #: AJ27105 13 21 GCCGCATGTC CSTACAGAAC TOGSTCCCAAA	31 PPASFNNIQT YKLEBENHEA 21 31 TACTGGGCTC CCTGCCATCA	AINKDQPANP ATCVEDVVYR 41 AGCGACACCGG GCATCACTGA TCTATGAATT	TEEYAQLFAA GDMLLEKIQS 51 CGAGCTATAT AAACGTGCTG TCACCTGGAG	
55	1 AMADRITGLOD LIARTAKDID ALADIAQSQL Seq ID NO: Nucleic Ac: Coding sequitary attorney are according to the coding sequitary and according accordi	11 AVNSLADGE VLIDSLESEE KTREGTHSQS 372 DNA seid Accession annes: 1-11 11 AGGIGGTIGAC AGGARAGIGAG CTCAAGGAACTAAG CTCACT AAGAAGGAGA ACTAAGGAACTAAGGAAGGACA ACTAAGGAAGAGAAGA	21 RAIGVLOCOS STAALQAASL LPDS plence n #: AJ27105 13 21 GCCGCATGTC GGTACGGAAC TOGGTCCCAAA AGAGCCTGTT TCAGTGTTGG CCTAACTGAAC TGATCGTTGG CCTAACTGAA	31 PPASPINIOT YKLEBENHEA 21 31 TACTGGGCTC CCTGCATCG GAGACAATG TACAACTGA GAGAGCTCA CTGGATGGA CTGGATGAT TTTATGTATA	AINKOQPANP ATCVEDVVYR 41 AGCGACACOG GCATCACNA TCTATGANT CCCAGAGGCA CAAAGCAGGA AAAGCAGGA AAAGCAAGA AATCTTGTGCA	TEEYAQLPAA GDMLLEKIGS 51 CGAGCTATAT AAAGGTGCTG TCACCTGGAG GGTAAACATT AAAGCGACCA AATGGAGCTC CTCTCCTGAA ATTCCTCCTGAA	60 120 180 240 300 360 420 480
55	1	11 ANNSLADOFC VLIDSLESSE KKRSOTHS/SS ANT STATEMENT AND STATEMENT AS AGGRETICAL TO AG	21 NATIOULOQUE STAALQASIL LPDS THEROE THEROE THEROE GCOGCATGTC COTACAGAA AGAGCCTOTT TOAGTCCTAA AGAGCCTATT TOAGTCCTAA AGAGCCTATT TOAGTCCTAA TOAGTCCTAA CTAACATA CTAACAGAC GCTTAACTTAA CTAACAGAC GCTTAACTTAA	31 PASPINIQT YKLEERNIFA 21 TACTIGGGCTC CCTGCCATCA GGAGGCATC CGAGGCATC CCTGGCATCA GGAGGCATC CCGGATCATA ACTATATTCT ACTAGTATA ACTATATTCT ACTAGTATA ACTATTTCT ACTATTCTGCA TTGGATTGGCA	ALINCOPANE ATCVEDVVVR 41 AGGGACACOG GCATCACTGA TCTATGAATT CCCMGAGGCA CAAGCAGGA ACTGTTGCA TCTTTGGGAAT GCCAGATGCT TCTTTGGGAAG TCTTTGGGAAGA TCTTGGAATTTT TCTGGGAAGA	51 CGAGCTATAT AAAGGTGCTG GGTAACATAT AAAGGTGCTG CTCTCCTGGAA ATGCTCTGGAA ATGCTCTGGAA ATGCTCTGGAA ATGCTCGGAA ATGCTCGGAA ATGCTCGGAA ATGCTCGGAA ATGCTCGGAA ATGCTCGGAA ATGCAGACC	60 120 180 240 300 360 420 480 600 660 720 780
55 60 65	1 MADRITCLOD LIARTANDID ALADINASC. Seg ID NO. NUCLeic ALADINASC. COding sequing the control of	11 ANNSLADOFC VLIBSLESSE KRRSGTHSQS 372 DNA seid Accession lence: 1-21 1 AGGRITAGAC AGGRITAGAC AGGRITAGAC AGGRITAGAC AGARATORA CTCTAGGACA TOTOTGACAT AGGRIGAGGAC AGARATORA TCCTTGCACAT TCCTACATT ATCATACTAGACA TAGGACAT ATCATAGGAC AGARATORA AGARATORA TAGGAAT GARATORA TAGGAAT GARATORA TAGAATTAGA AGGAATTAGAAGAATTATA TAGAATATGA AGGAATTAGAAGAATTATAGAATTAGAAGAATTAGAAGAA	21 IMAISYLOOGS STANLOADS IMAISYLOOGS STANLOADS LPDS IMAISY LPDS IMAISY	31 PARSPHRICT YKLEESSERA 11 STATEMENT PARSPHRICT YKLEESSERA STATEMENT PARSPHRICT ST	ALINKOOPAHP ATCVEDVVYR 41 ARGGACACCO GCATCACTAA TCHTAGAATT CCCAGAGGCA CTGATGOCAT ARAGCGAAGA TCTGTGGAAT TCTGTGGAAT TCCCAGGAGCA TCTGTGGAAT TCCCAGGAGCA TCTGGAAGA TCTGAGAGT TCAGAATTT TCACATGTT TCACATGTT TCACATATTT TCACATATTT TGACATATTT TGACATTT TGACATATT TT TGACATATT TGACATATT TGACATATT TGACATATT TGACATATT TGACATAT TT TGACATATT TT TT TGACATATT TT T	TEVAQLIPAA GEMELLEKTOS 51	60 120 180 240 300 360 420 540 600 600 720
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10	Seq ID NO: Nucleic Act Coding sequ	374 DNA sec d Accession sence: 1-11	#: NM_0163	95			
	1 ATGGAGAATC	11 AGGTGTTGAC	21 GCCGCATGTC	31 TACTGGGCTC	AGCGACACCG	51 CGAGCTATAT	60 120
15	CATTTCAAAG TTCTTAGACC ACAGTACAGA	CTCAAGGACA TTGTGAAACC AGAAAGTGAG	CGTACAGAAC TGGTGCCAAA AGAGCCTGTT TCAGTGGTGG TGATCGTTGG	GGAGACAATG TACAAACTGA GAGAGACTCA CTGGATGAAT	TCTATGAATT CCCAGAGGCA CAAAGCAGGA CTGATGOGGA	TCACCTGGAG GGTAAACATT AAAGCGACCA AATGGAGCTC	180 240 300 360
20	ACTOTTACAA TTCTCCTGGA TATGACACAT	TCTTTGTCAA TCCATACTGT	CCTAAATAAA AGGATACCTG CCTGACTGTG GGCTGACATG TGGAGTCACT	CGATTCIGTA ATGTATTTCT ACCTCACCGG	TCTTGGGAAA GCCAGATGCT TGCTGCCTTC	AGAGTCCTTT GGCAGTTGTG TCTGATCCAG	420 480 540 600 660
25	AAAGCTGTGG TTCTACATGC	TTTTCTTTGT TGACGTGCAT	TTTGTTTATC GTTTTATTG TGACATGGAT ACTGGGATGT CGGACGATTC TCTTCAGATT	TGGAGTGCAA TGGAAGGTGC	TTGAAATTTT TCACATGGCT	CAGGTACTCT TCGTTACACT	720 780 840 900 960 1020
30	ATAAATTTTC	GTCACCTTTA	TARACAGOSC TTTSGGAGGC	AGACIGAAAA	TGAGGGCAGG	CGCAGTGGCT	1080
35	Seq ID NO: Protein Acc		NP_0574				
	1	11	21 1	31 	41	51 	
40	FLDLVKPEPV RAKEEERLNK YDTFHTVADM	YKLTQRQVNI LRLESBGSPE MYFQQMLAVV	LRVELSDVQN TVQKKVSQMW TLTNLRKGYL ETINAAIGVT FYMLTCIDMD	ERLTKQEKRP FMYNLVQFLG TSPVLPSLIQ WKVLTWLRYT	LFLAPDFDRW FSWIFVNLTV LLGRNFILFI LWIPLYPLGC	RPCILGRESF IFGTMEENQN LVEAVSVIOS	120 180 240 300 360
45	STKKKDLDGF	LPV	KVRFSFFLQI	YLIMIPLGLY	INFRHLYKUK	REKTGEGEREK	360
50	Nucleic Ac Coding seq		Quence n #: NM_0059 1-270	31	41	51	
	1	ī	1	i	i	ï	
55	GTGAAACAAC TGCCAACCCA ATTCCAGAGC	CTTGCCAGCC	GCAGCCTTGC TCCACCCCAG GCCCTGCCAC CAAGGTGCCT GCAGAAGTAA	CCCAAAGTGC	CTGAGCCCTG	CAAGGAGCCC	120 180 240
60	Protein Ac		NP_0059				
65	1 MNSQQQKQPC IPEPCQPKVP	11 TPPPQFQQQQ EPCPSTVTPA	21 VKQPCQFPPQ PAQQKTKQK	31 EPCIPKTKEP	41 COPKVPEPCH	51 PKVPEPCQPK	60
70	Seq ID NO: Nucleic Ac Coding seq	uence:	n #: NM_0021 74-505		41	51	
	i	11	21	31	1	Ĩ	
75	CTACCTCGCT GTCGCGCTCG GAAGGGCCAC	AGCATGTCGG TCGCGCGCCG TACGCCGAGC	GCCGCGGCAA GCCGCGGCAA GCCTCCAGTT GCGTTGGCGC TCCTGGAGCT	GACTGGCGGC CCCAGTGGGC CGGCGCGCCA	AAGGCCCGCG CGTGTACACC GTGTACCTGG GCGGCCCGCG	CCAAGGCCAA GGCTGCTGCG CGGCAGTGCT ACAACAAGAA	120 180 240 300
80	GACGCGAATC GCTGCTGGGC GCTGCCCAAG CACCCAGGCC	ATCCCCCGCC GGCGTGACGA AAGACCAGCG	ACCTGCAGCT TCGCCCAGGG CCACCGTGGG ACTAAGAGGG TTTAAGGGCC	AGGCGATCCTG GCCGAAGGCG CCCGCGCCCGC	AACGACGAGG CCCTCGGGGG GGCCGGCGGC	AGCTCAACAA AGGCCGTGCT GCAAGAAGGC CCCAGCTCCC	360 420 480 540 600
85	TOGCOGCCCG	GCTCCCTGT	GGGCGGGGG CCGGCGGGG CCGCGGTGCG GACCTCCGTG	CCCTCCGGTA	TCCCCTCCCC TCCCGCACCG	CTTCCGGATG	660 720 780 840

		/086443	000000000	Genvaranon.	cagoogooo	ATOCOGAGTO	900
5	GCTAAGGGGC CAGGGCCGAG CGGCAGCTGC AGACGGCCGC GCCCCTTCTG AGGTCTGCGC	TGCGGGGAGG GTGGGCAGTC AGCCGGGGTG TGGCCGGGAG CGGCCGGGAC TGGGGCCGGG	COGCAGCACC CAGGCCGAGA TCTGGTACCC GCTTTGGTGG CCAGGCCTTT ACGAAGCACT TAGGGGGAGGC	TTCTGGAAGA GCCGGCGGCC CCCCGGCGTG GAGAGACGCG CACATCAGCT TGGTAACAGG CAGAGGCCTG	CTTGGCCTTC CTGAAGGTGA GTGCTTAGCC ATCGCCGGATT CTCCCTCCAT CACATCTTCC CAGTTTGGCT	OSCICTGACG GTGAGGCCCT CAGGACTITC TCGGTCTGGC CTTCATTCAT TCCCGAGTGA TCACGGCTGG	960 1020 1080 1140 1200 1260
10	CTATGTGGAC CCGACGCCGC CAGCACAAGT CTGCAGCTAA	AGCAAGAGTC CCCATTTCCC CGGTTAATCC CCCTTCCACG GATTGTTTT	GTTTTGCGGA TTCCAGCAAA CTGTCTGGAC ACTAGAACCT	ACCICGACTOG CTCAACTOGG TGAGCCTCCG	CAGCCAGGCC CAATCCAAGC TTGGCTTCTG	ACCTAGATAC ACCTAGAATT	1380 1440 1500 1560
15	Seq ID NO: Protein Acc	379 Protein	n sequence	96			
	1	11	21	31	41	51	
20	AEILELAGNA	arakaksess ardnektrii sggekatqas	PRHLQLAIRN	VHRLLRKGHY DEBLNKLLGG	AERVGAGAPV VTIAQGGVLP	MIČWANTEATL ATWANTEATL	60 120
25	Seq ID NO: Nucleic Aci Coding sequ	380 DNA sec id Accession mence:	puence 1 #: AL13694 184-864	2			
30	1	11	21	31	41	51	
30	DECORATIONS.	CAGAAGCTCG GCCGGGAGCC GGTCGACGCT	GGAGCGGCGG	AGGAGCCGGC	AGCAGCGGCG	COGCGGGCTC	60 120 180
25	GCGATGAAGA	TGGTCGCGCC	CTGGACGCGG	TTCTACTCCA	ACAGCTGCTG	CTTGTGCTGC	240 300
35	CATGTCCGCA	CCGGCACCAT TATTGAGTGC	CCTGCTCGGC	CCGGATCAGT	ATAACTTTTC	AAGTTCTGAA	360
	CTGGGGAGGTG	ACTITIGACTI	CATGGATGAT	GCCAACATGT	GCATTGCCAT	TGCGATTTCT	420
	CTTCTCATGA	TOCTGATATG CATTCTTCTG	TGCTATGGCT	ACTTACGGAG	CCCTGAACAT	GTTGGTTGCA	480 540
40	ATCACTGTGC	TTATTTATCC	ARACTCCATT	CAGGAATACA	TACGGCAACT	GCCTCCTAAT	600
	TTTCCCTACA	GAGATGATGT GCATTATCTT	CATGTCAGTG	AATCCTACCT	GTTTGGTCCT	TATTATTCTT	660 720
							780
45	ACTACGGTGC	TGCTACCCCC ACGTGTCTGC	GTATGATGAT	GCCACTGTGA	ATGGTGCTGC	CAAGGAGCCA	840 900
43	CTTTCCAGAC	ATCTGAGCAA	TAGTTOTOTT	ATTTCACTTT	TROCATRAGE	CTCTCTGAGC	960
							1020
		CTTTGCTAGA ACGGGCTTCA					1140
50							1200
	TOCCTOTOTT	TTGAAAATGT GAACAAAACC	AAAATAAAAC	CAAAAATAGA	CAACTTTTTC	CATTOTTOTA	1260
	ATTAGGTAAA	TAGAAGTCCT	TATGTATGTG	TTACAAGAAT	TTCCCCCCACA	ACATCCTTTA	1380
55	TOACTOARCT	TCAATGACAG AGAAAGCACC	TTTOTOTOTO	CTCCTARAGG	ATTTTCTCCA	TGGCCTGAAT	1440 1500
33	TAAGACCATT	AGAAAGCACC	AGGCCGTGGG	GCCTCGTATG	TOTTAGAGGG	TGGAATGGAT	1560
	GTGTTTGGCG	CTGCATGGGA	TCTGGTGCCC	CTCTTCTCCT	GGATTCACAT	CCCCACCCAG	1620
	GGCCCGCTTT	TACTAAGTGT	TOTGCCCTAG	ATTGGTTCAA	GGAGGTCATC	AAAAGGGTTT	1680 1740
60	TOTTTTCCCT	AATTGGGATA GCAAGCTACA	TCCTACTGCT	TTGAACTTCC	AAGTATGTCT	AGTCACCTTT	1800
		ACATTTTCAG ATTGCAAGGG					1860
	TGTTGGTTCA	TTATTGAATG	TGCTGTAAAT	TAAGTCGTTT	GCAATTAAAA	CAAGGTTTGC	1980
65	CCACATCCAA	AAAAAAAAA	YYYYY				
05	Seq ID NO: Protein Acc	381 Protei	n sequence CAB6687	16			
70	1	11	21	31	41	51	
/0	 MKMVAPHTRF	YSNSCCLCCH	VRTGTILIAV	WYLIINAVVL	LILLSALADP	DOYNPSSSEL	60
	GGDFRFMDDA	NMCIAIAISL	LMILICAMAT	YGAYKORAAW	IIPFFCYQIF	DFALNMLVAI	120
	TVLIYPNSIQ	EYIROLPPNF VLVYVTSNDT	PYRDDVMSVN TVI.I.PDVDDA	TUNCAAKEPP	FISIILTFKG PPVVSA	AFISCAMUCA	180
75							
	Seq ID NO: Nucleic Ac Coding seq	382 DNA sed id Accession mence:	quence n #: NM_0025 92-1774				
80	1	11	21	31	41	51	
	Charmooca c	AAGAACACTG	in the second se	TGGACGGGCC	CAGAGGANTO	CAGAGTTAAA	60
	COTTOLOGIC	CTGCGTCCGT	CACRATTURG	CATGGAATGT	CTCTACTATT	TCCTGGGATT	120
85	TOTAL CENTRAL	CONTRACATOR	TGCCACTTGA	TGCCGCCAAA	CHATTTCATG	ATGTGCTGGG	180 240
03	TGARAATGAC	TGGAATGAAA	AACTCTACCC	AGTGTGGAAG	CGGGGAGACA	GGTCTTCTGA TGAGGTGGAA	300
	AAACTCCTGG	AAGGGAGGCC	GTGTGCAGGC	GGTCCTGACC	AGTGACTCAC	CAGCOCTCGT	360

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	GGGCTCAAAT	ATAACATTTG	CGGTGAACCT	GATATTOOCT	AGATGCCAAA	AGGAAGATGC	420
	CAATGGCAAC	ATAGICTATG	AGAAGAACTG CATGGTCAGA	CAGAAATGAG	GCTGGTTTAT	CTGCTGATCC	480 540
			CTGATGGGAA	ACCTTTTCCT	CACCACCCCG	GATGGAGAAG	500
5	ATGGAATTTC	ATCTACGTCT	TCCACACACT	TGGTCAGTAT	TTCCAGAAAT	TGGGACGATG	660
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	COTGGTAACA	GATCAGATTC	CIGTGTTTGT	GACTATGTTC	CAGAAGAACG	ATCGARATTC	840
10	ATCCGACGAA	ACCITCCTCA	AAGATCTCCC	CATTATGTTT	GATGTCCTGA	TTCATGATCC	900
10	TAGCCACTTC	CTCAATTATT	CTACCATTAA ATACTGTGAA	CTACAAGTGG	AGCTTCGGGG	ATAATACTGG	960 1020
	CCTTABCCTC	ACTGTGAAAG	CTGCAGCACC	AGGACCTTGT	CCGCCACCGC	CACCACCACC	1080
	CAGACCTTCA	AAACCCACCC	CTTCTTTAGG	ACCTGCTGGT	GACAACCCCC	TGGAGCTGAG	1140
15		GATGAAAACT	GCCAGATTAA AGGTTAACAT	CAGATATGGC	CACTTTCAAC	TOATGOCOOT	1260
15	GCCATGGCCT	GARAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCATTCCCAC	1320
	GGAGGTCTCT	ACCATCATTT	CTGA CCCCAC	CTGCGAGATC	ACCCAGAACA	CAGTCTGCAG	1380
	CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
20	GACGTACTGT	CCTTACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAACA	GTGCCCTGAT	1560
	CTCCGTTGGC	TGCTTGGCCA	TATTTGTCAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAAACA	1620
	CAAGGAATAC	AACCCAATAG	AAAATAGTOO	TGGGAATGTG	GTCAGAAGCA	AAGGCCTGAG	1680 1740
	TGTCTTTCTC	CARGARTTTA	AAGCOGTGTT AAGGAGTTTC	TTALATTTCG	ACCURGINAN	TGAAGCTCAC	1800
25	TTTTCMGTGC	CATTGATGTG	AGATGTGCTC	GAGTGGCTAT	TAACCTTTTT	TTCCTAAAGA	1860
	TTATTGTTAA	ATACATATTG	TGGTTTGGGG	AAGTTGAATT	TTTTATAGGT	TAAATGTCAT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATACTGCA CTTTTCATTA	GUCAGCITCA	TTCACTTATA	AAGTCTTAGG	2040
	TARCTROTAG	CATACAAACA	CTGTGTCCCCG	AGAGTAAGGA	GAGAAGCTAC	TATTGATTAG	2100
30	3000m33000	AGGTTAACTG	CDAGAAGAGG	COGGATACTT	TCAGCTTTCC	ATGTAACTGT	2160
	ATGCATAAAG	CCAATGTAGT	CCAGTTTCTA TCCTGATGGA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220
	GTGCACACTT	GCTAGACTCA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
20	TGA CAACCTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCCAT	2400
35	GGACATITAG	TTAGTGCTTT	TTATATACCA TCGCTGCACA	GGCATGATGC	TGAGTGACAC	TCTTGTGTAT	2460
	ATTTCCAAAT	CONCRETENT	CATGGCAACT	TGATCAGTAA	GGATTTCACC	TCTGTTTGTA	2580
	ACTAAAACCA	TCTACTATAT	GTTAGACATG	ACATTCTTTT	TCTCTCCTTC	CTGAAAAATA	2640
40	AAGTGTGGGA	AGAGACAAAA	AAAAAAAA				
40	Sea ID NO:	383 Protein	sequence				
	Protein Ac	ression # ·	NP_0025	01			
				~-			
					41	51	
45	1	11	21 	31	41 	1	
45	1 MECLYYFIGE	11 -	21 AAKRFHDVLG	31 NERPSAYMRE	HNQLNGWSSD	ENDWNEKLYP	60
45	1 MECLYYFLGF WKRGDMRWK RNEAGLGADD	11 LLLAARLPLD NSWKGGRVQA YVYNSTAWSE	21 AAKRFHDVLG VLTSDSPALV DSDGENGTGO	31 MERPSAYMRE GSNITFAVNL SHHNVFFDGK	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR	ENDWMEKLYP NGNIVYERNC WMPIYVFHTL	120 180
	1 	11 LLLAARLPLD NSWKGGRVQA YVYNWTAWSE	21 AAKRFHDVLG VLTSDSPALV DSDGENGTOQ VTLGDOLMEV	31 NERPSAYMRE GSNITFAVNL SHENVFPDGK TUYBRHCRAY	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR VPIAOVKDVY	ENDWMEKLYP MGMIVYEKMC WMPIYVFHTL VVTDOIPVFV	120 180 240
45 50	1 	11 LLLAARLPLD MSHKGGRVQA YVYNUTAWS SVRVSVNTAW SOETFLKDLP	21 AAKRFHDVLG VLTSDSPALV DSDGENGTGQ VTLGPQLMEV INFDVLIHDP	31 MERPSAYMRE GSNITFAVNL SHENVFFDGK TVYRREGRAY SHFLNYSTIN	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR VPIAQVKDVY YKNSFGDNTG	 ENDWMEKLYP NGNIVYEKNC WMFIYVFHTL VVTDQIPVFV LFVSTMHTVN	120 180 240 300
	1 MECLYYFLGF VWKRGDMRWK RNEAGLSADP GQYFQKLGRC TMFQKMDRNS HTYVLNGTFS	11 LLLAARLPLD MSWKGGRVQA YVYNUTAWSE SYRVSVNTAN SDETFLKDLP LNLTVKAAAP	21 AAKRFHDVLG VLTSDSPALV DSDGENGTOQ VTLGPQLMEV IMPDVLIHDP GPCPPPPPPP	31 NERPSAYMRE GSNITFAVNL SHENVFPDGK TVYRRHGRAY SHELNYSTIN RPSKPTPSLG	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR VPIAQVKDVY YKWSFGDNTG PAGENPLELS	ENDWHEKLYP NGRIVYERNC WNFIYVFHTL VVTDQIPVFV LFVSTNHTVN RIPDENCQIN	120 180 240
	1 MECLYYFLGF VWERGDMRWK RNEAGLSADP GQYFQKLGRC TMFQKNDRNS HTYVLNGTFS RYGHFQATIT	LLLAARLPLD NSWKGGRVQA YYYNWTAWSE SVRVSVNTAN SDETFLKDLP LNLTVKAAAP IVEGILEVNI	21 AAKRFHDVLG VLTSDSPALW DSDGENGTGQ VTLGPQLMEV INFDVLIHDP GPCPPPPPPP IQMTDVLMEV TURR TRUGSG	31 	HNQLNGWSSD IFPRCQKEDA PPPHHPGWRR VFIAQVKDVY YKWSFGDNTE PAGNPLELS VYTQGSIPT DTSLALTSTL	ENDWHEKLYP NGNIVYERNC WNPIYVFHTL VVTDQIPVFV UFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	1 MECLYYFLGF VWERGDMRWK RNEAGLSADP GQYFQKLGRC TMFQKNDRNS HTYVLNGTFS RYGHFQATIT CEITQNTVCS PLRNUNSALI	11 LLLAARLPLD NSWKGGRVQA YYYNUTAUSE SYRVSVNTAN SDETFLKDLP LNLIVKAAAP IYPGILEVNI PUDVDEMCLL SVGCLAIFVT	21 AAKRFHDVLG VLTSDSPALV DSDGENGTOQ VTLGPQLMEV IMPDVLIHDP GPCPPPPPPP	31 	HNQLNGWSSD IFPRCQKEDA PPPHHPGWRR VFIAQVKDVY YKWSFGDNTE PAGNPLELS VYTQGSIPT DTSLALTSTL	ENDWHEKLYP NGNIVYERNC WNPIYVFHTL VVTDQIPVFV UFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420
	1 MECLYYFLGF VWERGDMRWK RNEAGLSADP GQYFQKLGRC TMFQKNDRNS HTYVLNGTFS RYGHFQATIT CEITQNTVCS PLRNUNSALI	LLLAARLPLD NSWKGGRVQA YYYNWTAWSE SVRVSVNTAN SDETFLKDLP LNLTVKAAAP IVEGILEVNI	21 AAKRFHDVLG VLTSDSPALW DSDGENGTGQ VTLGPQLMEV INFDVLIHDP GPCPPPPPPP IQMTDVLMEV TURR TRUGSG	31 	HNQLNGWSSD IFPRCQKEDA PPPHHPGWRR VFIAQVKDVY YKWSFGDNTE PAGNPLELS VYTQGSIPT DTSLALTSTL	ENDWHEKLYP NGNIVYERNC WNPIYVFHTL VVTDQIPVFV UFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	MECLYYFLGF VWKRGDMNK RNEAGLSADP GQYFQKLGRC TMFQKNDRNS HTYVLNGTFS RYGHFQATIT CBITQNTVCS PLRMANSALI FPGNQEKDPL	11	21 AAKRFHDVLG AAKRFHDVLG VLTSDSPALV USDGENGTOQ VTLOPQLMEV IMPDVLIHDP IQMTDVLMEV TVRRTFNGSG VISLLVYKKE Quence	31 MERPSAYME GSNITFAVNL SHENVFDOK TVYRHGRAY SHFLNYSTIN PWPESSLIDF TYCVNLTIGD KEYNPIENSP	HNQLNGWSSD IFPRCQKEDA PPPHHPGWRR VFIAQVKDVY YKWSFGDNTE PAGNPLELS VYTQGSIPT DTSLALTSTL	ENDWHEKLYP NGNIVYERNC WNPIYVFHTL VVTDQIPVFV UFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	1 MECLYYFLGF VMKRGDMMK RNEAGLSADP GCYFOXLGGC THFQXNDRNS HYVLNGTFS RYGHPQATIT CBITONTVCS PLRMANSALI FPGNQEKDPL SWCOLD ID MO: Nucleic Ac.	11 LLAARLPLD MSHKOGRVOA YVYNUTAWSE SVRVSWYTAN SDETFLKOLP LINLTVKAAAP IVEGLAIFUT LKNQEFKGVS 384 DNA seid d Accessio:	21 AAKRIHDVLG VLTSDSPALW DSDGENGTOQ VTLOPQLMEDV GPCPPPPPPP IQMTDVLMPV TVRRTFNGSG VISLLVYKKE Quence n #: NM 0011	31 NERPSAYME GSNITFAUNL SHEHNYPDGK TVYRHGRAY SHELNYSIN RPSKPTPSLG PWPESSLIDP TYCVHLILGD KEYMPIENSP	HNQLNGWSSD IFPRCQKEDA PPPHHPGWRR VFIAQVKDVY YKWSFGDNTE PAGNPLELS VYTQGSIPT DTSLALTSTL	ENDWHEKLYP NGNIVYERNC WNPIYVFHTL VVTDQIPVFV UFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	MECLYYFLGF VWKRGDMNK RNEAGLSADP GQYFQKLGRC TMFQKNDRNS HTYVLNGTFS RYGHFQATIT CBITQNTVCS PLRMANSALI FPGNQEKDPL	11 LLAARLPLD MSHKOGRVOA YVYNUTAWSE SVRVSWYTAN SDETFLKOLP LINLTVKAAAP IVEGLAIFUT LKNQEFKGVS 384 DNA seid d Accessio:	21 AAKRFHDVLG AAKRFHDVLG VLTSDSPALV USDGENGTOQ VTLOPQLMEV IMPDVLIHDP IQMTDVLMEV TVRRTFNGSG VISLLVYKKE Quence	31 NERPSAYME GSKITFAUNL SHHWYFDGK TVYRRHGRAY SHFLMYSTIN RPSKPTPSLG PWPESSLIDF TYCVML/ILGD KEYMPIEMSP	ENQLNOWSSD IFPRCOKEDA PPPHHEGARR VPIAQVKOVY YKNSFGDNTC PAGDNPLELS VYTOGGSTD DTSLALTSTL GNVVRSKGLS	ENDMNEKLYP NGRIVYERIC WNFIYVEHTL VYTDQIBYFV LFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS VFLNRAKAVF	120 180 240 300 360 420 480
50	1 MECLYYFLGF VMKRGDMMK RNEAGLSADP GCYFOXLGGC THFQXNDRNS HYVLNGTFS RYGHPQATIT CBITONTVCS PLRMANSALI FPGNQEKDPL SWCOLD ID MO: Nucleic Ac.	11 LLAARLPLD MSHKOGRVOA YVYNUTAWSE SVRVSWYTAN SDETFLKOLP LINLTVKAAAP IVEGLAIFUT LKNQEFKGVS 384 DNA seid d Accessio:	21 AAKRIHDVLG VLTSDSPALW DSDGENGTOQ VTLOPQLMEDV GPCPPPPPPP IQMTDVLMPV TVRRTFNGSG VISLLVYKKE Quence n #: NM 0011	31 NERPSAYME GSNITFAUNL SHEHNYPDGK TVYRHGRAY SHELNYSIN RPSKPTPSLG PWPESSLIDP TYCVHLILGD KEYMPIENSP	HNQLNGWSSD IFPRCQKEDA PPPHHPGWRR VFIAQVKDVY YKWSFGDNTE PAGNPLELS VYTQGSIPT DTSLALTSTL	ENDWHEKLYP NGNIVYERNC WNPIYVFHTL VVTDQIPVFV UFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	MECLYYFLGF VWKRGDMNK RNEAGLSADP GYFGKLGRC TMFQKNDRNS RYGHFQATIT CEITONTVCS PLRMANSALI FPGNQEKDPL Nucleic Ac- Coding seq	11 LLLARLPLD LLLARLPLD MSHWGGRVQA YYYMNTAWSE SYRVSWYTAM SDETFLKDLP LINLTWIANDPIVEGILEWNI PVDUDEMCLI SVGCLAIFUT LINUEFKGVS 384 DNA sei did Accessionence:	21	31 NERPSAYME GSKITFAUNL SHHWYFDGK TVYRHGRAY SHFLMYSTIN RPSKPTPSLG TYCVMLTLGD KEYNPIENSP	ENQLNGWSSD IFPRCOKEDA PFPHHEGWRE VPIAQVEDYY YKWSFGDNTG PAGENPLELS VYTOQGSIFT DTSLALTSTL GNVVRSKGLS	ENDWHEKLYP NGRITYERIC WRITYPHTL VYTD(19VFV LFVSTNHTVN RIPDENCQIN ISVDRDPAS VFLNRAKAVF	120 180 240 300 360 420 480
50 55 60	MECLYYFLGF VWKRGDMNK RNEAGLSADP GYFGXLGRC TMFQXNDRNS RYGHPQATIT CSITONTUCS PLRMNSALI FPGNQEKDPL Nucleic Ac. Coding sequ TCCATATTGT AATGAATTTT	11	21	31 MERPSAYMRE GSN ITFAUNL SHENVFDIGK SHENVFDIGK FPSKPIPSLG PWPESSLIDF TYCVM/LID KEYMPIENSP 34 31 CARAATRACT TTACTGAATC	 HNQLNGWSSD IFPRCOKEDA PFPHHEFORME VPIAQVKDVY XKHSFGDNTG PAGDNPLELS UVYTCQGSIPT DTSLALTSTL GNVVRSKGLS	ENDMNEKLYP NGRIVYEKIC WRITYPHTL VYTDQI ZEVE LEVSTRHITVN EVCTISDPA SVFLNRAKAVF 51 AAGTGGGTGG CATAGAAATG	120 180 240 300 360 420 480 540
50	MECLYYFLGF VMKMGDMRWK RNEAGLSADP GGYFONLGRC THMPOKNDRNS HTYVLMGTFS RYGHROATHT CEITONTVCS PLRMNSALI FPGMGEKDPL Seq ID MO: Nucleic Ac: Coding Seq I TCCATATTGT AATCAATTTT AATCAATTTT	LLLARRLPLD NSWEGGRVGA YVYNHTANG SVETTLKOLP YVYNHTAN SDETFLKOLP FILOULP PUDUPEMCLL SVGCLAIFVT LKNQEFKGVS 384 DNA seid Accessio: tence: 11 GGTTGCACCA TTTAATTTC	21	31 MERPSAYMRE GSN ITFANNL SHENYFDGK TVYRRHGRAY SHFLMYSTIG PWPESSLIDF TYCVILITIGA KEYNPIENSP 34 31 CARARTRACT TTACTGARTC	HNQLNGWSSD IFFRCQKEDA IFFRC	ENDWHEKLYP NGHIVIEKHC WHEIVEKHC WHEIVEKHC WHEIVEKHCH WHIDLENCH LFVSTHHTVH LFVSTHHTVH LFVSTHHTVH LFVSTHHTVH LFVSTHHTVH LFVSTHHTVH LFVSTHHTVH LFVSTHHTVH LFVSTHHTVH SIDDENCH SIDDENCH LFVSTHHTVH LFVSTHHT LFVSTHHTVH LFVSTHHTVH LFVSTHHT LFVSTHHTVH LFVSTHHT LF	120 180 240 300 360 420 480 540
50 55 60	1 BECLYYFLGF VMKRGDMRMK RNEAGLSADP GGYFGNLGRC HYPOKNDRNS HYVLNGTFS RYGHPGATL CEITONTUCS PLRMMNSLI FFGNGEKDPL Seq ID NO: Nucleic Acc Coding seq 1 CCATATTOT AATCAATTTT AATCAATTTT AATTGAATT ACCTRGCTAC	11 LLLARELPLD LLLARELPLD MSHKGGRVQA YYYRHTAMSE SYMSWITHEN SEFFIKEDLP LHENTWRAPP PUDIEMCLI SYGCLAIFUT LONGEFKGVS 384 DNA se id Accession ence 1 GCTTCCACCA AGCTTCCATCA AGCTTCCATCA AGCTTCCATCA AGCTTCCATCA AGCTTCCATCA AGCTTCCATCA AGCTTCCATCA AGCTTCCATCA AGCTTCCATCA CATATITITE CATATITUTE CATAT	21 AAKRFHDVLG VLTSDSPALM DSDGENGTOQ VTLGPQLMEV VTLGPQLMEV TURPDVLHED GPCPPPPPPP TVRRTFNGSG VISLLVYKKE THENCE THENCE CTGCCAATAA TTTGGATTCTT TTGGATTCTT TTGGATTCTT TTGGATTCTT	31 MREPSAYNES GSKITFAVUL SHENYFDOK TYVREIGANY SHEJMYSTIN FRSKTFSIS PMPSSSLIDF TYCVMILICAD KEYMPIENSP 34 31 CARAATAACT TTACTGAATC ACCAATTAC	I HNOLNGWSSD IFPROXEDA PPPHHFGWRR PPPHHFGWRR VFIAQVKDVY YKWSFGDWTG DYSLALTSTL GNVVRSKGLS 41 AGCARCCATG CAGRACACTG CAGRACACTG TGCAGAGATA	ENDMNEKLYP NGNIVYEKRC WNEIVYEKRC WNEIVYEKRL WYTDQIEVFU LFYSTNHTVN EVCTISDPAS VFLNRAKAVF 51 AAGTGGGTGG CATAGAAATG AGTTTACCTG	120 180 240 300 360 420 480 540
50 55 60	1 MECLYYLIGF WIREGORNEN RINGGIGENO PORTO CONTROL CON	11 LLLARRIPLD MSHKOGRUÇA VYUNITAMSE SVRIVNITAM SEBETILKUL SALAKUL SEBETILKUL SEBETILKUL SALAKUL SEBETILKUL S	21 AAKRPHDVLG AAKRPHDVLG VLTSDSPALW DEDGENGTOG VTLGPGLMEV VTLGPGLMEV VTLGPGLMEV TVRRTPRIGG VISLLVYKKE ZUENCE 1	31	I HIGHAGUSED I PERCOKEDA PEPHENGAREN PEPHENGAREN VETAQVICIDIY YKURSEDINIG PAGIONELES VITOGGIFT DISLALITSII GMYVESKGLS 41 AGGARCCATO CAGGARCACTO TGCANAGATA CACTITACAMA TGGANAGATA TGGANAGATA	ENDMNEKLYP NGSIVYEKNC WNPIYVEHC WNPIYVEHC VUTOQIPVEV LEVISTIBITO EVCTIISDEN EVCTIISDEN ISVPDRDPAS VFLNRAKAVF 51 ANATOGGTOG CATAGANATC AGTITAGCTC GRAGTAAGCA CAGTCTTCAG	120 180 240 300 360 420 540 540
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50 55 60 65	1 MECLYFIGF WINGODENK RENACLEAD OF THE METALLAND OF THE	11 LLLAARLPLD LLLAARLPLD MSHKOGRWQA MSKACACACACACACACACACACACACACACACACACACAC	21 AMS HEWIGE VICTORISES AND VICTO	31 NEEPPANREE NEEPPANREE NEEPPANREE NEET TPANREE SHETTINGE SHEDINGE SHEDIN	I HOLMOWSD I FPRCOXEDA I FPRCOXEDA I FPRCOXEDA PPHENDRING VI LAVINGTONI PAGONDIELS VITOGOSIETA GRAVES 41 I GRAVES GRACCATO CAGRACCATO CATCACACAT CATCACATT CATCACATT CATCACATT CATCACT CATTACT CAGTURATION CATTACATO CATTACATO CATTACATO CATTACATO CATTACATO CAGTURATO CAGTUR	EDMHERLYP NONIVYERIC WAPTIVYERI WATOLOFF LEVESTERTW RIPDENCIN	120 180 300 420 480 540 60 120 240 300 420 480 540 600
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50 55 60 65	1 MECLYYFLGF WINEGORNEN MECLYYFLGF WINEGORNEN MEN GEROACHAN MEN GEROAC	11 LLLAARLPLD I LLLAARLPLD I MSHUGGRVQA MSHUGGRVQA MSHUGGRVQA STANSWATAN SDETILMDIP IVEGILEVNI PVUDUENCLI SVOCLAF FOT LUNCEFRCUS 384 DNA se did Accessio- ience: 11 GCTTCCACCA AGCTTCCATA AGCTTCCATA AGCTCCATA AGCTCCATA AGCACACA CANAAAGCC CANAAAGCC TGAAGCTAT AGGACATAT AGGACATAT AGGACATAT AGGACATAC AGATTCCATA AGGACATCA AGATTCCATAC AGATTCATAC AGATTCCATAC AGATTCATAC AGATTCCATAC AGATTCCATAC AGATTCCATAC AGATTCCATAC AGATTCCATAC	21 AMS HIDVIG IAMS HIDVIG IAMS HIDVIG WIFSDSPAIN DSDGSMATO DSDGSMATO OTTOPOPPPP IQNTDVIMPV TYMER PIMSGS VISULVIKEE UNITED OTTOPOPPPPP IQNTDVIMPV TYMER PIMSGS VISULVIKEE UNITED OTTOPOPPPPP CTOCCANTAN CT	31 III PANNES GENTTPANNES GENTES GENTTPANNES GENTTPANNES GENTTPANNES GENTTPANNES GEN	ENQLISHES AND THE ACCOUNTS AND THE ACCOU	EDDMIRKLYP NONIVYERIC NONIVYERIC NONIVYERIC NONIVYERIC NONIVYERIC NONIVYERIC NONIVYERIC NONIVYERIC SUPERICA SUPERICA SUPERICA NAGORIA SUPERICA SUPE	120 180 240 300 360 420 480 540 120 240 300 420 480 660 660 660 6720
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		TGAAATGACT					1560
		GAGGCCATGC					1620
		TGACAAGTTC					1680
_		GAAGCAAGAG					1740
5		TGAGGCTGTC					1800
		GGAAGTCTGC					1860
		AGTTTAAATT					1920
		TCTCTTTAAT					1980
	AAAGACTTTT	ATGTGAGATT	TOCTTATCAC	AGAAATAAAA	TATCTCCAAA	TG	
10							

Seq ID NO: 385 Protein sequence Protein Accession #: NP_001125

	TIOCCIII ACI	acceptor #1					
15	1 MKWVESIFLI	11 FLLNFTESRT	21 LHRNEYGIAS	31 ILDSYQCTAE	41 SLADLATIF	51 FAQFVQEATY	60
	KRUSKMUKDA	LTAIEKPTGD	EOSSGCLENO	LPAPLEELCH	EKRILEKYGH	SDCCSQSEEG	120
	RHNCFLAHKK	PTPASIPLFQ	VPEPVTSCEA	YEEDRETFMN	KFIYEIARRH	PFLYAPTILL	180
	WAARYDKIIP	SCCKAENAVE	CPOTKAATVT	KELRESSLIN	QHACAVMENT	GTRTFQAITV	240
20		NPTEIQKLVL					300
	ECCKLTTLER	GOCITHAEND	EKPEGLSPNL	NRFLGDRDFN	QFSSGEKNIF	LASFVHEYSR	360
		LRVAKGYQEL					420
	KLGEYYLONA	FLVAYTKKAP	OLTSSELMAI	TRKMAATAAT	CCOLSEDKLL	ACGEGAADII	480
~-	IGHLCIRHEM	TPVNPGVGQC	CTSSYANRRP	CFSSLVVDET	YVPPAPSDDK	PIPHKDLCQA	540
25	QGVALQTMKQ SKTRAALGV	EPLINLVKQK	PQITEEQLEA	VIADFSGLLE	KCCQGQBQEV	CFAREGOKLI	600

Seq ID NO: 386 DNA sequence Nucleic Acid Accession #: NM_002205.1 Coding sequence: 1..3149

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	ATGGGGGGGGCC	GGACGCCAGA	STECCCTCTC	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
35	CGCCGACCCC	CGCTSSTGCC	GCTGCTGTTG	CTGCTSSTGC	CGCCGCCACC	CAGGGTCGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TOGAGTTTTA	CCGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
	CCCAAGGCTA	ATACCAGCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCCT	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAGG	CTCTCGGCTC	360
40	CTGGAGTCCT	CACTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCCTTGCAG	420
	TOGTTCGGGG	CAACAGTTCG	AGCCCATGGC	TCCTCCATCT	TGGCATGCGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTCAG	CTGGGCAGCA	600
	GGACAGGGTT	ACTGCCAAGG	AGGCTTCAGT	GCCGAGTTCA	CCAAGACTGG	COGTGTGGTT	660
45	TTAGGTGGAC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGTCTGCCAC	TCAGGAGCAG	720
	ATTGCAGAAT	CTTATTACCC	CGAGTACCTG	ATCAACCTGG	TTCAGGGGCA	GCTGCAGACT	780
		GTTCCATCTA					840
		ATGACACAGA					900
-0		CCATCCTTAA					960
50	CAGATGGCCT	CCTACTTTGG	CTATGCAGTG	GCCGCCACAG	ACGTCAATGG	GGACGGGCTG	1020
		TGGTGGGGGC					1080
	GAGGTGGGCA	GGGTCTACGT	CTACCIGCAG	CACCCAGCCG	GCATAGAGCC	CACGCCCACC	1140
	CITACCCTCA	CTGGCCATGA	TGAGTTTGGC	CGATTTGGCA	GCTCCTTGAC	CCCCCTGGGG	1200
55	GACCTGGACC	AGGATGGCTA	CAATGATGTG	GCCATCGGGG	CTCCCITTGG	TGGGGAGACC	1260
22	CAGCAGGGAG	TAGTGTTTGT	ATTTCCTGGG	GGCCCAGGAG	GGCTGGGGCTC	TAAGCCTTCC	1320
	CAGGTTCTGC	AGCCCCTGTG	GGCAGCCAGC	CACACCCCAG	ACTTCTTTGG	CTCTGCCCTT	1380
	CGAGGAGGCC	GAGACCTGGA	TGGCAATGGA	TATCCTGATC	TGATTGTGGG	GTCCTTTGGT	
	GTGGACAAGG	CTGTGGTATA	CAGGGGCCGC	CCCATCGTGT	CCGCTAGTGC	CTCCCTCACC	1500 1560
60	ATCTTCCCCG	CCATGTTCAA	CCCAGAGGAG	CGGAGCTGCA	GCTTAGAGGG	BOY CACCALLIA	1620
00		ACCTTAGCTT TOGAACTTCA					1680
		CCTCCAGGCA					1740
	CTGTTCCTGG	GCAGAGAGAT	GGCAACCCTG	ACCUAGACCC	TOCTONICON	GAGAGAGAGA	1800
	OBAGMOSATI	TTCACATCGC	TOWARD COTTO	TCCTTCCACC	CCCNACCCC	AGTGGACAGC	1860
65	CICICOCCON	GGCCAGCCCT	ACATTATCAC	FOCT TOOMCC	GCATAGAGGA	CARCICCTOR	1920
05	A TROTTER CTOCK	ACTGTGGAGA	MACABCATC	TGTGTGTGCCTG	ACCTGCAGCT	GGAAGTGTTT	1980
	CCCCACCACA	ACCATGTGTA	CCTGGGTGAC	PAGRATICOCC	TGAACCTCAC	TTTCCATGCC	2040
	CACAATCTCC	GTGAGGGTGG	CCCCTATGAG	COTCACOTTO	GCGTCACCGC	CCCTCCAGAG	2100
	CONCAGRACT	CAGGACTCGT	CAGACACCCA	GGGAACTTCT	CCAGCCTGAG	CTGTGACTAC	2160
70	TTTGCCGTGA	ACCAGAGCCG	CCTGCTGGTG	TGTGACCTGG	GCAACCCCAT	GAAGGCAGGA	2220
	CCCACTCTOT	GGGGTGGCCT	TOOGTTTACA	GTCCCTCATC	TCCGGGACAC	TAAGAAAACC	2280
	ATCCAGTITIG	ACTTCCAGAT	CCTCAGCAAG	AATCTCAACA	ACTOGGAAAG	CGACGTGGTT	2340
	TECTTTOGGE	TCTCCGTGGA	GGCTCAGGCC	CAGGTCACCC	TGAACGCTGT	CTCCAAGCCT	2400
	GAGGCAGTGC	TATTCCCAGT	AAGCGACTGG	CATCCCCGAG	ACCAGCCTCA	GAAGGAGGAG	2460
75	GACCTGGGGAC	CIGCIGICCA	CCATGTCTAT	GAGCTCATCA	ACCAAGGCCC	CAGCTCCATT	2520
		TGCTGGAACT					2580
	GTGACCAGAG	TTACGGGACT	CAACTGCACC	ACCAATCACC	CCATTAACCC	AAAGGGCCTG	2640
	GAGTTGGATC	CCCAGGGTTC	CCTGCACCAC	CAGCAAAAAC	GGGAAGCTCC	AAGCCGCAGC	2700
	TCTGCTTCCT	CGGGACCTCA	GATCCTGAAA	TGCCCGGAGG	CTGAGTGTTT	CAGGCTGCGC	2760
80	TGTGAGCTCG	GGCCCCTGCA	CCAACAAGAG	AGCCAAAGTC	TGCAGTTGCA	TTTCCGAGTC	2820
	TGGGCCAAGA	CTTTCTTGCA	GCGGGAGCAC	CAGCCATTTA	GCCTGCAGTG	TGAGGCTGTG	2880
	TACAAAGCCC	TGAAGATGCC	CTACCGAATC	CTGCCTCGGC	AGCTGCCCCA	AAAAGAGCGT	2940
	CAGGTGGCCA	CAGCTGTGCA	ATGGACCAAG	GCAGAAGGCA	GCTATGGCGT	CCCACTGTGG	3000
0.5	ATCATCATCC	TAGCCATCCT	GTTTGGCCTC	CTGCTCCTAG	GTCTACTCAT	CTACATCCTC	3060
85		GATTCTTCAA		CCATATOGCA	CCGCCATGGA	AAAAGCTCAG	3120
	CTCAAGCCTC	CAGCCACCTC	TGATGCCTGA				

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Seg ID NO: 387 Protein seguence Protein Accession #: NP_002196.1

5	1	11	21	31	41	51	
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	MGSRTPESPL	HAVOLRUGPR	RRPPLLPLLL	LLLPPPPPRVG	GFNLDARAPA	VLSGPPGSFF	60
	GESVEFYRPG	TDGVSVLVGA	PKANTSOPGV	LOGGAVYLCP	WGASPTOCTP	IBFDSKGSRL	120
	LESSLSSSEG	BEPVEYKSLO	WFGATVRAHG	SSILACAPLY	SWRTEKEPLS	DPVGTCYLST	180
10	DNFTRILEYA	PCRSDFSWAA	GOGYCOGGES	AEFTKTGRVV	LGGPGSYFWQ	GQILSATQBQ	240
	IAESYYPEYL	INLVOGOLOT	ROASSIYDDS	YLGYSVAVGE	PSGDDTEDFV	AGVPKGNLTY	300
	GYVTILNGSD	IRSLYNFSGE	QMASYFGYAV	AATDVNGDGL	DDLLVGAPLL	MDRTPDGRPQ	360
	EVGRVYVYLO	HPAGIEPTPT	LTLTGHDEFG	RFGSSLTPLG	DLEQDGYNDV	AIGAPFGGET	420
	COGVVFVFPG	GPGGLGSKPS	OVLOPINAAS	HTPDFFGSAL	RGGRDLDGNG	YPDLIVGSFG	480
15		PIVSASASLT					540
	GFTVELOLDW	OKOKGGVRRA	LFLASROATL	TOTLLIQNGA	REDCREMKIY	LRNESBFRDK	600
	LSPIHIALNE	SLDPOAPVDS	HGLRPALHYO	SKSRIEDKAQ	ILLDCGEDNI	CVPDLQLEVF	660
	GEONHVYLGD	KNALNLTPHA	ONVGEGGAYE	AELRVTAPPE	AEYSGLVRHP	GNFSSLSCDY	720
	PAVNOSRLLV	CELGNPMKAG	ASLWGGLRFT	VPHLRDTKKT	IQPDFQILSK	NUMBUSDAN	780
20	SPRLSVEAGA	OVTLNGVSKP	EAVLFPVSDW	HPRDOPOKEE	DLGPAVHHVY	ELINGGPSSI	840
	SOGVLELSCP	QALEGQQLLY	VTRVTGLNCT	THEPINPEGL	ELEPEGSLHH	OOKREAPSRS	900
	SASSGPOILK	CPEABCFRLR	CELGPLHOOE	SOSLOLHFRV	WAKTFLOREH	QPFSLQCEAV	960
	YKALKMPYRI	LPRQLPQKER	OVATAVONTK	AEGSYGVPLW	IIILAILPGL	PPPCFIAIF	1020
		PYGTAMEKAO					
25							

Seq'ID NO: 388 DNA sequence Nucleic Acid Accession #: NM_002425 Coding sequence: 26..1453

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	TGCCCAGCAA	TACCTAGAAA	AGTACTACAA	CCTCGAAAAG	GATGTGAAAC	AGTTTAGAAG	180
35		AATCTCATTG					240
	GGTGACAGGG	AAGCTAGACA	CTGACACTCT	GGAGGTGATG	CGCAAGCCCA	GGTGTGGAGT	300
	TCCTGACGTT	GGTCACTTCA	GCTCCTTTCC	TGGCATGCCG	AAGTGGAGGA	AAACCCACCT	360
	TACATACAGG	ATTGTGAATT	ATACACCAGA	TTTGCCAAGA	GATGCTGTTG	ATTCTGCCAT	420
	TGAGAAAGCT	CTGARAGTCT	GGGAAGAGGT	GACTCCACTC	ACATTCTCCA	GGCTGTATGA	480
40	AGGAGAGGCT	GATATAATGA	TCTCTTTCGC	AGTTAAAGAA	CATGGAGACT	TTTACTCTTT	540
	TGATGGCCCA	GGACACAGTT	TGGCTCATGC	CTACCCACCT	GGACCTGGGC	TTTATGGAGA	600
	TATTCACTTT	GATGATGATG	AAAAATGGAC	AGAAGATGCA	TCAGGCACCA	ATTTATTCCT	660
	CGTTGCTGCT	CATGAACTTG	GCCACTCCCT	GGGGCTCTTT	CACTCAGCCA	ACACTGAAGC	720
	TTTGATGIAC	CCACTCTACA	ACTCATTCAC	AGAGCTCGCC	CAGTTCCGCC	TTTCGCAAGA	780
45	TGATGTGAAT	GGCATTCAGT	CTCTCTACGG	ACCTCCCCCT	GCCTCTACTG	AGGAACCCCT	840
		AAATCTGTTC					900
		GCCATCAGCA					960
	TTGGCGAAGA	TOOCACTGGA	ACCCTGAACC	TGAATTTCAT	TIGATITICIG	CATTTTGGCC	1020
	CTCTCTTCCA	TCATATTTGG	ATGCTGCATA	TGAAGTTAAC	AGCAGGGACA	CCGTTTTTAT	1080
50	TTTTAAAGGA	AATGAGTTCT	GGGCCATCAG	AGGAAATGAG	GTACAAGCAG	GTTATCCAAG	1140
		ACCCTGGGTT					1200
		AAGAAAACAT					1260
		ATGGAGCAAG					1320
		GATGCTGTAT					1380
55	ACAGTTTGAG	TTTGACCCCA	ATGCCAGGAT	GGTGACACAC	ATATTAAAGA	GTAACAGCTG	1440
		TAGGCGAGAT					1500
		TAATGTATTA					1560
	GAAGAAGATG	AGCCTTGCAG	ATATCTGCAT	GTGTCATGAA	GAATGTTTCT	GGAATTCTTC	1620
		GAATTGCACT					1680
60	ATGTATTTTC	ATAGATGTGT	TATTACTICC	TCAATAAAAA	GITTTATTTT	GGGCCTGTTC	1740

Seq ID NO: 389 Protein sequence Protein Accession #: NP 002416

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	Ī	1	1	1	1	
MHLAFLVLLC	LPVCSAYPLS	GAAKEEDSNK	DLAQQYLEKY	YNLEKDVKQP	RRKDSNLIVK	60
KIOGMOKFLG	LEVICKLDID	TLEVMRKPRC	GVPDVGHPSS	FPGMPKWRKT	HLTYRIVNYT	120
						180
HAYPPGPGLY	GDIHFDDDEK	WTEDASGINL	FLVAAHELGII	SLGLPHSANT	EALMYPLYNS	240
FTELAQFRLS	QDDVNG IQSL	YGPPPASTEE	PLVPTKSVPS	GSEMPAKCDP	ALSFDAISTL	300
						360
IRGNEVQAGY	PRGIHTLGFP	PTIRKIDAAV	SDKEKKKTYF	FAADKYWRFD	ENSOSMEQGF	420
PRLIADDFPG	VEPKVDAVLQ	AFGFFYFFSG	SSQFEFDPNA	RMVTHILKSN	SWLHC	
	1 	1 11 HILAFLYLLC LPVCSAYPLS KIQSMQKFLG LEVTGKLDTD DDLPBDAVDS ALEKALKVME HAYPPGPGLY GDIFFDDDKK FTELAGFELS CDUVNG IOSL RGEVLEFKDR YFWRSHNIP TRANEWQAGY PRGIFTLGFP	1 11 21 1	HHAPLYLLC LPYCSAYPLS GAAKEEDSKK DLAQYLERY KICSGKGFLG LEYTKELDIT TLEVEKFRE GYPENGHES POLPEDADAS ATKELAKYME RYPLTYSKL YEEGADIMS I HAYPPGGLY GUTHETDDEK WTEDAGSTILL PUMAHELGHE FELAGYPLS GOUNNETGSL KOPPDASTEE HYPKTSKYPS RGEYLFFKOR YYMRISHKOP EPPFILISAF PIPSLSSYLDA REGREYGASY PROGUSTIGPS PUTRKIDAN ZOBEKKTYP	1 11 21 31 41 11 11 11 11 11 11 11 11 11 11 11 11	

Seq ID NO: 390 DNA sequence Nucleic Acid Accession #: NM_002421.2 Coding sequence: 1..1409

80 31 41 51 ATGGACAGCT TECCTCCACT GEOCUTICTS CHITTCTIGGG GEOFAGATAT ACACAGCTTC COAGGACT TECCTCCACT AGAGCAGAT GEOGACTAG TECCAGAGATA GEOGACATAG TECCAGAATA CETTGAGAACACA AGAGCAGAT GEOGACTAG TECCAGAATA CETTGAGAATAT CACAGACAT TECCAGAATAT TECCAGATAT TECCAGATAT TECCAGATAT TECCAGATAT TETTGAGCATAT AGAGCAAT GEOGAGATC TITTGAGCATA AACTUACTUG GAAACCAGAT CETTGAGCAGT GEOCAGATT GEOGAGATC CATTGAGCAGT GEOCAGATT GEOGAGATC CATTGAGCAGT GEOCAGATT GEOCAGATT GEOGAGATC CATTGAGTT GEOCAGATT GEOCAGATT GEOGAGATC GEOCAGATT GEOCAGATT GEOCAGATT GEOCAGATT GEOGAGATC GEOCAGATT 120 180 85 240

	WO 02	/086443					
		AGGGGAACCC	TCGCTGGGAG	CAAACACATC	TGACCTACAG	GATTGAAAAT	360
	TACACGCCAG	ATTTGCCAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAACTC	420
	TGGAGTAATG	TCACACCTCT	GACATTCACC	AAGGTCTCTG	AGGGTCANGC	AGACATCATG	480 540
5	ATATCTTTTG	TCAGGGGAGA CTTTTCAACC	TCATCGGGAC	AMCTUTCUTT	ATGATGGACC	TOGAGGAAAT	600
,	GAAAGGTGGA	CCAACAATTT	CAGAGAGTAC	ATTGGAGGG	GTGTTGCGGC	TCATGRACTC	660
	GGCCATTCTC	CCAACAATTT TTGGACTCTC	CCATTCTACT	GATATOGGGG	CTTTGATGTA	CCCTAGCTAC	720
	ACCTTCAGTG	GTGATGTTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
	GGACGTTCCC	AAAATCCTGT	CCAGCCCATC	GGCCCACAAA	CCCCAAAAGC	ATGTGACAGT	840
10	AAGCTAACCT	TTGATGCTAT	AACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900
	TTCTACATGC	GCACAAATCC TGCCAAATGG	CTTCTACCCG	GAAGTTGAGC	TCAATTTCAT	TTCTGTTTTC	1020
	TOGCCACAAC	AAGGGAATAA	GCTTGAGGCT	CTTICACCAC	ACABTOTOCT	ACACCCATAC	1080
	CCCAAGGACA	TCTACAGCTC	CTTTGGGGCT	CTAGAACTG	TGARGCATAT	CGATGCTGCT	1140
1.5	CTTTCTGAGG	ABAACACTGG	ADDRACCTAC	TTCTTTGTTG	CTAACAAATA	CTGGAGGTAT	1200
	GATGAATATA	AAAACACTGG AACGATCTAT	GGATCCAGGT	TATCCCAAAA	TGATAGCACA	TGACTTTCCT	1260
	GGAATTGGCC	ACAAAGTTGA	TGCAGTTTTC	ATGAAAGATG	GATTTTTCTA	TTTCTTTCAT	1320
	GGAACAAGAC	AATACAAATT	TGATCCTAAA	ACGAAGAGAA	TTTTGACTCT	CCAGAAAGCT	1380
20	AATAGCTGGT	TCAACTGCAG	GAAAAATTAG				
20	O TD 100	391 Protein					
	Protein Ac		NP_0024	12.1			
	1	11	21	31	41	51	
25	1	1	1	1	1	1	
	MHSFPPLLLL	LFWGVVSHSF FGLKVTGKFD	PATLETQEQD	ADPAĞKAPEK	YYNLKNDGRQ	VEKRRNSGPV	60 120
	VEKLKOMQEF	FGLKVTGKPD	ABTLKVMKQP	RCGVPDVAQF	VLTECNPRWE	QTHLTYRIEN	180
	YTPDLPRADV	DHAIEKAFQL IGGDAHFDED	PRICERRE	AVSEGUADIM NT.UDVA AV	GUGLGLGUARD	DIGNIMATOR	240
30	TERRITOR AC	DDIDGIQALY	CBSONBACEL	GROTEKACIO	KLTPDAITT	RGEVMPPKOR	300
50							360
	PEDLYSSEGE	PRTVKHIDAA	LSEENTGKTY	PEVANKYNRY	DEYKRSMDPG	YPKMIAHDFP	420
	GIGHKVDAVF	PRTVKHIDAA MKDGFFYFFH	GTRQYKFDPK	TKRILTLQKA	NSUFNCRKN		
25							
35	Nucleic Ac	392 DNA sec id Accession uence: 11	1 #: NM_002	421.2			
				31	41	51	
40	1	11	21	31	41	1	
	ATGCA CAGCT	TTCCTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTC	ACACAGCTTC	60
	CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
	TACTACAACC	TGAAGAATGA	TGGGAGGCAA	GTTGAAAAGC	GGAGAAATAG	TGGCCCAGTG	180
	GTTGAAAAAT	TGAAGCAAAT	GCAGGAATTC	TTTGGGGCTGA	AAGTGACTGG	GAAACCAGAT	240
45	CCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCTGATGT	GGCTCAGTTT	300
	GTCCTCACTG	AGGGGAACCC	TOGCTGGGAG	CANACACATC	TGACCTACAG	GATTGAAAAT	360
			AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAACTC	420
	TACACGCCAG	ATTTOCCARG			AGGGTCAAGC		
	TGGAGTAATG	TCACACCTCT	GACATTCACC	MUGGICICIO			480
50	TGGAGTAATG ATATCTTTTG	TCACACCTCT	GACATTCACC	AACTCTCCTT	TTGATGGACC	TGGAGGAAAT	540
50	TGGAGTAATG ATATCTTTTG CTTGCTCATG	TCACACCTCT TCAGGGGAGA CTTTTCAACC	GACATTCACC TCATCGGGAC AGGCCCAGGT	AACTCTCCTT	ATGCTCATTT	TGGAGGAAAT	540 600
50	TGGAGTAATG ATATCTTTTG CTTGCTCATG GAAAGGTYGGA	TCACACCTCT TCAGGGGAGA CTTTTCAACC CCAACAATTT	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC	AACTCTCCTT ATTGGAGGGG AACTTACATC	ATGCTCATTT	TGGAGGAAAT TGATGAAGAT TCATGCCCTC	540
50	TGGAGTANTG ATATCTTTTG CTTGCTCATG GAAAGGTGGA GGCCATTCTC	TCACACCTCT TCAGGGGAGA CTTTTCAACC CCAACAATTT TTGGACTCTC	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATTCTACT	AACTCTCCTT ATTGGAGGGG AACTTACATC GATATCGGGG	ATGCTCATTT GTGTTGCGGC CTTTGATGTA	TGGAGGAAAT TGATGAAGAT TCATGGCCTC CCCTAGCTAC	540 600 660
	TGGAGTAATG ATATCTTTTG CTTGCTCATG GAAAGGTGGA GGCCATTCTC ACCTTCAGTG GGACGTTCCC	TCACACCTCT TCAGGGGAGA CTTTTCAACC CCAACAATTT TTGGACTCTC GTGATGTTCA AAAATCCTGT	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAG CCAGCCCATC	AACTCTCCTT ATTGGAGGGG AACTTACATC GATATCGGGG GATGACATTG GGCCCACAAA	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCCAAAAGC	TGGAGGAAAT TGATGAGAT TCATGCCCTC CCCTAGCTAC AGCCATATAT ATGTGACAGT	540 600 660 720 780 840
50 55	TGGAGTAATG ATATCTTTTG CTTGCTCATG GAAAGGTGGA GGCCATTCTC ACCTTCAGT GGACGTTCCC LAGCTAACCT	TCACACCTCT TCAGGGGAGA CTTTTCAACC CCAACAATTT TTGGACTCTC GTGATGTTCA AAAATCCTGT TTGATGCTAT	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAG CCAGCCCATC AACTACGATT	AACTCTCCTT ATTGGAGGGG AACTTACATC GATATCGGGG GATGACATTG GGCCCACAAA CGGGGAGAAA	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCCAAAAGC TGATGTTCTT	TGGAGGAAAT TGATGAAGAT TCATGCCCTC CCCTAGCTAC AGCCATATAT ATGTGACAGT TAAAGACAGA	540 600 660 720 780 840 900
	TGGAGTAATG ATATCTTTTG CTTGCTCAGA GAAAGGTGGA GGCCATTCTC ACCTTCAGTG GGACGTTCCC AAGCTAACCT TTCTACATGC	TCACACCTCT TCAGGGGAGA CTTTCAACC CCAACAATTT TTGGACTCTC GTGATGTTCA AAAATCCTGT TTGATGCTAT GCACAAATCC	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAT CCAGCCCATC AACTACGATT CTTCTACCCG	AACTCTCCTT ATTGGAGGGG AACTTACATC GATATCGGGG GATGACATTG GGCCCACAAA CGGGGAGAAG GAAGTTGAGC	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCCAAAAGC TGATGTTCTT TCAATTTCAT	TOGACGAAAT TGATGAAGAT TCATGCCTC CCCTAGCTAC AGCGATATAT ATGTGACAGT TAAAGACAGA TTCTGTTTTC	540 600 660 720 780 840 900 960
	TGGAGTANTG ATATCTTTG CTTGCTCATG GANAGGTGGA GGCGATTCTC ACCTTCAGTG GGAGGTTCCC ANGCTANCCT TTCTACATGC TGGCGACNAC	TCACACCTCT TCAGGGGAGA CTITTCAAC CCAACAATTT TTGGACTCTC GTGATGTTCA AAAATCCTGT TTGATGCTAT TGCACAAATCC TGCCAAATGG	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATCTACT GCTAGCTCAG CCAGCCCATC AACTACGATT AACTACGATT AACTACGATG GCTTGAAGCT	AACTCTCCTT ATTGGAGGG AACTTACATC GATATCGGG GATGACATG GGCCCACAAA CGGGCAGAAC GAAGTTGAGC GCTTACGAAT	ATGCTCATIT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCCGACAG	TOGACGAAAT TGATGAAGAT TCATGCCTC CCCTAGCTAC AGCCATATTA ATGTGACAGT TAAAGACAGA TTCTGTTTTC AGATGAAGTC	540 600 660 720 780 840 900 960 1020
	TGGAGTAATG ATATCTTTTG GAAAGGTGGA GGCCATTCTC ACCTTCAGTG GGCAGTTCCC AAGCTACCT TTCTACATGC TGGCCACAAC CGGTTTTCCA	TCACACCTCT TCAGGGGAGA CTTTTCAACC CCAACATTT TTGGACTCTC GTGATGTTCA AAAATCCTGT TTGATGCTAT GCACAAATCC TGCCAAATGG TACCAAATGG	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAG CCAGCCCATC AACTACGATT CTTCTACCCG GCTTGAAGGT GTTTGAAGGT	ARCTCTCCTT ATTGGAGGG RACTTACATC GATATCGGG GATGACATTG GGCCCACAAA CGGGGAGAAG GAGTTGAGC GTTACGAAT GTTACGAAT	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCCAAAAGC TGATGTCTT TCAATTTCAT TTGCCGACAG AGAATGTGCT	TGGAGGAAAT TGATGAGGAT TCATGCCCTC CCCTAGCTAC AGGCATATAT ATGTGACAGT TAAAGACAGA TTCTGTTTTC AGATGAAGTC ACACGGATAC	540 600 660 720 780 840 900 960 1020 1080
55	TGGAGTANTG ATATCTTTTG CTTGCTCATG GAAAGGTGGA GGCCATTCTC ACCTTCAGTG GGACGTTCCC AAGCTAACCT TTCTACATG TGCCACAAC CCGAGGACA CCCAGGGACA	TCACACCTCT TCAGGGAGAA CTTTCAACC CCAACAATTT TTGGACTCTC GTGATGTTCA AAAATCCTGT TTGATGCTAT GCACAAATCC TGCCAAATGC AAGGGAATAA TCTACAGGCTC	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAT CCATCCATC AACTACGATT CTTCTACCCG GCTTGAAGCT GTACTGGGCT CTATTGGCTTC	ARCTCTCCTT ATTGGAGGG ARCTTACATC GATATCGGG GATGACATTG GGCCCACAAA CGGGGAGAAC GAAGTTGAGG GCTTACGAAT GTTCAGGGAC CCTAGGACTG	ATGCTCATTT GTGTTTGCGGTA ATGCATCCA CCCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCCGACAT AGAATGTGCT TGAAGCATAT TGAAGCATAT	TGGAGGAAAT TGATGACGAT TCATGCCTC CCCTAGCTAC AGGCATATAT ATGTGACAGT TAAAGACAGA TTCTGTTTTC AGATGAAGT ACACGGATAC CGATGCTGCT	540 600 660 720 780 840 900 960 1020 1080 1140
	TGGAGTANTG ATATCTTTIA CTTGCTCATG GAAAGGTGGA GGCATTCTC ACCTTCAGTG GGACGTTCCC AAGCTAACCT TTCTACATG CGGTTTTTCA CCCAAGGAC CTTTCTGAGG	TCACACCTCT TCAGGGGAGA CTTTTCAACC CCACAATTT TTGGACTCTC GTGATGTTCA AAATCCTGT TTGATGCTAT GCACAAATCC TGCCAAATGG AAGGGAATAA TCATACAGCTC AAAACACTGG	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAG CCAGCCCATC AACTACGATT CTTCTACCCG GCTTGAAGCT GTACTGGGCT CTTTTGGCTT CAAAACCTAC	ARCTCTCCTT ATTGGAGGG RACTTACATC GATATCGGGG GATGACATTG GGCCCACAAA CGGGGAGAAC GAAGTTGAGC GCTTACGAAT GTTCAGGGAC CTTCAGGGAC TTCTTTGTTG	ATGCTCATTT GTGTTGCGGTA ATGGCATCCA CCCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCCGACAG AGAATGTGCT TGAAGCATAT CTAACAAATA CTAACAAATA	TGGAOGAAAT TGATGAGAT TCATGCCTC CCCTAGCTAC AGCCATATAT ATGTGACAGT TTAAAGACAGA TTCTGTTTTC AGATGAAGTC ACACGGATAC COATGCTGCT CTOGAGGTAT	540 600 660 720 780 840 900 960 1020 1080 1140
55	TGGAGTANTG ATATCTTTTTG CTTGCTCATG GAAAGGTGGA GGCCATTCTC ACCTTCAGTG GGAGGTTCCC AAGCTAACCT TTCTACATGC TGGCCACAAC CGGTTTTTCA CCCAAGGACA CTTTCTGAGG GATGLATATA	TCACACCTCT TCAGGGGAGA CTTTTCAACC CCAACATTT TTGGACTCTC GTGATGTTCA AMAATCCTGT TTGATGCTAT GCACAATTG TGCCAAATGC AAGAGGAATAT TCTACAGCTC AAAAACACTGG AAGGAATCA AAGACACTGG	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAG CCAGCCCATC AACTACGAT CTTCTACCG GCTTGTAAGCT GTTAGTGAGCT GTTAGTGGGCT CTTTGGCTTC AARAACCTAC GABTCAGGGT	ARCTCTCCTT ATTGGAGGGG ARCTTACATC GATATCGGGG GATGACATG GGCCCACAAA CGGGGAGAAG GAAGTTGAGC GCTTACGAAT GTTCAGGGAC CCTAGGAACTC TTCTTTGTTG TATCCCAAAA	ATGCTCATTT GTGTTTGCGGC CTTTGATGTA ATGGCATCCA CCCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCGGACAG AGAATGTGCT TGAAGCATAT CTAACAAATA TGATAGCACAC	TOGAOGAAAT TGATGACGAT TCATGCCTC CCCTAGCTAC AGOCATATAT ATOTGACAGA TICTGTTTTC AGAAGACAGA TICTGTTTTCC ACACGGATAC COATGCTGCT CTGAGGTAC TGACTTTCCT	540 600 660 720 780 840 900 960 1020 1080 1140
55	TGGAGTANTG ATACTTTTG CTTGCTCATG GAAAGGTGGA GGCGATTGTC ACCTTCAGTG GGAGGTTCCC AAGCTAACCT TTCTACATGC CGGTTTTTCA CCCAAGGACA CTTCTGAGG GATGAATATA GGAATTGACA GGATTGATGAGCA ACTTCTGAGG GATGAATATA AGAATTGACA GGATTGACA AGAATTGACA AGAATTACA AGAATTGACA AGAATTACA AGAATTA	TCACACETT TCAGGGGGGA CTTTCAACC CCACACATT TTGGACTCTC GTGATGTTCA NAAATCCTGT TTGATGCTAT TTGATGCTAT TCACAGGTC AAGGAATAC CTGCCAAATGG AAGGAATAC AAACACTGG AACACTGG AACACTGG AACACTGG AACACTGGAACACACAGTTGA ACAAAGTTGA	GACATTCACC TCATCGGGAC AGGCCCAGGTAC CCATTCTACT CCATTCTACT CCAGCCCATC AACTACGATT CTTCTACCG GCTTGAAGCT CTTTGACGTC AAAAACCTAC GGATCCAGGTT AAAAACCTAC GGATCCAGGTT TGCAGTTTTC	AACTCTCCTT ATTGGAGGGG AACTTACATC GATATCGGG GATGACATTG GGCCCACAAA GGCCCACAAA GTTTAGGAGAC CTTACGAAC CTTAGGAAC CCTAGGACC CCTAGGACT TCTTTTTGTTG TATCCCAAAA	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCCGACAG AGAATGTGCT TGAAGGCATAT CTAACAAATA TGATAGCAC GATTTTCTA GATTGCTA GATTTCTA	TOGROGRAPAT TGATGRAGAT TCATGCCTC CCCTAGCTAC AGCCATATAT ATGTGRACAGT TARAGACAGA TTCTGTTTTC AGATGRAGTC CGATGCTGCT CTGAGGTAT TGACTTCCT TGACTTTCCT TTCTTTCCAT	540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260
55	TGGAGTAATG ATATCTTTIG GAAAGTGGA GGCCATTGZC ACCTTCAGTG GGACTTCZC ACCTTCAGTG GGACTTCCC CAGGTAACCT TCTTCAGATG CGGTTTTTCA CCCAGGACC TTTTCAGAGG GATGAATATA GGAATTGGC GGACAAAGAC GGATTATCA GGAATTGGAG GAAAGAAAGAC GGAAAAGAA	TCACACCTCT TCAGGGGAGA CTTTTCAACC CCAACATTT TTGGACTCTC GTGATGTTCA AMAATCCTGT TTGATGCTAT GCACAATTG TGCCAAATGC AAGAGGAATAT TCTACAGCTC AAAAACACTGG AAGGAATCA AAGACACTGG	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC GCTAGCTCAG GCTAGCTCAG GCTAGCTCAG GCTAGCTCAG GCTAGCAGATTAC TCTTACCGG GCTTGGAGCT CTTTGGCTTC GAACACCAC GGATCCAGGT TGCAGTTTTC TGATCTAGATTTT TGATCTCAGATTTTC TGATCCTAAA	AACTCTCCTT ATTGGAGGGG AACTTACATC GATATCGGG GATGACATTG GGCCCACAAA GGCCCACAAA GTTTAGGAGAC CTTACGAAC CTTAGGAAC CCTAGGACC CCTAGGACT TCTTTTTGTTG TATCCCAAAA	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCCGACAG AGAATGTGCT TGAAGGCATAT CTAACAAATA TGATAGCAC GATTTTCTA GATTGCTA GATTTCTA	TOGROGRAPAT TGATGRAGAT TCATGCCTC CCCTAGCTAC AGCCATATAT ATGTGRACAGT TARAGACAGA TTCTGTTTTC AGATGRAGTC CGATGCTGCT CTGAGGTAT TGACTTCCT TGACTTTCCT TTCTTTCCAT	540 600 660 720 780 840 900 900 1080 1140 1200 1260 1320
55	TGGAGTAATG ATATCTTTIG GAAAGTGGA GGCCATTGZC ACCTTCAGTG GGACTTCZC ACCTTCAGTG GGACTTCCC CAGGTAACCT TCTTCAGATG CGGTTTTTCA CCCAGGACC TTTTCAGAGG GATGAATATA GGAATTGGC GGACAAAGAC GGATTATCA GGAATTGGAG GAAAGAAAGAC GGAAAAGAA	TCACACCTT TCAGGGGGA CTITICAACC CCACACATTI TGGACTCTC GTGATGTTCA AMAATCCTGT TTGATGCTAT GCACAATGC AGGGAATGC AAGGGAATAC CTACAGCTC AAAACACTGA AACACATGA AAAACATGA AATACAAATT	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC GCTAGCTCAG GCTAGCTCAG GCTAGCTCAG GCTAGCTCAG GCTAGCAGATTAC TCTTACCGG GCTTGGAGCT CTTTGGCTTC GAACACCAC GGATCCAGGT TGCAGTTTTC TGATCTAGATTTT TGATCTCAGATTTTC TGATCCTAAA	AACTCTCCTT ATTGGAGGGG AACTTACATC GATATCGGG GATGACATTG GGCCCACAAA GGCCCACAAA GTTTAGGAGAC CTTACGAAC CTTAGGAAC CCTAGGACC CCTAGGACT TCTTTTTGTTG TATCCCAAAA	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCCGACAG AGAATGTGCT TGAAGGCATAT CTAACAAATA TGATAGCAC GATTTTCTA GATTGCTA GATTTCTA	TOGROGRAPAT TGATGRAGAT TCATGCCTC CCCTAGCTAC AGCCATATAT ATGTGRACAGT TARAGACAGA TTCTGTTTTC AGATGRAGTC CGATGCTGCT CTGAGGTAT TGACTTCCT TGACTTTCCT TTCTTTCCAT	540 600 660 720 780 840 900 900 1080 1140 1200 1260 1320
55	TGGAGTANTE ATACTTTTG CTTGCTCATG GAAAGGTGGA GGCGATTGTC ACCTTCAGTG GGAGGTTGCC AAGCTACCT TTCTACATGC TGGCACACAC CCCAAGGACA CCTTTCTGGGG GATGTTTTCT GGGAATATATA GGAATAGGA AATAGCTGGT	TCACACTCT TCAGGGAGA CTTTTCAACC CCACACTTTT TGGACTCTC GTGATGTTCA AAAATCCTT TGAAGCTAT GCACAATCC TGCCAAATCC TGCCAAATCC AAGACACTC AAAACACTTA AAAATCTAACACTC AAAACACTTA AAAACTTAAACACTTA AAAAGTTAA AATACAAATT TCAAAGTCAA	GACATTCACC TCATCGGGC AGGCCCAGGT CAGAGGTTAC CCATCCTACT GCTAGCTCAG CCAGCCATC AACTACGAT CTTCTACCG GCTTGAGCT GTACTGGGCT CAGAGCT GTACTGGGCT AAAAACTTAC GATCGAGCT GGATCGAGT TGCAGTT TGCAGTT TGCAGTT TGCAGTT TGCAGTT TGCAGTT TGCAGTT	AACTCTCCTT ATTGGAGGGG AACTTACATC GATATCGGG GATGACATTG GGCCCACAAA GGCCCACAAA GTTTAGGAGAC CTTACGAAC CTTAGGAAC CCTAGGACC CCTAGGACT TCTTTTTGTTG TATCCCAAAA	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCCGACAG AGAATGTGCT TGAAGGCATAT CTAACAAATA TGATAGCAC GATTTTCTA GATTGCTA GATTTCTA	TOGROGRAPAT TGATGRAGAT TCATGCCTC CCCTAGCTAC AGCCATATAT ATGTGRACAGT TARAGACAGA TTCTGTTTTC AGATGRAGTC CGATGCTGCT CTGAGGTAT TGACTTCCT TGACTTTCCT TTCTTTCCAT	540 600 660 720 780 840 900 900 1080 1140 1200 1260 1320
55	TGGAGTANTG ATARCTTTTG CTTGCTCATG GAAGGTATCTC ACCTTCAGTG GGAGGTTCCC AAGCTACCT TTCTACATGC TGGACTTTCTC TGGACTACCT TCTACATGC GGATTTTTCA CCCAMGGACA CTTTCTGAGG GATGAATATA GGAATTGCCC GGAACAAGAC AATACCTGGT Seq ID NO:	TCACACTICT TCAGGIGAGA CTITTCAACC CCAACAATT TTGGACTCTC GTGATGTCA AMAATCCTUT TTGATCTAT TGCACAATCC TGCCAAATCC AAGAGTTGA AAGAGTTGA AAGAGTTGA AATACAAATT TCAACTGCAG 393 Prote:	GACATTCACC TCATCGGCT AGGCCCAGGT CAGAGAGTAC CCATCTACT GCTAGCTCAG GCTAGACTACT CTCTTACCCG GCTTGAAGCT CTCTTACCGCT CAGACTACGCTC AAAAACCTAC GGATCCAGGT TAGAGCT AAAAACTAC GGATCCAGGT TGCAGTTTTC TGAAAAATTAG AAAAAATTAG in sequence	AACTCTCCTA ATTGGAGGA AACTTACATC GATAACATG GATGACATTG GGCCCACAAA GGGGGGAGAG GAAGTTGAGAAT GTTCAGGAAT GTTCAGGACT TTCTTGTTG TATCCCAAAA ATGAAAGATC AAGGAGAGAGAAAAAAAAAA	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCCGACAG AGAATGTGCT TGAAGGCATAT CTAACAAATA TGATAGCAC GATTTTCTA GATTGCTA GATTTCTA	TOGROGRAPAT TGATGRAGAT TCATGCCTC CCCTAGCTAC AGCCATATAT ATGTGRACAGT TARAGACAGA TTCTGTTTTC AGATGRAGTC CGATGCTGCT CTGAGGTAT TGACTTCCT TGACTTTCCT TTCTTTCCAT	540 600 660 720 780 840 900 900 1080 1140 1200 1260 1320
55 60 65	TGGAGTANTS ATATCTTTES CTTGCTCATG GANAGOTGGA GGCCATTCTC ACCTCAGTG GGAGGTTCCC ANGCTAACCT TCCTACATGC TTCTTCAGTG GGACTTCTCC CCCAGGACAC CCCAGGACAC CCTTTCTGGAGG GATGAATTGGCC GGACAAAATATATA GGAATTGGCC GGACAAAGAC AATAGCTGGT Seq ID NO: Protein Ac	TCACACCTCT TCAGGGGAGA CTTTCAACC CCACCAATTCT TTGGACTCTC GTGATGTTCA ARAATCCTUT TTGATGCTAT TTGATGCTAT TGCACAATCC TGCCAAATCC TGCCAAATCC AAGGGAATAC AAAACACTGG AACAACTCT AAAACACTGG AACAACTTCAACTGCAC 393 Protecession #:	GACATTCACC TCATGGGAC AGGCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAG CCAGCCATC AACTACGATT CTTCTACCCG GCTTGAACGT CTTCTACCGG CTTGAACGT CTAGCGCT CTTGGCTCC GAATACCATC TGAATCCAGT TGCAGTCT TGCAGTTCT TGCATCC TGATCCTAAA GAAAAATTAG in sequence NF_002-	AACTCTCCTA ATTGGAGG AACTTACATC GATAACATC GATCACATTG GGCCCACAAA COGGGAGAAG GATTGAGAT GCTTACGAAT GCTTACGAAT TTCTTTGTTG TATCCCAAAA ATGAAAGATC ATGAAACATC ATGA	ATGCTCATTI GTGTTGCGGC CTTTGATGTA ATGGCATCCA ATGGCATCCA TCAGTTCTT TCAGTTTCTT TCAGTTCAT TTGCCGACAG AGAATGTCCT TGAAGCACAT CTAACAAATGTCT TGAAGCACAT CTAACAAATA TGATAGCACA GATTTTCTA TTTTGACTCT	TOGAGGAME TGATGAGAGAT TCATGCCCTC CCCTAGCTAC AGCCATATAT ATUTGACAGT TAAAGACAGA TICHGTTTTC ACAGGGATAC CGATGCTGCT CTGGAGGTAT TGACTTCCT TTGCTTTCAT CCAGAAAGCT	540 600 660 720 780 840 900 900 1080 1140 1200 1260 1320
55	TGGAGTANTG ATARCTTTTG CTTGCTCATG GAAGGTATCTC ACCTTCAGTG GGAGGTTCCC AAGCTACCT TTCTACATGC TGGACTTTCTC TGGACTACCT TCTACATGC GGATTTTTCA CCCAMGGACA CTTTCTGAGG GATGAATATA GGAATTGCCC GGAACAAGAC AATACCTGGT Seq ID NO:	TCACACTICT TCAGGIGAGA CTITTCAACC CCAACAATT TTGGACTCTC GTGATGTCA AMAATCCTUT TTGATCTAT TGCACAATCC TGCCAAATCC AAGAGTTGA AAGAGTTGA AAGAGTTGA AATACAAATT TCAACTGCAG 393 Prote:	GACATTCACC TCATCGGCT AGGCCCAGGT CAGAGAGTAC CCATCTACT GCTAGCTCAG GCTAGACTACT CTCTTACCCG GCTTGAAGCT CTCTTACCGCT CAGACTACGCTC AAAAACCTAC GGATCCAGGT TAGAGCT AAAAACTAC GGATCCAGGT TGCAGTTTTC TGAAAAATTAG AAAAAATTAG in sequence	AACTCTCCTA ATTGGAGGA AACTTACATC GATAACATG GATGACATTG GGCCCACAAA GGGGGGAGAG GAAGTTGAGAAT GTTCAGGAAT GTTCAGGAC TTCTTGTTG TATCCCAAAA ATGAAAGATC AAGAAGAGAGAGAAAAGATG AAGAAGAGAGAAAAAAAA	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCCA CCCAAAAGC TGATGTTCTT TCAATTTCAT TTGCCGACAG AGAATGTGCT TGAAGGCATAT CTAACAAATA TGATAGCAC GATTTTCTA GATTGCTA GATTTCTA	TOGROGRAPAT TGATGRAGAT TCATGCCTC CCCTAGCTAC AGCCATATAT ATGTGRACAGT TARAGACAGA TTCTGTTTTC AGATGRAGTC CGATGCTGCT CTGAGGTAT TGACTTCCT TGACTTTCCT TTCTTTCCAT	540 600 660 720 780 840 900 900 1080 1140 1200 1260 1320
55 60 65	TGGAGTANTS TATATTTTG CTTGCTCATG GAAAGGTGGA GGCGATTGTG GAAGGTTGCA GGCGATTCTGG GAGGTAACCT TTCTACATG TGGCACAAC CGGATTTTTCA CGCACAAC CCCAAGGACA CTTTCTGGGG GATCAAATATCA GGAAATAGCT GGAACAAGAC AATAGCTOOT Seq ID NO: Protein Ac	TCACACCTCT TCAGGGGAGA CTTTCAACC CCAACCACTC CCAACCACTC CCAACCACTC TTGGACTCT ANAATCCTCT TTGATCTAT GCACAATCC TGCCAAATCC AAAGCCTAT ACAAAGTTA TCAACTGCAG 393 Prote: cession #: 11	GACATTCACC TACTGGGAC AGGCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAG CCATCCTACT GCTAGCTCAG CCATCCTACC GCTAGCCAGC CCTTCTACCCG GCTTGAAGCT GCTTAGCAGCT CTTGAGCCTC AACAACACCAGC CTTACCAGGT TGAGTTTC TGAGTTT TGAGTTT TGAGTTT TGAGTTT TGAGTT TGAGT TGAGTT TGAGT	AACTCTCCTI ATTGGGGGG AACTTACATC GATATOGGG GATACATC GACATCACATC GGCCCACAAAA COGGCAGAAC COGGCAGAAC COTTACGAAC CCTACGAAC TCTTTGTTG TATCCCAAAA ATGAAAGATC ACGAAGAGAC 112.1 31	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCA CCCCAAAAGC TGATGTTCAT TCAATTTCAT TTCCATCTCAT AGAATGTCT TGAAGCATAT TGATAGCACA AGATGTCT TTAGACATAT TGTAGCACA ATTTTGACTCT	TOGAGGAAGT TGATGAGGAGT TGATGAGGAGT TGATGAGGAGT AGGGATATTA ATTIGAGAGT TAAAGACAGA TI CTGTTTTC AGATGAAGT ACAGGGATAC TGAGTTGCT TGAGTTTCCT TGAGTTTCCT TGAGTTTCCT TGAGTTCCT TGAGTTACA CCAGAAAGGT 51	540 600 720 780 840 900 960 1080 1140 1260 1320 1380
55 60 65	TGGAGTANTS TATATTTTG CTTGCTCATG GAAAGGTGGA GGCGATTGTG GAAGGTTGCA GGCGATTCTGG GAGGTAACCT TTCTACATG TGGCACAAC CGGATTTTTCA CGCACAAC CCCAAGGACA CTTTCTGGGG GATCAAATATCA GGAAATAGCT GGAACAAGAC AATAGCTOOT Seq ID NO: Protein Ac	TCACACCTCT TCAGGGGAGA CTTTCAACC CCAACCACTC CCAACCACTC CCAACCACTC TTGGACTCT ANAATCCCOT TTGGACTCT ANAATCCCOT TTGGACATCC ANAATCCCOT TGCCAAATCC ANAACCCTC ANAACCTC ANACCTC ANACCT ANACCTC ANACCTC ANACCTC ANACCT ANAC	GACATTCACC TACTGGGAC AGGCCAGGT CAGAGAGTAC CCATTCTACT GCTAGCTCAG CCATCCTACT GCTAGCTCAG CCATCCTACC GCTAGCCAGC CCTTCTACCCG GCTTGAAGCT GCTTAGCAGCT CTTGAGCCTC AACAACACCAGC CTTACCAGGT TGAGTTTC TGAGTTT TGAGTTT TGAGTTT TGAGTTT TGAGTT TGAGT TGAGTT TGAGT	AACTCTCCTI ATTGGGGGG AACTTACATC GATATOGGG GATACATC GACATCACATC GGCCCACAAAA COGGCAGAAC COGGCAGAAC COTTACGAAC CCTACGAAC TCTTTGTTG TATCCCAAAA ATGAAAGATC ACGAAGAGAC 112.1 31	ATGCTCATTT GTGTTGCGGC CTTTGATGTA ATGGCATCA CCCCAAAAGC TGATGTTCAT TCAATTTCAT TTCCATCTCAT AGAATGTCT TGAAGCATAT TGATAGCACA AGATGTCT TTAGACATAT TGTAGCACA ATTTTGACTCT	TOGAGGAAGT TGATGAGGAGT TGATGAGGAGT TGATGAGGAGT AGGGATATTA ATTIGAGAGT TAAAGACAGA TI CTGTTTTC AGATGAAGT ACAGGGATAC TGAGTTGCT TGAGTTTCCT TGAGTTTCCT TGAGTTTCCT TGAGTTCCT TGAGTTACA CCAGAAAGGT 51	540 600 720 780 840 900 960 1020 1140 1260 1320 1380
55 60 65	TOGAGTANTS TATATTTTES CTTGCCATG CANAGGTGGA GGCGATTGTC AGCTTCAGTG GGAGCTTCCC AGCTTACCC TGGCGCACACC TGGCCACACC CCCAAGGACA CTTCTGGGG GATGATTTCA CCCAAGGACA CTTCTGGAGG GATGAATATTGC GGAACAAGAC AGAATATGGC GGAACAAGAC AGAATATGGC GGACAGAC Seq ID NO: Protein &c L MHSFPPLLLLL MESFPPLLLL VEKLKOMGFF	TCACACCTCT TCAGGGGGAC CTTTCAGCC CCACCATTT TCGAGCTCAGC GTGATCTCAGCC GTGATCTCT GTGACTCTC ANACCCTCT TCGCCAATGC TCGCCAATGC TCGCCAATGC TCGCCAATGC AAGGGTGA AAGGGATTA ACCACTGC AAACGATCTA ACAACTTCC ACACCTGC ACACCTGC ACACCTGC ACACCTGC ACACCTGC ACACCTGC ACACCTGC ACCACCTGC ACC	GACATTCACC GACAGATCACC AGGCCAGGT CAGGAGGATAC CCATTCTACT GCAGGAGGATAC CCATTCTACT GCAGGAGGATAC CTCTCACCG GCATGCCAGG AACAACCTAC AAAAACTACAT TGAGCCTAAA GAAAAATTAG in sequence NF_002- 21	AMCTOCOTT ATTGGAGGG AACTTACATC GATATOGGG GATATOGGGG GATATOGGGG GATATOGGGG GATATOGGGG GATATOGGGG GATATOGGGG GATTATOGGATA COGCICAGAAC CTTCAGGATA CTTCAGGATA ATGAAAGATA ATGAAAGATA 112.1 31 11 VDLVOKYLEK RGGSVDVAGE	ANGECEATT GOTTHOGOGE GTTOTANTA ANGECHECE CCCARANCE TOCHOTETE TOCHOTETET TOCHOTETET TOCHOTETET TOCHOTETET TOCHOTECT TOCHOTETET TOCHOTECT	TOGACCAAAT TCATGACAAAA TCATGCCTTC CCCTAGCTAAA GCCATACTA AGCCATATA ATTGTACAGT TAAAAAAAACAA TCATGTACAGT AAAAAAAAACAA TCATGTACAGT TCATGTTTC AGATGAAAAAAAAACAA TCATGTACAGT TTCTTTTCAT TCATTTCAT TCATTTCAT TCATTTCAT TCATTTCAT TCATTTCAT VEKERRISGEV VEKERRISGEV VEKERRISGEV TCATGAAGAAAACT	540 600 720 780 840 900 900 1020 11400 1260 1320 1380
55 60 65 70	TOGGETAME ANACOTTAGE GAAAGCTAACT GAACCTTCAGE GAACCTTCAGE GAACCTTCAGE GAACCTTCAGE GAACCTTCAGE COGCACAGA COGTTTTTCA COGCACAGA COTTTCTGAGE COTTTCTGAGE COTTTCTGAGE COTTTCTGAGE COTTTCTGAGE COTTTCTGAGE GAACAAGC ATTACTGOT Seq ID NO Protein Ac 1	TCACACCTCT TCACGGGGAA CTTTCACC CCACACATT TGGACTCAC GTCATCACC GTCATCACC ANALTCCTT TTGATCCTAA ACACCTC ANACCTCT ACACCTC ANACCTCT ANACCTCT ANACCTCT ANACCTCT ANACCTCC ANA	GACATTCACC GACAGO AGSCCCAGO AGSCCCAGO AGSCCCAGO CCATCTACT GCAGGAGATAC CCATCTACT GCAGGAGATAC CTCTACCC GCTTGACCT GACACCAC AACAACCTAC TOCATCTACT AAAAACTACAT TOCATCTTTCACCC GATTGACTT AAAAACTACAT GAAAATTAG AAAAATTAG AAAAAATTAG AAAAATTAG AAAAAATTAG AAAAATTAG AAAAAATTAG AAAAAATTAGAAATTAGAA	AMCTOCTET ATTGGAGGG AACTTACATC GATATCGAGG GATATCGAGG GATATCGAGG GATATCGAGG GATATCGAGG GATATCGAGG GATATCGAGG GATATCGAGG GATATCGAGA GATATCGAGAT GATATCGAGAT GATTCAGGAA TOTTCAGGAAT TATTCCAJAAA ACGAAGGAACG TATCCAJAAA ACGAAGGAACA CCAJAACG TATCCAJAAA ACGAAGGAACA CCAJACACA TATCCAJAAA ACGAAGGAACA CCAJACACACACACACACACACACACACACACACA	ANGECEATT GYGTTGGGGC GTTTGAGTA ANGGCATCG CCCCAAAAGC CCCCAAAAGC TCAATTCAT TCAATTCAT TCAATTCAT TCAATTCAT TCAATTCAT TCAATTCAT TTAGACCATA TCAAAACAG GATTTTCAT TTTTAACCTT 41 YYNLKHOGRO VLITEGHREWE LIFFWEGHBGG VLITEGHREWE	TOCACOLAMI TOCACOLAMI TOCACOCTO COCTAGOTA TOCACOCTO COCTAGOTA TOCACOCTO COCTAGOTA AGOCATATA AGOCATATA TAMAJACAGA TICAGOTTO AGACGAGA TAMAJACAGA TICAGOTTO TOCACOCTO COMAGGATA COMAGCAC 51 VECCRISSOR V	540 600 720 780 840 900 960 1020 1140 1260 1320 1380
55 60 65	TOGGTTATC ATACTTITE CTTGCTCATG ANAGGTOAG AGCCATTCTC AAAGCTAACT TCTACATG CGAATTCTC CGAAGGCA CTTCTCTGGG GGAATTCTC CGAAGGCA CTTCTGGGG GAAATACA CGCAAGGCA ATACCTC GGAAATACA Seq ID NO 1 MSSPPLLLL MSSPPLLLL MSSPPLLLL MSSPPLLLL MSSPPLLLL MSSPPLLLL MSSPPLLLL MSSPPLLL MSSPPLL MSSPRL MSSPR	TCACACCTCT TCACGGGGGA CTTTCACC CCACACATT TCGACCCCAC GCACACATT TTGACCTCA GCACACATT TTGACCTCA ARACCCTCT TTGACCTCA ARACCCTCT TTGACCTCA ARACCCTCT ARACCCTCA ARACCCTCA ARACCCTCA ARACCCTCA ARACCCTCA ARACCACTCA ARACCACTCA ARACCACTCA ARACCACTCA ARACCACTCA ARACCACTCA ARACCACTCA ARACCACTCA ARCCAGTCA ARCCAG	GACATTCACC GACAGO AGSCCCAGOT CAGAGAGATA CAGAGAGATA CAGAGAGATA CATACACCA CATACACAC CATACACCA CATACACAC CATACACCA CATACACACAC	AACTCTCTT ATTGGAGGG AACTTACATC GATATCGGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGAG GATATCAGGAG GATATCAGGAG GATATCAGGAG GATATCAGAA GATCAGAACTG TTCATTCAGTAG TATCAGAACTG TTCTTCTTGTGT TATCAGAACTG TTCTTCTTGTGT AATGAAAGAAGAA 112.1 31 yDLVGKYLER ECGUPUDVAGF EC	ANGECHATT GYGTTUGGGE GYTTAGAGTA ANGGENECA CCCCAAAAGC TCAGATTCAT TCAGATTCAT TCAGATTCAT TCAGATTCAT TCAGATCAG AGAAAGC GATTTCAC GATTTCAT TTTTAGACCAGA TTTTCAC GATTTCAT TTTTAGACCAGA VINLKNOGRG VINLKNOGRG GRIGGERG GR	TOGAGGAANT TOGAGGAANT TOGAGGAANT TOGAGGAGA TOGAGGAGA AGCCATATAT ANTIGAGGAG TANAMACAGA TACAGGATATA AGCCATATAT ANAMACAGA TACAGGATATA TOGAGTATC AGAGGAGATAC AGAGGAGATAC AGAGGAGATAC TOGAGGATAC TOGAGGATAC TOGAGGATAC TOGAGGATAC TOGAGGATAC TOGAGGATAC TOGAGGATAC COMMANAGC TOGAGGATAC TOGAGGATAC COMMANAGC TOGAGGATAC TOGAGATAC TOGAGATAC TOGAGGATAC TOGAGATAC TOGAGTAC	540 660 720 780 840 900 1020 1140 1200 1260 1380
55 60 65 70	TOORTHMEN ATACTITES CTRUCTORED CONCENTRATE	TCACACCTCT TCACGGGGAA CTTTCACC CCACACATT TTGACCTCAC GCACACATT TTGACCTCA ARATCCTT TTGACCTCA ARATCCTT TTGACCTCA ARATCCTT TTGACCTCA ARACCACTC ARACACTCA ARACCACTC ARACACTCA ARACACTCA ARACACTCA ARACACACTCA ARACACACTCA ARACACATCA ARACACATCA ARACACATCA ARACACATCA ARACACATTA ARACACATTA ARACACATTA ARACACATTA ARACACATTA ARACACTCA ARACACATTA ARACACAT	GACATTCACC GACATTCACC AGGCCAGGT CAGGAGAGTAC CAGGAGAGTAC CAGGAGAGTAC CAGGAGAGTAC CAGGAGAGTAC CAGGAGAGTAC CAGGAGAGTAC CAGGAGAGTAC CAGGAGAGTAC CAGGAGTAC CAGGAG	AMCTOCOTT ATTGGAGGG AACTTACATC GATATCGGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGAG GATATCAGGAG GATATCAGGAG GATATCAGAA TATCAGAACTA TATCAGAACTA TATCAGAACTA TATCAGAACTA TATCAGAAGAA 112.1 31 yDLVOKYLER ECGUPUNAGE ECGU	ANGECHATT GYGTHOGGGE GYTTAGAGTA ANGGENECA CCCCAAAAGC TOGATTCAT TOGATTCAT TOGATTCAT TOGATTCAT TOGATTCAT TOGAGCAGA AGANOSO CTAGAAAGC GATTTTCAT TTTTGATCTCAT TYNLKNDGRG VINLKNDGRG GRISGLGLBGT KJFBAGTTTA KJFBAGTTTAT TYNLKNDGRG GRISGLGLBGT KJFBAGTTTAT KJFBAGTTTAT TYNLKNDGRG GRISGLGLBGT KJFBAGTTTAT KJFBAGTTAT KJFBAGTTTAT KJ	TOGACCIANT TOGATGAGAM TOGATGCOTT COCTAGCTAG TOGATGAGAM TOGATGCOTT COCTAGCTAG AGCCATATA ANTIGACAGA TANAGAGAGA TANAGAGAGA TANAGAGAGAT TANAGAGGAGA TANAGAGGAGA COGATTCC TATCATTTCC TTCTTCTCT TTCTTTCTC TTCTTTCT	540 660 720 840 900 1020 1140 1260 1320 1380
55 60 65 70	TOORTHMO ATACTITES CTROCCARD OF A TACTITES CTROCCARD OF A TACTITES CTROCCARD OF A TACTICATE OF A	TOACHCOTOR TOAGGGGAA CTITICAACC COACAATIT TOGAACTCAC GTGATGTTCA TOAGGGAATA TOAGCTAC TOCCAATGCA AAGGGAATA AAGGGAATA AATACAGCT AAAAGCACC 393 Proce cession #: 11 1 LPHGUVSHEP FOLKVITCH DUDLIGHTARPGL	GACATTCACC GACATTCACC TCATCGGGAC AGGCCCAGGT CAGGACGATAC CCATCTACT CCATCACC	AMCTOCOTT ATTGGAGGG AACTTACATC GATATCGGGG GATGCACTTG GGGCCACAAA CGGGGAGAAG GGTCACAAAA CGGGGAGAAA ATGAAACATC TCCTTAGGGAGA ACGAAGAGAGAA ATGAAACATC TCCTTAGGGAGAA ACGAAGAGAGAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAAA ATGAAACATC ACGAAGAGAAAA ACGAAGAGAAA ACGAAGAGAAAA ACGAAGAGAAAA ACGAAGAAGAAA ACGAAGAAGAAAA ACGAAGAAGAAAA ACGAAGAAGAAAA ACGAAGAAGAAAAAAAA	ANGOCHATT GYGTMOGOGO GTTTAGAGTA ANGOGNACO CCCCABAGC TOANTOTAT TOANTTCAT TOANTTCAT TOANTTCAT TOANTCACT TOANTCACT TOANTCACT TOANTTCAT TATACACAG ANTITICAT TATTOACCCC 41 LYYMLKHDGRO GULTEGHERE GISLGLEHOT LIFFWEGHER GISLGLEHOT LIFFWEGHER LIFFWEGHER GISLGLEHOT LIFFWEGHER LIFFWEG	TOGACCIANT TOGATGAGAM TOGATGCOTT COCTAGCTAG TOGATGAGAM TOGATGCOTT COCTAGCTAG AGCCATATA ANTIGACAGA TANAGAGAGA TANAGAGAGA TANAGAGAGAT TANAGAGGAGA TANAGAGGAGA COGATTCC TATCATTTCC TTCTTCTCT TTCTTTCTC TTCTTTCT	540 660 720 780 840 900 1020 1140 1200 1320 1380
55 60 65 70 75	TOORTHMO ATACTITES CTROCCARD OF A TACTITES CTROCCARD OF A TACTITES CTROCCARD OF A TACTICATE OF A	TCACACCTCT TCACGGGGAA CTTTCACC CCACACATT TTGACCTCA GTATTTTGACTC GTACATCT GTACATCT GTACATCT GTACACCTC ANARCCTOT TTGACCTAC ANARCCTOT TTGACCACTC ANACCTC	GACATTCACC GACATTCACC TCATCGGGAC AGGCCCAGGT CAGGACGATAC CCATCTACT CCATCACC	AMCTOCOTT ATTGGAGGG AACTTACATC GATATCGGGG GATGCACTTG GGGCCACAAA CGGGGAGAAG GGTCACAAAA CGGGGAGAAA ATGAAACATC TCCTTAGGGAGA ACGAAGAGAGAA ATGAAACATC TCCTTAGGGAGAA ACGAAGAGAGAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAAA ATGAAACATC ACGAAGAGAAAA ACGAAGAGAAA ACGAAGAGAAAA ACGAAGAGAAAA ACGAAGAAGAAA ACGAAGAAGAAAA ACGAAGAAGAAAA ACGAAGAAGAAAA ACGAAGAAGAAAAAAAA	ANGOCHATT GYGTMOGOGO GTTTAGAGTA ANGOGNACO CCCCABAGC TOANTOTAT TOANTTCAT TOANTTCAT TOANTTCAT TOANTCACT TOANTCACT TOANTCACT TOANTTCAT TATACACAG ANTITICAT TATACACAG ANTITICAT TATTOACTCT VYNLKHOGGO VLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE LIEF	TOGACCIANT TOGATGAGAM TOGATGCOTT COCTAGCTAG TOGATGAGAM TOGATGCOTT COCTAGCTAG AGCCATATA ANTIGACAGA TANAGAGAGA TANAGAGAGA TANAGAGAGAT TANAGAGGAGA TANAGAGGAGA COGATTCC TATCATTTCC TTCTTCTCT TTCTTTCTC TTCTTTCT	540 660 720 840 900 1020 1140 1260 1320 1380
55 60 65 70	TOORTHMO ATACTITES CTROCCARD OF A TACTITES CTROCCARD OF A TACTITES CTROCCARD OF A TACTICATE OF A	TOACHCOTOR TOAGGGGAA CTITICAACC COACAATIT TOGAACTCAC GTGATGTTCA TOAGGGAATA TOAGCTAC TOCCAATGCA AAGGGAATA AAGGGAATA AATACAGCT AAAAGCACC 393 Proce cession #: 11 1 LPHGUVSHEP FOLKVITCH DUDLIGHTARPGL	GACATTCACC GACATTCACC TCATCGGGAC AGGCCCAGGT CAGGACGATAC CCATCTACT CCATCACC	AMCTOCOTT ATTGGAGGG AACTTACATC GATATCGGGG GATGCACTTG GGGCCACAAA CGGGGAGAAG GGTCACAAAA CGGGGAGAAA ATGAAACATC TCCTTAGGGAGA ACGAAGAGAGAA ATGAAACATC TCCTTAGGGAGAA ACGAAGAGAGAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAAA ATGAAACATC ACGAAGAGAAAA ACGAAGAGAAA ACGAAGAGAAAA ACGAAGAGAAAA ACGAAGAAGAAA ACGAAGAAGAAAA ACGAAGAAGAAAA ACGAAGAAGAAAA ACGAAGAAGAAAAAAAA	ANGOCHATT GYGTMOGOGO GTTTAGAGTA ANGOGNACO CCCCABAGC TOANTOTAT TOANTTCAT TOANTTCAT TOANTTCAT TOANTCACT TOANTCACT TOANTCACT TOANTTCAT TATACACAG ANTITICAT TATACACAG ANTITICAT TATTOACTCT VYNLKHOGGO VLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE LIEF	TOGACCIANT TOGATGAGAM TOGATGCOTT COCTAGCTAG TOGATGAGAM TOGATGCOTT COCTAGCTAG AGCCATATA ANTIGACAGA TANAGAGAGA TANAGAGAGA TANAGAGAGAT TANAGAGGAGA TANAGAGGAGA COGATTCC TATCATTTCC TTCTTCTCT TTCTTTCTC TTCTTTCT	540 660 720 840 900 1020 1140 1260 1320 1380
55 60 65 70 75	TOGATTATO ATACTTES CTROCTORIO CTROCTORIO CTROCTORIO CONTROL AGGINACT TECHNOTIC CONTITUTA CONTITU	TORACTOT TORAGOGNA AND TORAGOGNATA AND TORAGOGNATA AND TORAGOGNATA TORACOCCA AND TORACOCCA AND TORAGOGNATA TORACOCCA AND TORACOC	GACATTCACC GAGGAGATA AGGCCAGGT CAGGAGAGATA AGGCCAGGT CAGGAGAGATA AGCTACAGAGAGAGAGA AACTACGAT CTTTGACGTA AACTACGAT CTTTGACGTA AAAAACCTAC TTGACCTAA GAAAAACTAC IN SEQUENCE NF_002 21 PATLETGEO AGTLTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	AMCTOCOTT ATTGGAGGG AACTTACATC GATATCGGGG GATGCACTTG GGGCCACAAA CGGGGAGAAG GGTCACAAAA CGGGGAGAAA ATGAAACATC TCCTTAGGGAGA ACGAAGAGAGAA ATGAAACATC TCCTTAGGGAGAA ACGAAGAGAGAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAAA ATGAAACATC ACGAAGAGAAA ATGAAACATC ACGAAGAGAAAA ATGAAACATC ACGAAGAGAAAA ACGAAGAGAAA ACGAAGAGAAAA ACGAAGAGAAAA ACGAAGAAGAAA ACGAAGAAGAAAA ACGAAGAAGAAAA ACGAAGAAGAAAA ACGAAGAAGAAAAAAAA	ANGOCHATT GYGTMOGOGO GTTTAGAGTA ANGOGNACO CCCCABAGC TOANTOTAT TOANTTCAT TOANTTCAT TOANTTCAT TOANTCACT TOANTCACT TOANTCACT TOANTTCAT TATACACAG ANTITICAT TATACACAG ANTITICAT TATTOACTCT VYNLKHOGGO VLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE LIEF	TOGACCIANT TOGATGAGAM TOGATGCOTT COCTAGCTAG TOGATGAGAM TOGATGCOTT COCTAGCTAG AGCCATATA ANTIGACAGA TANAGAGAGA TANAGAGAGA TANAGAGAGAT TANAGAGGAGA TANAGAGGAGA COGATTCC TATCATTTCC TTCTTCTCT TTCTTTCTC TTCTTTCT	540 660 720 840 900 1020 1140 1260 1320 1380
55 60 65 70 75	TOCHTANCE AT THE TOCHTANCE AT THE TOCHTANCE AND	TOAGACCTOT TOAGGGGAG CTTTTAACC COACAATTT TOAGGGGAG CTTTTAACC COACAATTT TOAGCGAG GTGAAGTTCA AMAATCCTOT TOAGCGAATGG AAAGGGACTAAC AAAGGACTTA AAAAGGACTTA AAAAGGACTTA TOAACTCCG 393 PTOCCCCCSSION 8: 11 11 11 11 12 14 15 16 16 17 17 17 17 17 17 17 17 17 17 17 17 17	GACATTCACC TACTOGOSA AGGCCOAGOT AGGCCOAGOT AGGCCOAGOT AGGCCOAGOT AGCCCOAGOT AACTACCOAT A	AACTCTCTT ATTGGAGGG AACTTACATC GATATCAGGG GATACACTG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGAG GATATCAGAG GATATCAGAG GATATCAGAG TTCTTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTGTTG TTCTTTGTTG TTCTTGTTG TTCTTGT TTCTTGT TTCTTGT TTCTTGT TTCTTGT TTCTTG TTCTTGT TTCTTGT TTCTTGT TTCTTG TTCTTGT TTC	ANGOCHATT GYGTMOGOGO GTTTAGAGTA ANGOGNACO CCCCABAGC TOANTOTAT TOANTTCAT TOANTTCAT TOANTTCAT TOANTCACT TOANTCACT TOANTCACT TOANTTCAT TATACACAG ANTITICAT TATACACAG ANTITICAT TATTOACTCT VYNLKHOGGO VLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE LIEF	TOGACCIANT TOGATGAGAM TOGATGCOTT COCTAGCTAG TOGATGAGAM TOGATGCOTT COCTAGCTAG AGCCATATA ANTIGACAGA TANAGAGAGA TANAGAGAGA TANAGAGAGAT TANAGAGGAGA TANAGAGGAGA COGATTCC TATCATTTCC TTCTTCTCT TTCTTTCTC TTCTTTCT	540 660 720 840 900 1020 1140 1260 1320 1380
55 60 65 70 75	TOGGNETAMO ATACOTTES CHACTORIS CHACT	TORACCTOT TORAGGIAN CTITUTA ACC CTITUTA ACC CTITUTA ACC CTITUTA ACC CTITUTA ACC CTITUTA ACC ACC GREATITA ANALTICIT TORATOT TORATOT TORATOT TORATOT TORATOT ANACATOT TORATOT	GACATTCACC TOATCAGA AGGCCOAGOT AGGCCOAGOT AGGCCOAGOT AGGCCOAGOT AGCACCAGA AGGCCOAGOT ACTACCAGA A	AACTCTCTT ATTGGAGGG AACTTACATC GATATCAGGG GATACACTG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGAG GATATCAGAG GATATCAGAG GATATCAGAG TTCTTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTGTTG TTCTTTGTTG TTCTTGTTG TTCTTGT TTCTTGT TTCTTGT TTCTTGT TTCTTGT TTCTTG TTCTTGT TTCTTGT TTCTTGT TTCTTG TTCTTGT TTC	ANGOCHATT GYGTMOGOGO GTTTAGAGTA ANGOGNACO CCCCABAGC TOANTOTAT TOANTTCAT TOANTTCAT TOANTTCAT TOANTCACT TOANTCACT TOANTCACT TOANTTCAT TATACACAG ANTITICAT TATACACAG ANTITICAT TATTOACTCT VYNLKHOGGO VLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE LIEF	TOGACCIANT TOGATGAGAM TOGATGCOTT COCTAGCTAG TOGATGAGAM TOGATGCOTT COCTAGCTAG AGCCATATA ANTIGACAGA TANAGAGAGA TANAGAGAGA TANAGAGAGAT TANAGAGGAGA TANAGAGGAGA COGATTCC TATCATTTCC TTCTTCTCT TTCTTTCTC TTCTTTCT	540 600 720 840 900 1020 1140 1260 1320 1380
55 60 65 70 75	TOGGNETAMO ATACOTTES CHACTORIS CHACT	TOAGACCTOT TOAGGGGAG CTTTTAACC COACAATTT TOAGGGGAG CTTTTAACC COACAATTT TOAGCGAG GTGAAGTTCA AMAATCCTOT TOAGCGAATGG AAAGGGACTAAC AAAGGACTTA AAAAGGACTTA AAAAGGACTTA TOAACTCCG 393 PTOCCCCCSSION 8: 11 11 11 11 12 14 15 16 16 17 17 17 17 17 17 17 17 17 17 17 17 17	GACATTCACC TOATCAGA AGGCCOAGOT AGGCCOAGOT AGGCCOAGOT AGGCCOAGOT AGCACCAGA AGGCCOAGOT ACTACCAGA A	AACTCTCTT ATTGGAGGG AACTTACATC GATATCAGGG GATACACTG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGAG GATATCAGAG GATATCAGAG GATATCAGAG TTCTTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTGTTG TTCTTTGTTG TTCTTGTTG TTCTTGT TTCTTGT TTCTTGT TTCTTGT TTCTTGT TTCTTG TTCTTGT TTCTTGT TTCTTGT TTCTTG TTCTTGT TTC	ANGOCHATT GYGTMOGOGO GTTTAGAGTA ANGOGNACO CCCCABAGC TOANTOTAT TOANTTCAT TOANTTCAT TOANTTCAT TOANTCACT TOANTCACT TOANTCACT TOANTTCAT TATACACAG ANTITICAT TATACACAG ANTITICAT TATTOACTCT VYNLKHOGGO VLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE LIEF	TOGACCIANT TOGATGAGAM TOGATGCOTT COCTAGCTAG TOGATGAGAM TOGATGCOTT COCTAGCTAG AGCCATATA ANTIGACAGA TANAGAGAGA TANAGAGAGA TANAGAGAGAT TANAGAGGAGA TANAGAGGAGA COGATTCC TATCATTTCC TTCTTCTCT TTCTTTCTC TTCTTTCT	540 600 720 840 900 1020 1140 1260 1320 1380
55 60 65 70 75	TOGGNETAMO ATACOTTES CHACTORIS CHACT	TORACCTOT TORAGGIAN CTTITLACC CTTITLACC CTTITLACC CTTITLACC CTTITLACC CTTITLACC CTTITLACC GRANTICA ANALTICIT TORACTOT GRANTICA ANALTICIT TORACC ANALTICIT TORACC ANALTICIT TORACC ANALTIC ANACC ANALTIC ANACC ANALTIC ANACC TORACC ANALTIC ANACC TORACC	GACATTCACC TOATCAGA AGGCCOAGOT AGGCCOAGOT AGGCCOAGOT AGGCCOAGOT AGCACCAGA AGGCCOAGOT ACTACCAGA A	AACTCTCTT ATTGGAGGG AACTTACATC GATATCAGGG GATACACTG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGGG GATATCAGAG GATATCAGAG GATATCAGAG GATATCAGAG TTCTTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTTGTTG TTCTTGTTG TTCTTTGTTG TTCTTGTTG TTCTTGT TTCTTGT TTCTTGT TTCTTGT TTCTTGT TTCTTG TTCTTGT TTCTTGT TTCTTGT TTCTTG TTCTTGT TTC	ANGOCHATT GYGTMOGOGO GTTTAGAGTA ANGOGNACO CCCCABAGC TOANTOTAT TOANTTCAT TOANTTCAT TOANTTCAT TOANTCACT TOANTCACT TOANTCACT TOANTTCAT TATACACAG ANTITICAT TATACACAG ANTITICAT TATTOACTCT VYNLKHOGGO VLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE GISLGLEHOT KLITEURIPREE LIEFWECHBE LIEF	TOGACCIANT TOGATGAGAM TOGATGCOTT COCTAGCTAG TOGATGAGAM TOGATGCOTT COCTAGCTAG AGCCATATA ANTIGACAGA TANAGAGAGA TANAGAGAGA TANAGAGAGAT TANAGAGGAGA TANAGAGGAGA COGATTCC TATCATTTCC TTCTTCTCT TTCTTTCTC TTCTTTCT	540 600 720 840 900 1020 1140 1260 1320 1380

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ATGGTCAGAA AGCCTGTTGT GTCCACCATC TCCAAAGGAG GTTACCTGCA GGGAAATGTT AACGGGAGGC TGCCTTCCCT GGGCAACAAG GAGCCACCTG GGCAGGAGAA AGTGCAGCTG 120 AAGAGGAAAG TCACTTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTGGAGCA GGAATCITCA TOTOTOCTAA GOGCGTGCTC CAGAACACGG GCAGCGTGGG CATGTCTCTG VANDALLIA TUTURUTU MAGGITTOTIC CARANGOS CONGOTTOS CONTECTION CONCENTRATOR CONTECTION CONTE 300 360 420 540 10 600 660 TITANAGACG COTITICAGG AAGAGATICA AGTATTACGC GGTTGCCACT GGCTTTTTAT 720 TATOGRATOT ATGCATATGC TEGCTOGTTT TACCTCAACT TIGTTACTGA AGAAGTAGAA AACCCTGAAA AAACCATTCC CCTTGCAATA TGTATATCCA TOGCCATTGT CACCATTGGC 840 15 TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAATG CTGAGGAGCT GCTGCTTTCA AATGCAGTGG CAGTGACCTT TTCTGAGGGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG 900 960 ATCTTTGTTG CCCTCTCCTG CTTTGGCTCC ATGAACGCTG GTGTGTTTGC TGTCTCCAGG 1020 TTATTCTATG TTGCGTCTCG AGAGGGTCAC CTTCCAGAAA TCCTCTCCAT GATTCATGTC 1080 COCAAGCACA CTCCTCTACC AGCTGTTATT GTTTTGCACC CTTTGACAAT GATAATGCTC TTCTCTGGAG ACCTGGACAG TCTTTTGAAT TTCCTCAGTT TTGCCAGGTG GCTTTTTATT 1200 GGGCTGGCAG TTGCTGGGCT GATTTATCTT CGATACAAAT GCCCAGATAT GCATCGTCCT 1260 TTCARGOTGC CACTOTTCAT COCAGCTTTG TTTTCCTTCA CATGCOTCTT CATGGTTGCC CTTTCCCCTC ATTTGGACCC ATTTAGTACA GGGATTGGT TCGTCATCAC TCTGACTGAT CATCATCTTT TATTATTAGG GACAGGARA COCAGTGGTT TAGAATAATG 1320 1440 2.5 TCAGAGAAAA TAACCAGAAC ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG 1500 TORGRAMA TARCOUGHAC RITHORANTA KINCHORAG THERACUSE MEMAKITANG TETRIGARCHA ATGORGTERA GARCITIGOR ATCHGOCCAN GOGGGARCAC MARAFAGGAR TITTIACITC ATTITCTICAN AGCCHAGAG ATTACACIT TOGGATAAN CAMAMGAGAT CAGITHATTIT TATTCATATA TITTAGCATA TICGACITA TITCIANGRA MITHAGITAT AACCCTAGOT AGTHARAGAA AGGGARTAG CAGITHATTOT AGGGGCGA CANTCTTON 1560 1620 1680 1740 30 GTCTCTGATA CCTACCTATT GGGGTTAGGA GAAAAGACTA GACAATTACT ATGTGGTCAT 1800 TOTOTACAAC ATATOTTAGO ACGGCAAAGA ACCTTCAAAT TGAAGACTGA GATTTTTCTG 1860 TATATATOGG TITTGTAAAG ATGGTTTTAC ACACTACAGA TGTCTATACT GTGAAAAGTG 1920 TTTTCAATTC TGAAAAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT 1980 ATTITACATI GACATIGCAT IGCTICCCCI TAGATACCAA ITTAGATAAC AAACACICAT 35 GCTTTANTGG ATTATACCCA GAGCACTITG AACAAAGGTC AGTGGGGATT GTTGAATACA 21.00 GOTTIANGO ATRATOCOS GACOLTTU ANCAMOSTO ADTOSCATO TOTRANANO
TRABAGNAS TRATOCOS GACOLTTU ANCAMOSTO ADTOSCATO TOTRANANO
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TRACOCOS T 2160 2220 2340 40 2400 2460 2520 2580 CTTCAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAACATA AAAATTGCAA 45 AAGAAATGTC GCTGTAAATA AGATTTACAA CTGATGTTTC TAGAAAATTT CCACTTCTAT 2700 ATCTAGGCTT TGTCRGTAAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA CTGATAAGAA GAAAATTGAA ATGAGAATCT GTGGATAAGT GTTTGTGTTC AGAAGATGTT 2760 2820 GTTTTGCCAG TATTAGAAAA TACTGTGAGC CGGGCATGGT GGCTTACATC TGTAATCCCA 2880 GCACTTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCGG GAGTTCTAGA CCAGCCTGAC 2940 50 CARCATGGAG ARACCCCATC TCTACTARAR ATACARARTT AGCTGGGCAT GGTGGCACAT 3000 GCTGGTAATC TCAGCTATTG AGGAGGTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGAG GAGGTTGCAG TGAGCCAAGA TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT CCATCTCCAA AAAAANAAAA AAAA 3060 55 Seq ID NO: 395 Protein sequence Protein Accession #: NP 055146.1 80 40 60 120

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	1	1	1	1	1		
60	MVRKPVVSTI	SKGGYLOGNV	NORLPSLGNK	EPPGQEKVQL	KRKVTLLRGV	SILICTLICA	
	GIFISPKGVL	QNTGSVGMSL	TIMTVOGVLS	LFGALSYABL	GTTIKKSGGH	YTYILEVPGP	13
	LPAFVRVKVE	LLIIRPAATA	VISLAFGRYI	LEPFFICCEI	PELAIKLITA	VGITVVMVLN	14
	SMSVSHSARI	OIFLIFCKLI	AILIIIVPGV	MOLIKGOTON	PKDAFSGRDS	SITRLPLAFY	2
	YGMYAYAGWF	YLNFVTEEVE	NPEKTIPLAI	CISMAITIGV	YVLTNVAYFT	TINABELLLS	3
65	NAVAVTESER	LLGNFSLAVP	IFVALSCFGS	MINGGVFAVSR	LFYVASREGH	LPEILSMIHV	3
		VLHPLTMIML					4
	FKVPLFIPAL	FSFTCLFMVA	LSLYSDPFST	GIGFVITLTG	VPAYYLFIIW	DKKPRWFRIM	4
	SEKITRTLQI	ILEVVPEEDK	L				
70							

Seq ID NO: 396 DNA sequence Nucleic Acid Accession #: NM_006528 Coding sequence: 57..764

75	1	11	21	31	41	51	
	1	1	1	1	1		
		GCTTTCTCGG					60
		CCCCCTGGGG					120
~~		TCAGGAGCCA					180
80		CCGGGCCCTA					240
		GTACGGGGGC					300
		TTGCTGGAGG					360
		GTGTGAGGGG					420
0.0		CTTTTCCGGT					480
85		TATGGGCTTC					540
		ACTGTGCTCT					600
	CCTGTGATGC	TITCACCTAT	ACTGGCTGTG	GAGGGAATGA	CANTAACTTT	GTTAGCAGGG	660

5	GCTTTGCCAG ATCTTGTTTG GCATGAGGAA TTCAAAAATT TTTAATTTAT	086443 ACGIGCATGI TAGAATCCGG TCITTATGGC ACAATCATT TGGATTITIT GGTTCAACTG CACCATTICA AGACAATATA	AAAATTCGGA TTATTTGCCT GGTGATTTAT TATATATAAC TTTGTGAGAC TTGGGGTCGT	AGAAGCAATT TTATGGTTGT TCACCAGTTT TAGCTGCTAT GAATTCTTGC	TTABACATTC ATCTGAAGAA TTATTABTAC TCABATGTGA ARTGCATAAG TCAGAAGAGG	TTAATATGTC TAATATGACA AAGTCACTTT GTCTACCATT ATATAAAAGC ATCATAACTG	720 780 840 900 960 1020 1080
10	Seq ID NO: Protein Acc	397 Protein	sequence P_006519				
15	CROFLYGGCE	11 ILLEPLTEAA GNANNFYTWE HRNRIENRFP CGGNINNFVS	ACDDACWRIE DEATCMGFCA	KVPKVCRLQV PKK1PSFCYS	SVDDQCBGST PKDEGLCSAN	VTRYYFNPRY	60 120 180
20	Seq ID NO: Nucleic Ac:	398 DNA se id Accession Lence: 11	quence		PREMORIENT	RANGE	
25	CCCGAGTTTG	11 CCAGCCTCCC AGGTGGCCAC	CTGGATCAAA	ATCACCCTTA	TTCTGGTGTA	CCTGATCATC	60 120
30	TTCGTGATGG AAAGGATACT TTGGTGTTCC ACGTCCAGCT GCTACGCTGC	GCCTTCTGGG TGCAGAAGGA TCATCGGCAT ACACCCTGTC TGCACGTGCT AGGCTGTGTC	GAACAGCGTC GGTGACAGAC GCCCATGGAG CTGCAAGCTG GACGCTCAGC	ACCATTCGGG CACATGGTGA TTCTACAGCA CACACTTTCC TTTGAGCGCT	TCACCCAGGT GTTTGGCTTG TCATCTGGAA TCTTCGAGGC ACATCGCCAT	GCTGCAGAAG CTCGGACATC TCCCCTGACC CTGCAGCTAC	180 240 300 360 420 480
35	GTCACCTCCG GTGAACGTGC CAGCCCGAGA CAGTCCAGCA	CCCTGGTGGC CCAGCCACCG CCTCCAATAT TCTTCGGCGC	ACTGCCCTTG GGGTCTCACT GTCCATCTGT CTTCGTGGTC	TGCAACCGCT ACCAACCTCT TACCTCGTGG	TGGGTACTGA CCAGCACCCG CCAGCCGCTG TCCTGCTCTC	GTACCCCCTG CCACCACGAG GACCGTGTTC CGTAGCCTTC	540 600 660 720 780
40	ACCATCATCT ACCATCATCT ATTCGGAGGA	ACATGATGCA COCAGCTGAG TOCTGAGGCT TCATGGCTGC TCCTCCTCCC	GAAGTCCGAG GATTGTTGTG GGCCAAACCC CTTCTCGGAG	AGCGAAGAGA ACATTGGCCG AAGCACGACT ACGTTTTTCT	GCAGGACCGC TATGCTGGAT GGACGAGGTC ACCTCAGCTC	GCCCAACCAG CTACTTCCGG GGTCATCAAC	840 900 960 1020
45	TGCGGCCTGT ACCACCGACA TCTGCAAGGA TCTAAGTCCC	ACACGGTGTC CGCTGCAGCA GCGCCCGCTT GAACTGAGAA AGTCATTGAG CAGAGAATGG	CGCCAACCAC TGTGCAGCGC GATTTTCTTA TCTCGAGTCA	GAGAAGCGCC CCGTTGCTCT AGCACTTTTC CTAGAGCCCA	TGCGCGTACA TCGCGTCCCG AGAGCGAGGC ACTCAGGCGC	GCGCCAGTCC CGAGCCCCAG	1140 1200 1260 1320
50	Seg ID NO:		in sequence	CATGAMGTT	GA.		
55	1 MASPSLPGSD	11 CSQIIDHSHV HMVSLACSDI	21 PEPEVATWIK	31 ITLILUYLII PYSTIWNPLT	41 FVM3LLGNSV TSSYTLSCKL	51 TIRVTQVLQK HTFLFEACSY	60 120
60	ATLLHVLTLS VNVPSHRGLT MCWNNMQVLM IRRIMAAAKP CRLSLOHANH	PERYIAICHP CNRSSTRHHE KSQKGSLAGG KHDWTRSYFR EKRLRVHAHS LEPNSGAKPA	PRYKAVSGPC QPETSNMSIC TRPPQLRKSE AYMILLPPSE TTDSARFVQR	QVKLLIGFVW TNLSSRWTVF SBESRTARRQ TFFYLSSVIN PLLFASRRQS	VTSALVALPL QSSIFGAPVV TIIPLRLIVV PLLYTVSSOO	LEAMGTBYPL YLVVLLSVAF TLAVCWMPNQ PRRVFVQVLC	180 240 300 360 420
65	Seq ID NO: Nucleic Ac Coding seq	400 DNA s id Accessio uence: 28	n #: NM_00	6475.1			
70	TTGCTGCTTA	11 CAACGGAGAG TTGTTAACCC GGGGTCGGGA	TATAAACGCC	AACAATCATT	ATGACAAGAT	GATTTTGGGC	60 120 180
75	ACCAMANAGA AANACGACTG TGCCCAGCAG ACAACGCAGC TTCACTTACT	ARTACTTCAG TTTTATATGA TTTTGCCCAT GCTATTCTGA TTGCACCGAG	CACTTGTAAG ATGTTGCCCT TGACCATGTT CGCCTCAAAA TAATGAGGCT	AACTGGTATA GGTTATATGA TATGGCACTC CTGAGGGAGG TGGGACAACT	AAAAGTCCAT GAATGGAAGG TGGGCATCGT AGATCGAGGG TGGATTCTGA	AATGAAAGGC GGGAGCCACC AAAGGGATCC TATCCGTAGA	240 300 360 420 480 540
80	AAGAGAATGT TTGGGGCTTT ATCCATGGGA	GCAACGTGAA TGACCAAGGA TCATTAA CCA ACCAGATTGC CCTCAATTCA	TTATCCTAAT AACAAATGGT AGACTTCATT	GGCATGATTA GGGGTTGTCA GTTGTCCATG GAAGCAGAAG	TTCCTTCAAT CTGTTAATTG TCATTGACCG ATGACCTTTC	TGCTCGAATC TGCTCGAATC TGTGCTTACA ATCTTTTAGA	600 660 720 780
85	GCAGCTGCCA TTTGCTCCCA	TCACATCGGA CCAATGAGGC TGGCTTCCGA TTATGGGAGG	CATATTGGAG TTTTGAGAAA AGCTCTTATG	GCCCTTGGAA CTTCCACGAG AAGTACCACA	GAGACGGTCA GTGTCCTAGA TCTTAAATAC	AAGGTTCATG TCTCCAGTGT	900 960 1020

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		GTGACAGTAT	AACAGTAAAT	GGAATCAAAA	TOGTGAACAA	AAAGGATATT	1080
	GTGACAAATA	ATGGTGTGAT	CCATTTGATT	GATCAGGTCC	TAATTCCTGA	TTCTGCCAAA	1140
	CAAGTTATTG	AGCTGGCTGG CTGCTCTGAG	AAAACAGCAA	ACCACCTTCA	COGATCTTGT	GGCCCAATTA	1200 1260
5	GCATTTTTTTTTTT	ATGATACTCT	CAGCAGATGGT	CAGCGCCTCC	TTAAATTAAT	TCTGCAGAAT	1320
	CACATATIGA	AAGTAAAAGT	TGGCCTTAAT	GAGCTTTACA	ACGGGCAAAT	ACTGGAAACC	1380
	ATCGGAGGCA	AACAGCTCAG	AGTCTTCGTA	TATCGTACAG	CTGTCTGCAT	TGAAAATTCA	1440 1500
	TGCATGGAGA	AAGGGAGTAA CAGAGAAATC	CCTCCATCAA	AACGGTGCGA BBGTTBBBBC	AAGATAAGGG		1560
10	TTCCTCAGCC	TACTTGAAGC	TGCAGACTTG	AAAGAGCTCC	TGACACAACC	TGGAGACTGG	1620
	ACATTATTTG	TGCCAACCAA	TGATGCTTTT	AAGGGAATGA	CTAGTGAAGA	AAAAGAAATT	1680
	CTGATACGGG	ACAAAAATGC AAGGATTTGA	TCTTCAAAAC	ATCATTCTTT	ATCACCTGAC	ACCAGGAGTT	1740
	AAAATCTTTC	TGAAAGAAGT	AAATGATACA	CTTCTGGTGA	ATGAATIGAA	ATCAAAAGAA	1860
15	TCTGACATCA	TGACAACAAA	TGGTGTAATT	CATGITGTAG	ATAAACTCCT	CTATCCAGCA	1920
	GACACACCTG	TTGGAAATGA	TCAACTGCTG	GAAATACTTA	ATAAATTAAT	CANATACATC	1980 2040
	CAAATTAAGT	TTGTTCGTGG	GGAACCAAAA	ATTANAGTGA	TTGAAGGCAG	TCTTCAGCCT	2100
	ATTATCABAA	CTGAAGGACC	CACACTAACA	AAAGTCAAAA	TTGAAGGTGA	ACCTGAATTC	2160
20	AGACTGATTA	AAGAAGGTGA	AACAATAACT	GAAGTGATCC	ATGGAGAGCC	AATTATTAAA	2220
	AAATACACCA	AAATCATTGA TTACAGGTCC	TGGAGTGCCT	GTGGAAATAA	CTGAAAAAAA	BACACGAGAA	2280
	BAACGAATCA BCBCBBCBBB	CTCTGAAGAA	ATTGTTACAA	GAAGAGGTCA	CCAAGGTCAC	CAAATTCATT	2400
	GAAGGTGGTG	ATGGTCATTT	ATTTGAAGAT	GAAGAAATTA	AAAGACTGCT	TCAGGGAGAC	2460
25	ACACCCGTGA	GGAAGTTGCA	AGCCAACAAA	AAAGTTCAAG	GTTCTAGAAG	ACGATTAAGG	2520 2580
	GAAGGTCGTT	CTCAGTGAAA CCTTAGAAAA	ATCCAAAAAC	CAGAAAAAA	TCAGGAACTG	AAACATCAGC	2640
	ACABAGAAGC	AATCATCAAA	TAATTCTGAA	CACAAATTTA	ATATTTTTTT	TTCTGAATGA	2700
••	CANADCATCAC	GGAAATTGTG	GAGTTAGCCT	CCTGTGGTAA	ACCAATTGAA	GAAAATATAA	2760
30	CACCTTACAC	CCTTTTTCAT	CTTGACATTA	AAAGTTCTGG	CTAACTTTGG	AATCCATTAG	2820
	AGAAAAATCC	CACCODAGCCT	ATTCATTACA	TTATGGATAC	ATRABANTOCA	CGCAAGCCAT	2940
	TATCTCTCCA	TOGGAAGCTA	AGTTATAAAA	ATAGGTGCTT	GGTGTACAAA	ACTTTTTATA	3000
25							3060
35	CAACTAATTT	TGTACTCTCA TTCAATAAAA	GAATGTTTGT	CATATGCTTC	TTGCAATGCA	AAATTTTTTAA	3120 3180
	ATTCAGAAAA	ACTCAAGATT	TARGTTANAA	AGTGGTTTGG	ACTTGGGAA	AUG. LUNCIN	5200
40	Seq ID NO: Protein Acc	ession #: 1	in sequence IP_006466.1				
	1	11	21	31	41	51	
	Ī	Ī	1	1	1	1	
45	MIPPLPMFSL	LLLLIVNPIN	ANNHYDKILA	HSRIRGRDQG	PNVCALQQIL	GTKKKYFSTC	60 120
40	KNWYKKSICG	SFTYFAPSNE	AMPAILMENTE	POLESMYNVE	TANALHSHMI	NKRMLTKDLK	180
	NGMIIPSMYN	NLGLFINHYP	NGVVTVNCAR	IIHGNQIATN	GVVHVIDRVL	TOIGTSIQDF	240
	IEAEDDLSSF	RAAAITSDIL	EALGRDGHFT	LFAPTNEAFE	KLPRGVLERF	MGDKVASEAL	300 360
50	MKYHILNTLO		PETLEGNTIE	LCI.AGAI.PDD	GEVTI.LADIM	NAFSDDTLSM	420
20	TROUT TROOP	POUTPLACED.					
	VORLLKLILO	KOVIBLACKO NEILKVKVGL	MELYMGQILE	TIGGKQLRVF	VYRTAVCIEN	SCMEKGSKQG	480
	VQRLLKLILQ	KQVIBLAGKQ NHILKVKVGL TIKPARKSIH	NELYNGQILE EKI-KODKRES	TIGGKQLRVF	UVERTAVCIEN	SCMEKGSKQG WTLFVPTNDA	480 540
	VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE	KQVIBLAGKQ NHILKVKVGL IIKPAEKSLH ILIRDKNALO	NELYMGQILE EKLKODKRFS NIIIYHLTPG	TIGGKQLRVF TFLSLLEAAD VFIGKGFEPG	VYRTAVCIEN LKELLTOPGD VTNILKTTOG	WTLFVFTNDA SKIPLKEVND	480 540 600
55	VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVNELKSK	KQVIBLAGKQ NHILKVKVGL IIKPAEKSLH ILIRDKNALQ BSDIMTTNGV	NELYNGQILE EKLKQDKRFS NIILYHLTPG IHVVDKLLYP	TIGGKQLRVF TFLSLLEAAD VFIGKGFEPG ADTPVGNDQL	VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY	SCMEKGSKQG WTLFVPTNDA SKIPLKEVND IQIKFVRGST	480 540 600 660 720
55	VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVNELKSK FKEIPVTVYT TEVIHGEPII	KQVIBLAGKQ NEILKVKVGL IIKPAEKSLH ILIRDKNALQ ESDIMTTNGV TKIITKVVEP KKYTKIIDGV	MELYNGQILE EKLKQDKRFS NIILYHLTPG IHVVDKLLYP KIKVIEGSLQ PVBITEKETR	TIGGKQLRVF TFLSLLEAAD VFIGKGFEPG ADTPVGNDQL PIIKTEGPTL EERIITGPEI	VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKIEGEPE KYTRISTGGG	SCMEKGSKQG WTLPVPTNDA SKIPLKEVND IQIKFVRGST FRLIKEGETI ETEETLKKLL	480 540 600 660
55	VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVNELKSK FKEIPVTVYT TEVIHGEPII	KQVIBLAGKQ NHILKVKVGL IIKPAEKSLH ILIRDKNALQ BSDIMTTNGV TKIITKVVEP	MELYNGQILE EKLKQDKRFS NIILYHLTPG IHVVDKLLYP KIKVIEGSLQ PVBITEKETR	TIGGKQLRVF TFLSLLEAAD VFIGKGFEPG ADTPVGNDQL PIIKTEGPTL EERIITGPEI	VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKIEGEPE KYTRISTGGG	SCMEKGSKQG WTLPVPTNDA SKIPLKEVND IQIKFVRGST FRLIKEGETI ETEETLKKLL	480 540 600 660 720
	VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVMBLKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKP Seq ID NO:	KQVIELAGKQ NHILKVKVGL IIKPAEKSH ILLIRDKNALQ ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 402 DNA Bec	THE	TIGGKQLRVF TFLSILLEAD VFIGKGFEPG ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN	VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKIEGEPE KYTRISTGGG	SCMEKGSKQG WTLPVPTNDA SKIPLKEVND IQIKFVRGST FRLIKEGETI ETEETLKKLL	480 540 600 660 720
55 60	VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVMELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKP Seq ID NO: Nucleic Ac:	KQVIELAGKQ NHILKVKVGL IIKPAEKSLH ILIRDKNALQ ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEOGDGHLFE 402 DNA Bee td Accession	MELYNGQILE EKLKQDKRFS NIILYHLTPG HHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEBIKRLLQG Quence 1 #: NM_002	TIGGKQLRVF TFLSILLEAD VFIGKGFEPG ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN	VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKIEGEPE KYTRISTGGG	SCMEKGSKQG WTLPVPTNDA SKIPLKEVND IQIKFVRGST FRLIKEGETI ETEETLKKLL	480 540 600 660 720
	VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVMELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKP Seq ID NO: Nucleic Ac:	KQVIELAGKQ NHILKVKVGL IIKPAEKSH ILLIRDKNALQ ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 402 DNA Bec	NELYNGQILE EKLKQDKRFS NILYHLTPG IHVVDKLLYP KIKVIEGSLQ PVEITSKETR DEBIKRLLQG Quence 1 #: NM_002	TIGGKQLRVF TPLSLLEAAD VPIGKGFEPG ADTPVGNDQL PIIKTEGPTL EBRIITGPEI DTPVRKLQAN	LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL	SCMEKGSKQS WTLFVPTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ	480 540 600 660 720
	VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVMELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKP Seq ID NO: Nucleic Ac:	KQVIELAGKQ NHILKVKVGL IIKPAEKSLH ILIRDKNALQ ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEOGDGHLFE 402 DNA Bee td Accession	MELYNGQILE EKLKQDKRFS NIILYHLTPG HHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEBIKRLLQG Quence 1 #: NM_002	TIGGKQLRVF TFLSILLEAD VFIGKGFEPG ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN	VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKIEGEPE KYTRISTGGG	SCMEKGSKQG WTLPVPTNDA SKIPLKEVND IQIKFVRGST FRLIKEGETI ETEETLKKLL	480 540 600 660 720
60	VORLIKLILQ RNGAIHIFRE FKGMTSESKE TLLUMBLKSK FKEIPUTVYT TEVIHGEPII QEEVTKUTKP Seq ID NO: Nucleic Ac: Coding sequ	KQVIBLAGKQ NEILKUKVGL IIKPAEKSLH ILIRDKNALQ BSDIMTINGV TKHITKVVEP KKYTKIIDGV IEGGDGHLFE 402 DNA see dd Accession dence: 404	MELINGQILE EKLKQDKRFS NIILYHLTPG IHVVDKLLYP KIKVIEGSLQ PVEITSKETR DEBIKRLLQG Quence 1 #: NM_002 1 #: NM_002	TIGGOLAVF TFLSLLEAAD VFIGKOFEPG ADTPVGNDQL FIIKTEGFTL EERIITGFEI DTPVRKLQAN 2416	VYPRAVCIEN LELLTQPGD VTNILKTIQG LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL	SCMEKGSKQS WTLFVPTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ	480 540 600 660 720
	VQRLKKLILQ RNGAHHIFRE FKGMYSESKE TLLVMELMSK FKEIPUTVYT TEVIHGEPII QBEVTKVTKP Seq ID NO: Nucleic Ac: Coding sequ	KQVIBLAGKQ NEILKUKVGL IIKPAEKSLH ILIRDKNALQ BSDIMTTNGU ESDIMTTNGU KKYTKIIDGV IEGGDGHLFE 402 DNA sec ich Accession ience: 40	MELINGILE EKLKQDKRPS NILLYHLTPG IHVVDKLLYP KIKVIEGSL PVEITEKETR DEBIKRLLQG QUENCE 14: NM_002 117 21 GGAACTCCAT	TIGGOQLAVF TFLELLEAD VFIGKGFEPG ADTPVGHEQL PIIKTEGFTL EERIITGPEI DTPVRKLQAN 2416 31 TCTATCACTA ATTCGAGTGC	VYRTAVCIEN LWELLTOPED VTNILKTTOG LEILNKLIKY TKVKIEGER KYTRISTGGG KKVQGSRRRL 41 TGAAGAAAAG	SCHEKGSKOG WILFUPTNDA SKIPLKEVND 101KFVRGST PRLIKEGETI ETESTLKKLL REGRSQ 51 1 TGGTGTTCTT AGTAGTGAGA	480 540 600 660 720 780
60	VQRLKALIQ RNGAHIFRE FKGMTSEEKE TLLVMELMSK FKEIPUTVYT TEVHKGEPII QBEVTKVIKP Seq ID NO: Nucleic Ac: Coding sequ 1 ATCCAATACA TTCCTCTTGS AACGGTCGCT	KQVIELACKQ NEILKVKYGL IIRPAEKSLH ILIRDKNALQ ESDIMITING	MELINGOILE EKLKQDKRPS NIILYHLTPG IHVVDKLLYP KIXVIEGSLQ PVEITSKETR DEBIKRLLQG quence 1 #: NM_002 117 21] GGAACTCCAT GCTGGTTCTG CAGCACCAAC	TIGGROLAVE TFLSILEAAD VFICKGFEPG ADTPUGHDQL EERIITGPEI DTPVRKLQAN 2416 31 TCTATCACTA ATTGGAGTGC CAAGGGACTA	VYRTAVCIEN LKELLTOPED VINILKITOG LEILNKLIKY KVKIEGER KYTRISTGGG KKVQGSRRRL 41 TGAAGAAAAG AAGAAACAC	SCHEKGSKQE WITEPURNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI ETESTLKKLL REGRSQ 51 I TOGTGTTCTT AGTAGTGAGA ATTCCTTGAAA	480 540 600 720 780
60	VQRLKALIQ RNGAHIFRE FKGMTSEEKE TLLWMELMSK FKEIPUTVIKF TEVINGEPII QESTTAVIKF Seq ID NO: Coding seq 1 ACCATACA TTCCTCTTGG AAGGGTCGCT	KQVIELACKQ MHILKVKVOL IIRPAEKSLH ILIRDKNALQ ESDIMITINGV ESDIMITINGV KKYTKIIDGV IEGGDGHLFE 402 DNA Sec 404 Accession cence: 40 11. GGACTGACTT GCATCATCTT GTTCCTGCAT AATTIGCCCC	NELINGOILE EKIKODKRPS NIILYHLTPG IHVVDKLLYP KIKVIEGH PVEITEKETR DEBIKKLLQG quence 1 #: NM_002 117 21] GGGAACTCCAT GCTGGTTCTG CAGCACCAAC AAGCCCTTCC	TIGGGQLAVF TFLSILEAAD VFIGKGFEPG ADTPVGHDQL PIINTEGFTL EERIITGFEI DTPVRKLQAN 2416 31 TCTATCACTA ATTGGAGTGC CAAGGGCTA TGGGAGAAAA	VYRTAVCIEM LWELLTOPED VINILKTIQG LEILNKLIKY KVKIESEPE KYTRISTGGG KKVQGSRRRL 41 TGAAGAAAAG AAGGAACCCC TCCACCTACA TTGAAATCAT TTGAAATCAT	SCHEKGSKOG WITEPUTNDA SKIPLKEVND 101KFVRGST FRLIKEGETI ETESTLKKLL REGRSQ 51 TOGTGTTCTT AGTAGTGAGA ATCCTTGAAGA ATCCTTGAAGT	480 540 600 720 780
60	VORLIKILLO RINGAHIFRE FKOMTSEEKE TLLVNELKSK FKEIPUTYT TEVHIGBEII TEVHIGBEII OBETTKVTKP Seq ID NO: Nucleic Ac. Coding sequ ATCCAATACA ATCCCATTOG AAGGGTOGT	KQVIELACKQ MHILKVKVGL IIRPAEKSLH ILIRDKNALQ ESDIMITING ESDIMITING ESDIMITING ESDIMITING ESDIMITING ENDIMITING ENDIMITING IEGGDGHLFE 402 DNA Sec dd Accession cence: 40 11. GGACTGACTT GGACTGACTT GTCCTGCAT TAATTIGCCCC TTCAAACATG	MELINGOILE EKIKADKRPS NIILYHITPG IHVVDKLLYP KIKVIEGSLQ PVELISKETR DEEIKRLLQG QUENCE 1 #: NM_002 117 21 GGAACTCCAT GGGACCAC CAGCACCAC TCTAAACCCA TCTAAACCCA TCTAAACCCA	TIGGRQLAVE TFLSILEAAD VFIGKFESE ADTEVURDOL PIIKTEGPTL EERIITOPEI DTFVKKLQAN 2416 31 TCTATCACTA ATTGGAGNGC CAAOGGACTA GGGGAAAAA GATTCAGCAG	VYRTAVCIEM LKELLTOPED VINILKITOG LEILINKLIKY KVKIESEPE KYTRISTGG KKVQGSRRRL 41 TGAAGAANAA AAGGACCCC TCCACCTACA ATGTGAAGAA	SCHEKGSKOG WITEPUTNDA SKIFLESVND IQIIFWRGST FRLIKEGETI ETESTLKKLL REGRSQ 51 TOGTGTTCTT AGTAGTGAGA ATCCTTGAAA TCGTACACTG ACTAGTAAAAA	480 540 600 720 780
60	VQRLKALIQ RNGATHIFRE FKGMTSEEKE TLLVWELMSK FKEIFVTYT TEVINGEFII OBEVTKVTKF Seq ID NO: Nucleic Ac: Coding seq 1 ACCATACA TTCCTCTTGG AAGGGTCGCT GACCTTAAAC AAGGGTCGCT AAGATGGGAAA	KQVIELACKQ MEILKYKYOL IIRPAEKSLH ILIKDKHALQ ESDIMITINGV TKIITKVVEF 402 DNA ses 402 DNA ses 403 GAGTGACTT GCATCATCTT STTCCTGCAT AATTIGCCC TTCAARGACTG AACAGGTCAG TGAARGTCA	MELINGILE BEKLAGNKRPS NILLYHLTPG IHVVDKLLYP PUBLISKETE DEBIKRLLQG QUEENCE QU	TIGGOLAVE TFLSILEAAD VFICKOFERG ADTPVGHDQL PIINTEGFTL EERIITGFEI DTPVRKLQAN 31	VYRTAVCIEM LKELLTOPED VINILKITOG LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41	SCHEKGSKOG WITEPUTNDA SKIPLKEVND IQIKFWRGST FRLIKEGETI ETBETLKKLL REGRSQ 51 TOGTGTTCTT AGTAGTGAGA ACTGATAAA ACTGATAAA ACTGATAAAAA ACTGATAAAAAA ACTGATAAAAAA	480 540 600 720 780 60 120 180 240 300 360 420
60	VORLIKILLO RINGAHIFRE FKGMTSEEKE FKGMTSEEKE FKEIPUTUYT TEVHIGBEII CODING Nucleic Ac Coding sequ Coding sequ ATCCAATACA TTCCTCTTGG AAGGGTGGT AAGGGTGGT AAGGGAGA AAGAATGGAG AAGAAAGTGAC	KQVIELAGKQ MRILKVKYGL IIRDAEKSHH ILIEDKNAKUGL ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGRLFE 402 DNA sec dd Accession cence: 40 11 GGAGGAGAGTT GGATCATCTT GTTCCTGCAT AATTIGCCOC TTCAAACATG TGAAAGTTCG TGAAAGTTCG TGAAAGTTCG TGAAAGTTCG TGAAAGTTCG TGAAAGTTCG TGAAAGTTCA	NELINGOILE EKLKQNKPS NIILYHITPG IHVVDKLLYP KIKVIEGSLQ PVEITEKETR LTR LTR LTR LTR LTR LTR LTR LTR LTR L	TIGGRQIAVE TFLSILEAAD VFIGKFESG ADTPVGEDCL PILTEGPTL ERRITTGPEI DTFVYKLQAN 2416 31 TCTATCACTA ATTGGAGGGC CAAGGGACTA ATTGGAGGACTA GATTCAGCAG GATTCAGCAG GATTCAGCAG AAGCAAAAGA GATTCAGCAG AAGCAAAAGAA CGTTCTCTCT	VYRTAVCIEM LKELLTOPED VINILKITOE LEILNKLIKY TKVKIEGEPE KYTRISIGGE KKVQGSRRRL 1 TGAAGAAAAG AAGGACCCC TCCACCTACA ATGTGAAGAA AAAAGAAGAA TTTTAAATTAT	SCHERGSKOG WITEPUTNDA SKIFLKEVNI DIINFVRGST FRLIKEGETI ETESTLKKLL REGRSQ 51 TOGTGTTCTT AGTAGTGAGA ATCCTTGAAA ATCCTTGACACT ACTGATTAAAA TACATAAAAA TACATAAAAAA TACATAAAAAA	480 540 660 720 780 60 120 180 240 300 360 420 480
60 65 70	VORLIKILIO RINGAHIFRE FKOMTSEKE FALL GEVENTSEKE FALL GEVENTSEKE FKOMTSEKE FKOMTSEKEE FK	KOVIELAGKO MILLGENCO MILLG	NELINGILE EKLKQNKPS NILLYHITPG IHVVDKLLYP KIKVIEGSLQ PVEITSKER DEBIKRLLQG QUENCE 117 21] GGGACTCCAT GCTGGTTCTG CAGCACCAAC CAAAGAAA AAGCCTTCA CTTAAACCAA TCTGTGTTAA TCTGTGTTAA	TIGGRQLAVE TFLSLLEAD VFIGKOFSEG ADTPVGHDQL FIKTEGFTL ERRITIGFEI DTPVRKLQAN 2416 31 TCTATCACTA ATTGGAGTGC CAAOGGACTA TGCAAGAAAGA GATTCAGCAG AAGCAAAGAA GGTTATTGAA	VYRTAVCIEM LKELITOPED VINILKITOPE LEILMKLIKY TKVKIEGEPE KKYOGSRRRL 1 TGAAGAAAAA AAGGAACCC TCCACCTACA TTGAAAATCAT ATGTGAAGAA ATGGGAAAAA AAAAGAACAC TTTAATTAT TTGAATAGAA	SCHEKGSKOG WITEPUTNDA SKIPLKEVND IQIKFWRGST FRLIKEGETI ETBETLKKLL REGRSQ 51 TOGTGTTCTT AGTAGTGAGA ACTGATAAA ACTGATAAA ACTGATAAA ACGGTATAA ACGGTATAA ACGGTATAA	480 540 600 720 780 60 120 180 240 300 360 420
60	VORLIKALIO, ROMANHIFE R FROMYSEKE FROMYSEKE FROMYSEKE FROMYSEKE FROMYSEKE FROMYSEKE FROMYSEKE FROMYSEKE FROMYSEKE 1 ACCAATACA TCCTCTTGG AACGATGGAA AAGGGGGGAA AAGGGGGAA AAGGATGGAA AAGAATGGAA AAGAATGGAA ATTCCTTAGAA AAGAATGAA AAGAATGAA AAGAATGAA AAGAATGAA AAGAATGAA ATTCCTTAGAA AAGAATGAA ATTCCTAAACA AATTACTTCAAAAGAA ATTACTTCAAAAGAA ATTACTTCAAAAGAAAAAAAAAA	KQVIELAGKQ MINILAGWAG	MELYNQTILE EKIKQDKRFS NILLYHLTFG INIVOKLLYP KIKVIEGSIQ PVETTEKETE DEBIKRILGG INFO COMPANION OF THE STATE OF T	TIGGGOLAW THISALEAN VFIGKOPERO ADTPVIGHOU PILKTEGPTL ERRITOPEL 2416 31 1 CTATCACTA ATTGAGGGC CAAOGMACTA TIGGGGAANA GUTTCACGG ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA ANGCHANGA COTTACTACCA CTACCACCA CTACCACCA CTACCACCA CTACCACCA CTACCACCA CTACCACCA	VYPTAVCIES LIKELITYPOU VINI LIKETO LIELIMKLIKY TKYKI ROBPE KKVYGSRRRL 41 TGAAGAAMA AAGGAACCCC TTGAAATCAT ATGGAGAAAA AAGAATCAA TTGAATGAATCAT TTGAATGAATAA AAGAATCAA	SCHERGSKCS SCHERGSKCS SCHERGSKCS SKIPLERIND 1016FVRGST FFLIKROBET FFLIKROBET FFLIKROBET 1 TOGTOTTCTT AOTAGTAGAA ACCTGAAAAA TOCTGACACA ACCTGAAAAA ACCTGAAAAA ACCTGAAAAA ACCTGAAAAA ACCTGAAAAA ACCTGAAAAA ACCTGAAAAA ACCTGAAAAA	480 540 660 720 780 60 120 180 240 300 360 420 540 660
60 65 70	VORLIKATIO ROBANTESE ROMANIFESE FROMTSESE FROMTSES F	KQVIELAGKQ MINILAGWAG MINILAGWAG BBDIMTINGU HISPARAGLA	MELYNQGILE EKIKQDKRFS NILUFHLTFG INIVOMELUF KIKUIGSHQ PVEITSKETE DEBIKKILQG 117 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TIGGROLAW THISLIEAD VI IGROPEO ADTOVIDUD IN THEOPTH ERRITOPED DTOVAKLOAM 2416 31 1 TCTATCACTA ATTGGAGGIAG TGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	VYPTAVCIEN LIKELITYPOU VINI LIKETOO LELIJAKULIK TRUKTOO LELIJAKULIK TKYKI EGESPE KKVQGSRFRL 41 1 1 1 1 1 1 1 1 1	SCHEKGSKOS SCHEKGSKOS SILPLENDA IOIKFVAGT FELIKEGETI FELIKEGETI FESTERIKUL REGRSQ 51 TOGTGTTCTT TOGTGTTCTT TOGTGTTCTAAAA ATCCTTGAAAA TACCTTGAAAA TACCTTGAAAA TACCTTGAAAA TACCTGAAAAT TACCTACACAC ACTTGAAAAAA TACCTGAAAAA	480 540 660 720 780 60 120 180 240 300 420 480 660 660 6720
60 65 70	VORLIKATIO ROMANIFER ROMAN	KQVIELAGKQ MINILAGWAG	NELYMOGILE EKIKODKARS NILUTHUTPG INTUVENCE NILUTHUT	TIGGKOLAWF THEALEAN VFICKOFEN ANDYWOUNDL PILKTEOPTH ERRITTOPH TCHACACTA ANTOGRACIA TCHACACTA ANTOGRACIA TGCORGANA ANTOGRANA AN	VYPTAVCIES LIKELITYPOU VINI LIKETOG LIELIMKLIKY TRVKI BEBEB KKVITI STOGO KKVOGSRREL 41 I TORAGMANAG ANGGRACOCC TTORAGMANAG ANGGRACOCC TTORAGMANAG ANTOGRAGA TTORAGRAGA TTORAGRAGA TTORAGT TTORATTAT TTORATGRAGA ANGANATCA ANGGRAGA TTORAGT TT	SCHERGSKCS SCHERGSKCS SCHERGSKCS SKIPLERIND 1016FVRGST FPLIKEGIETI FPLIKEGIETI FPLIKEGIETI FRETERIKUL REGRESQ 51 I TOGTOTTOTT AUTHOTHOGA AUTOCHAANA TOCHACHOO ACTURATIAN ACATCAANAA COCTAANAA TOCHACACC CCACANAGA CCCCCACACC CCCCACACC CCCACACC CCCCACACC CCCACACC CCCCACACC CCCACACC CCCACC CCCACACC CCCACC CCCACACC CCCACACC CCCACACC CCCACC CCCACC CCCCACC CCCACC CCCACC CCCACC CCCACC CCCACC CCCCACC CCCACC CCCACC CCCACC CCCACC CCCACC CC	480 540 660 720 780 120 120 120 240 300 360 420 480 540 660 720
60 65 70 75	VORLIKATIO ROMANIFER FROMTSENE FROMTSENE FROMTSENE FROMTSENE TAVHESPI OBSTRATE ACCATTACA ACCATT	KQVIELAGKQ MILLAGKQ MILLAGKQ MILLAGKA MILLAGKAL BEDIMTINGV TILTKVMBA LIGOMORILE 402 DNA sec 404 Accessio Lences 40 11 11 GOAGRICA GOAGRACATC GOAGRACATC TICTAGAA AATTIGACC TICTAGAA AATTIGACC TICTAGAA AATTIGACC TICTAGAA AATTIGACC TICTAGAA AATTIGACC TICTAGAA AATTIGACC TICTAGAA TICTAGAC TICTAGAA TICT	MELYMOGILE EKIKQDKAFS NILUTHUTPG INTOVINUE PROPERTY	TIGOROLAW THEALEAN ANTOWORDLO FILKTEOPTH ERRITOPE 11 CTATCACTA ATTOMOTOC CAMOGRACIA OTTOMOTOC CAMOGRACIA OTTOMOTOC CAMOGRACIA OTTOMOTOC CAMOGRACIA OTTOMOTOC ANTOMOTOC CAMOGRACIA OTTOMOTOC ANTOMOTOC CAMOGRACIA OTTOMOTOC ANTOMOTOC CAMOGRACIA OTTOMOTOC ANTOMOTOC CAMOGRACIA OTTOMOTOC ANTOMOTOC CAMOGRACIA OTTOMOTOC OTTOMOTOC OTTOMOTOC OTTOMOTOC OTT	VYPTAVCIES LEGILIPOUS VINILATTO LEGILIPOUS VINILATT	SCHERSKYC KITEVETHEN SILTELERINA JOJINEVRST SILTELERINA JOJINEVRST STEETLIKKL REGRESQ STEETLIKKL REGRESQ STEETLIKKL REGRESQ ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA ACTIOTIONA CONTINUES ACTIOTIONA CONTINUES CO	480 540 600 600 720 780 120 180 240 300 3420 480 540 600 600 780 840 900
60 65 70	VORLINGIAL OF THE MACHINETS OF T	KOVIELAGICA NILIKANYALI ILIBANHALA NILIKANYALI ILIBANHALA SEDIHTTMAV TRIITKVYBE KKYTRIIDAV 10 GAAGGACTACT GCATCATCT GATTTAACC CTCTATGATTCT GCATCATCATCT GATTTAACCA CTCCATCATCATCT GCATCATCATCT GCATCATCATCATCT GCATCATCATCT GCATCATCATCATCT GCATCATCATCT GCATCATCATCT GCATCATCATCT GCATCATCATCATCATCT GCATCATCATCATCATCATCATCATCATCATCATCATCATC	NELYMOGILE EXIKQUERE'S NILLYHLTPG INIVOMALLY KIKVIBGBLQ PVEITSERT 1 #1 MM_002 117 21 GGRGGTTCTG GGRGGTTCTG CGGGCCCCAC AAGCCCTCC CCCAAAACAAA AAACTCCTAG TAGAACAAA AAAACTCCAAG CCACACCAC GACCACCAC CCCAAAACAAA AAAACTCCAAG CCACACCACC CCAAAACAAA AAAACTCCAAG CCACACCACCACC CCACAACACACACCCCC CAAAACACACACCCCC CAAAACACACACACCCCCACAAACAAA AAAACTCCAAG CCACACCCCCC CAAAACACCCCCCC CAAAACCCCCCC	TIGGROLAWY TIGGROLAWY TIGGROSSO ANDEVOUNDLY TIETHEDPTL ERRITIOPEL TOTALCACTA ATTOGRASTIC CARAGGACTA TGCAGAGATA TGCAGAGATA AGCTACTACA AGCTACTACA AGCTACTACA AGCTACTACA AGCTACTACA CONTICACAC CONTICACAC AGCTACTACAC	VYPTAVCIES LEGILITYOUS LEGILITY LEGI	SCHERGES (COMENCES) WILEVERION SITELERINA I (1) (1) (NEVRSST) FELLIRGIETI FELLIRGIETI STESTLINGLI REGREQ 51 1	600 1200 7800 1200 2400 3000 4200 5400 6600 7200 8400 9000 9600
60 65 70 75	VORLINGIAL OF THE PROPERTY OF	KQVIELAGKQ NILIKANKOL IIIRAEKSLH IIIRAEKSLH IIIRAEKSLH IIIRAEKSLH IIIRAEKSLH IIIRAEKSLH IIRAEKSLH IIR	NELYMOGILE EXIKADKARS NILIYHITSG INIVONALIY EXIKADKARS NILIYHITSG INIVONALIY EXIKTIBASHQ PRETIRETS BERIFALLOG PRETIRETS GENOTICAS GORGATICAS ANACCOCTO COMMANDA ANACCOCTO COMMANDA ANACCOCTO COMMANDA ANACCOCTO GAG COMMANDA ANACCOCTO GAG COMMANDA ANACCOCTO GAG COMMANDA CTITOTOCTO GAG CACAGCOCTO GAG COMMONDA COMMANDA GAG COMMANDA GAG COMMANDA GAG COMMANDA GAG COMMANDA GAG COMMANDA GAG GAG COMMANDA GAG GAG COMMANDA GAG GAG GAG COMMANDA GAG GAG GAG GAG GAG GAG GAG	TIGGGOLAW THEASLEAN ADTEVORED FILENDER	VYPTAVCIES LIKELITYPOU VINI LIKTUGO LIELIJAKULINY LIELIJAK	SCHERSKICH KITEVETRIS SILTELERINA JOINTONT TO INTEREST	480 540 660 720 780 120 120 180 300 360 424 480 660 660 660 720 780 880 880 890 960 960
60 65 70 75	VORLIKALIO ROMANITAR ROMAN	KQVIELAGKQ NNILKAKWAOI IIIRARAHA IIIRAKAHA IIRAKAHA IIRAKA	NELYNGOLLE SELKGDKARS NILITHITSG INTUNDIKALTS NILITHITSG INTUNDIKALTS PWEITSKETR DEELKELLGG QUARTICLE GGAACTCCAT GGAACTCCAT CAGCACCACC AAGCCTTCAA AAAACTCAT CCTAAACAAAA AAAACTCAA CCTACCACAAAAAAAA	TIGGGOLAW THE STATE OF THE STAT	VYPTAVCIES LEGILIPOLIS LEGILIP	SCHERSKE SCH	600 1200 7800 6600 6600 1200 1800 2400 3000 5400 6600 7200 9000 8400 9000 10200 9000 10200 9000 10200
60 65 70 75 80	VORLINGIAL OF THE MANAGEMENT O	KOVIELAGION NILIKANYOLI IIIRARIALI BILITANIA BILITA	NELYNGOLLE SELKGDKARS NILITHITSG INTUNDIALITS INTUNDIALIT	TIGGGOLAW THE STATE OF THE STAT	VYRTAVCIES LIGHLITHOUS VINILIATION VINILIATION VINILIATION VINILIATION VINILIATION KKYVQSBRRIL 41	SCHERSKYC KITEVPHENS SITPLEFAND SITPLEFAND SITPLEFAND SITPLEFAND SITPLEFAND FOR SITPLEFAND FOR SITPLEFAND FOR SITPLEFAND SITPLEFAND FOR SITPLEFAND FOR SITPL	600 1200 6600 6600 7800 8600 1800 3600 4200 9600 1000 1000 1000 1000 1000 1000 10
60 65 70 75	VORLINGIAL VORLINGIA PROMATHER PROMYSERSE PROMYSERSE PROMYSERSE PROMYSERSE SEGID NO: Nucleic No: Coding segi A TCOATACA TCOCATOG AAGOOTOGC AAGOOTO	KOVIELAGIKO KILIKUWALI ILIKONALO ILI	NELYMOGILE EXILAGIDARS NILLYBULTHON SELICATION OF THE PROPERTY	TIGGROLAW THE STATE OF THE STAT	VYRTAVCIES LEGILITATO VINILIATION VINILIATION VINILIATION VINILIATION VINILIATION ATTOMATICAL ATTOMAT	SCHERSKÖG KITLENDRA SKITLENDRA SCHERS STATISANA KONTAGNA ACCIOLAGA ACCATALA AASTINANA KOSTINANA TICHNANGA COCCATALA AGOTTAGARA ACCATALAGA ACCAT	480 600 660 720 780 120 180 240 360 360 660 660 660 660 660 1020 1080 1020 1080 1020 1040 1040 1040 1040 1040 1040 104
60 65 70 75 80	VORLINGIAL OF THE STATE OF THE	KOVIELAGION NILIKANYOLI IIIRARIALI BILITANIA BILITA	NELYMOQILE EKIKGURAFS NILUMIENS NILU	TIGGEOLEWE THE SECTION OF THE SECTIO	VERTANCIES LEGILIQUEO LEGILIQUE LEGILIQUEO LEGILIQUEO LEGILIQUEO LEGILIQUEO LEGILIQUEO LEGILIQUE LEGILIQUEO LEGILIQUEO LEGILIQUEO LEGILIQUEO LEGILIQUEO LEGILIQUE LEGILIQUEO LEGILIQUEO LEGILIQUE LEGILI	SCHERSKÖG KYTLEVERDEN SOLIKEVRIGET SOLIKEVRIGET ETESTLIKULT ETESTLIKULT ETESTLIKULT AUTHOTIONA AUTOTIONA A	600 1200 6600 6600 7800 8600 1800 3600 4200 9600 1000 1000 1000 1000 1000 1000 10

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	AGATTGTCAG	CTCCTTGAGG	GCAAGAGCCA	CAGTATATTT	CCCTGTTTCT	TCCACAGTGC	1440
	CTAATAATAC	TGTGGAACTA	GGTTTTAATA	ATTTTTTAAT	TOCTGGCTAC	ATGGGCAGGA	1500 1560
_	CTAGCCTCTG	GTAACCTCTT	ACTTATTATC	TTCAGGACAC	TCACTACAGG	GACCAGGGAT	1620
5	GATGCAACAT	CCTTGTCTTT	TTATGACAGG GGATATTCTG	ATGTTTGCTC	AGCTTCTCCA	ACAATAAGAA	1680 1740
	AAAATCATAT	AATCTTA CAA	TGAAAAGGAC	TTTATAGATC	AGCCAGTGAC	CAACCTITTC	1800
	CCAACCATAC	AAAAATTCCT	TTTCCCGAAG	GAAAAGGGCT	TTCTCAATAA	GCCTCAGCTT	1860
10	TCTAAGATCT	AACAAGATAG	CCACCGAGAT TGTTTCAGAG	CCTTATCGAA	ACTCATTTA	GGCAAATATG	1920
10	TCTCCCATGA	AGAAAGGGAA	CGGTGAAGTA	CTAAGCGCTA	GAGGAAGCAG	CCAAGTCGGT	2040
	TAGTGGAAGC	ATGATTGGTG	CCCAGTTAGC	CTCTGCAGGA	TGTGGAAACC	TOCTTCCAGG	2100 2160
	CTTTCCCC3.2.3	TOGA D TO A CT	AGGAGAGGTT GCTCACACTG	CTICATIVA TITT	AGAGTGCTGT	CCGGTGGAGA	2220
15	TCCCACCCGA	ACGTCTTATC	TAATCATGAA	ACTCCCTAGT	TCCTTCATGT	AACTTCCCTG	2280
	ASTOTASAAA	GIGITTICATA	AATTTGAGAG AACCAAAGAC	TCTGTGACCC	ACTTACCTTG	CATCTCACAG	2340 2400
	TCATTTATCA	TATATATACA	TACATGCATA	CACTCTCAAA	GCAAATAATT	TTTCACTTCA	2460
-00	AAACAGTATT	GACTTGTATA	CCTTGTAATT	TGAAATATTT	TCTTTGTTAA	AATAGAATGG	2520
20	TATCAATAAA	TAGACCATTA	ATCAG				
	Seq ID NO:	403 Protein	sequence				
	Protein Acc	cession #: 1	IP_002407				
25	1	11	21	31	41	51	
	HENCOGUI DI I	07777777770	OGTPVVRKGR	COCTOMINAT	THEOREMAN	OPADODSCEK	60
	IEIIATLKNG	VOTCLNPDSA	DAKEPIKKME	KOVSOKKKOK	NGKKHOKKKV	LKVRKSQRSR	120
30	QKKTT						
50	Sea ID NO:	404 DNA sec	ruence				
	Nucleic Act	Ld Accession	1 #: NM_006	670			
	Coding sequ	uence: 85	1347				
35	1	11	21	31	41	51	
	1	1	CCAGCCTCCC		1	amongs conn	60
	Agemenaggg	AAACGCGAGC	CGCGATGCCT	GGGGGGGTGCT	CCCGGGGGGCCC	COCCAGCCGGG	120
40	GACGGGCGTC	TGCGGCTGGC	GCGACTAGCG	CTGGTACTCC	TGGGCTGGGT	CTCCTCGTCT	180
40	TOTOCCACCT	CCTCGGCATC	CTCCTTCTCC	TCCTCGGCGC	CGTTCCTGGC		240 300
	CGCACAGTCA	AGTGCGTTAA	CCGCAATCTG	ACCGAGGTGC	CCACGGACCT	GCCCGCCTAC	360
	GTGCGCAACC	TCTTCCTTAC	CGGCAACCAG	CTGGCCGTGC	TCCCTGCCGG	CGCCTTCGCC	420
45	CGCCGGCCGC	CGCTGGCGGA	GCTGGCCGCG GCATCTGCCC	AGCCTGGGGG	AGCTCGACCT	CAGCCACAG	480 540
73	CCACTGGCCG	ACCTUAGEOU	CTTCGCTTTC	TOGGGGGAGGA	ATGCCAGCGT	CTCGGCCCCC	600
	AGTCCCCTTG	TGGAACTGAT	CCTGAACCAC	ATCGTGCCCC	CTGAAGATGA	GCGGCAGAAC	660 720
	CGGAGCTTCG	AGGGCATGGT	GGTGGCGGCC	CTUTTACCTGC	CGCGGGGATGT	GCTGGCCCAA	780
50	CTGCCCAGCC	TCAGGCACCT	GGACTTAAGT	AATAATTCGC	TOSTGAGCCT	GACCTACGTG	840
	TOCTTCCGCA	ACCTGACACA	TCTAGAAAGC TGAGTTGCAA	CTCCACCTGG	AGGACAATGC	TTTCCTGGAC	900 960
	AACAATCCCT	GGGTCTGCGA	CTGCCACATG	GCAGACATGG	TGACCTGGCT	CAAGGAAACA	1020
55	GAGGTAGTGC	AGGGCAAAGA	CCGGCTCACC	TGTGCATATC	COCCAAAAAAAT	GAGGAATCGG	1080
33	CAAACCTCTT	AACTCAACAG	TGCTGACCTG GGGTATTGTT	GACTGTGACC	CGATTCTTCC	CCCATCCCTG	1140
	GTTTTGTATT	TGAACCGCAA	GGGGATAAAA	AAGTGGATGC	ATAACATCAG	AGATGCCTGC	1260
	AGGGATCACA	TGGAAGGGTA	TCATTACAGA	TATGAAATCA	ATGCGGACCC	CAGATTAACA	1320
60	CATGAGATGT	AGACTTAAGC	TGTCTGAGAA	CTAGGCTTGC	TOCACTTTCA	TOCTOCACTA	1440
	TAGATACAAC	GGACTTTGAC	TAAAAGCAGT	GAAGGGGATT	TGCTTCCTTG	TTATGTAAAG	1500
	TTTCTCGGTG	TGTTCTGTTA	ATGTAAGACG CAACACGTAT	ATGAACAGTT	GTGTATAGTG	AGCATGAACA	1560 1620
	TGGGCTTCTT	GCTGTCTGTC	TCTCTCTCAG	TACAGTTCAA	GGTGTAGCAA	GTGTACCCAC	1680
65	ACAGATAGCA	TTCAACAAAA	GCTGCCTCAA	CTTTTTCGAG	AAAAATACTT	TATTCATAAA	1740
	CTGCAGACGT	TAGCAGGCTC	ACCTAAGTTG TTCAAAATAA	CTCCATGGTG	CACAGGAGCA	CCTGCATCCA	1860
	AGAGCATGCT	TACATTTTAC	TGTTCTGCAT	ATTACAAAAA	ATAACTTGCA	ACTTCATAAC	1920
70	TTCTTTGACA	AAGTAAATTA	CTTTTTTGAT	TGCAGTTTAT	ATGAAAATGT	ACTGATTTTT	1980 2040
70	ATTCTTAAAA	GAA	ATCLAACCGA	CIGARITOTI	AAGGGGGGGG	MOUNTAINS	2040
	Seq ID NO:	405 Protein cession #: 1	sequence P 006661				
75			_				
	1	11	21	31	41	51	
	MPGGCSRGPA	AGDGRLR LAR	LALVLLOWVS	SSSPTSSASS	FSSSAPFLAS	AVSAQPPLPD	60
80	OCPALCECSE	AARTVKCVNR	NLTEVPTDLP	AYVRNLFLTG	NQLAVLPAGA	PARRPPLABL	120
0U	NHIVDDEDED	ONE SEEGMEN	LPSLRQLDLS AALLAGRALQ	GLERLELAGN	HPLYLPRDUT.	AOLPSIRHID	180 240
	LISMISTATE	VVSERNITHI.	ESTABLISHMAL.	KVLHNGTLAR	LOGLPHIRVE	LDNNPWVCDC	300
	HMADMVTWLK	ETEVVQGKDR	LTCAYPEKMR IKKWMHNIRD	NRVLLELNSA	DLDCDPILPP	SLQTSYVFLG	360
85	LVLADIGATE	DEVLIENCE	TVENDUMIND	ACRUMINOTE	TUTETHANDER	маноонову	

Seq ID NO: 406 DNA sequence Nucleic Acid Accession #: Eos sequence

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WO 02/086443 Coding sequence: 1..927

1	11	21	31	41	51	
						60
						120
TTCTCCTCCT	CGGCGCCGTT	CCTGGCTTCC	GCCGTGTCCG	CCCAGCCCCC	GCTGCCGGAC	180
CAGTGCCCCG	CGCTGTGCGA	GTGCTCCGAG	GCAGCGCGCA	CAGTCAAGTG	CGTTAACCGC	240
AATCTGACCG	AGGTGCCCAC	GGACCTGCCC	GCCTACGTGC	GCAACCTCTT	CCTTACCGGC	300
						360
						420
						480
						540
CCCTGGGTCT	GCGACTGCCA	CATGGCAGAC	ATGGTGACCT	GGCTCAAGGA	AACAGAGGTA	600
GTGCAGGGCA	AAGACCGGCT	CACCTGTGCA	TATCCGGAAA	AAATGAGGAA	TCGGGTCCTC	660
						720
						780
						840
CACATGGAAG	GGTATCATTA	CAGATATGAA	ATCAATGCGG	ACCCCAGATT	AACAAACCTC	900
AGTTCTAACT	CGGATGTCCT	CGAGTGA				
	ATGCCTGGGG CTAGCGCTGG TCTCCTCCT CAGCGCTGG AATCTGACCG AACCGGGGG AGCCTCAGGC CGCAGCGGG CCCTGGGTCT GTGCAGGCCA TTGGAACTCA TCTTATGTCT TATTTGAACC	ATOCTOGOGO GOTOCTOCOC CTAGOCCTOGO GOTOCTOCOC CTAGOCCTOGO COCCTOGO CACTOCOCCO GOCCOCOTO CACTOCOCCO GOCCOCOTO CACTOCOCCO GOCCOCOTO CACTOCOCCO COCCOCOC CACCOCOCOC GOCACCOCO CACCOCOC GOCACCOCO COGCOTOCO GOCACCOCO COCCO GOCACCOCO COCCO GOCACCO COCCO GOCACO GOCACCO GOCACCO GOCACCO GOCACO GOCACCO	11 21 11 21	1 12 23 31 31 31 31 31 31 31 31 31 31 31 31 31	1 1 21 31 41 41 41 41 41 41 41 41 41 41 41 41 41	1 11 21 31 31 51 51 51 51 51 51 51 51 51 51 51 51 51

Seq ID NO: 407 Protein sequence

	Protein	Addession	3:	Eos	sequence	
25	1	11		21	3	

1	11	21	31	41	51	
1	1	1	1	1	1	
MPGGCSRGPA	AGDGRLRLAR	LALVLLCHVS	SSSPTSSASS	FESSAPFLAS	AVSAQPPLPD	60
QCPALCECSE	AARTVKCVNR	NLTEVPTDLP	AYVRNLFLTG	NQLASNHFLY	LPRDVLAQLP	120
SLRHLDLSINI	SLVSLTYVSF	RNLTHLESLH	LEDNALKVLH	NGTLABLOGL	PHIRVFLONN	180
PWVCDCHNAD	MYTWLKETEV	VQGKDRLTCA	YPEKMRNRVL	LEUNSADLDC	DPILPPSLQT	240
SYVFLGIVLA	LIGAIFLLVL	YLNRKGIKKW	MHNIRDACRD	HMEGYHYRYE	INADPRLINL	300
SSNSDVLE						
	QCPALCECSE SLRHLDLSHN PWVCDCHNAD SYVFLGIVLA	MPGGCSRGPA AGDGRLRLAR QCPALCECSE AARTVKCVNR SLRHLDLSHNI SLVSLTYVSP PWVCDCHNAD MVTWLKETEV SYVFLGIVLA LIGAIFLLVL	MPGGCSRGPA AGDORLRJAR LALVILGHVS QCPALCECSE ARTYKCVNR NITEVPTDLP SLRRIDJENN SLVSLTYVSP RILTHLESLAP PWVCDCHMAD MVTMLKETEV VQGEDRLTCA SYVFLGIVLA LIGAIFILUU YLNRKGIKKN	MPGGCSRGPA AGDORLRLAR LALVLLOWVS SSSPTSSASS QCPALCEGSE ARRYKCVNR NLTEVPTDLP ATVENTELIAG SLENLDLSHN SLVSLITVSF RHLTHLESLH LEDNALKVLH PWVCDCHRAD MVYMLKETEV VQGKDRLTCA YPERMERRVL SYVFLGIVLA LIGAIFLLU YLNRKDIKKO MENIROACH	MOGGERGPA ADDRIRLAR TALVILLOW'S SSPTSSASS FESSAPILAS QUEALGEGES ARKYWCYNN NIEPFPTUP AYWRHEIMON NILASNIFLUS ERRILLDENN SVENITY'S PINTHIBISHA BEDNALWAN HOTHAREAGGI. PRIVOCHMAD MYTHIBEST VOCKORLICA YPERWRRWL LELMSADUR SYVELGIYLA LIGATILLWI, YLMROGINSH MINIBOACH BHEGVETKYE SYVELGIYLA LIGATILLWI, YLMROGINSH MINIBOACH BHEGVETKYE	MOGGERGEA ADDERLALE LAUVLIGHVS SSSTISASS FESSAPPLAS AVSAOPPLED CCHALCESE ARTYKCHRE NITEYPTDLE ATVENLERIC NOLASHREYL DERVLAQLE FENDLISH SVELTYSP SHLUHESSH LEDNALVUM NOTLASKOLD PHENFLENE PRVCOCHAD MYTHLESEN VQCEDLICA PERMERRUL LEDNADALC DELUBEACH SVEYLCHVAL LOGATELLU VLENKRIKSH MEMIREACH BENGENTERS IMADERLIN

35 Seq ID NO: 408 DNA sequence Nucleic Acid Accession #: NM_000095.1 Coding sequence: 26..2299

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		CTCGGCGCGT					120
		CGGGAACTGC					180
		GTCAGGGAGA					240
	GCGGCAGCAG	CAGTCAGGAGA	act conference	P COCCEPT COCCEPT	GIGNIGONGS	mocherocore	300
45		TGCTTCCCCG					360
73		GCGGGCTTCA					420
	ccccracccc	TGCTTCCCCC	CUGGCAACGG	CICGUACIGO	ACCGACGICA	MCCOMOLOCYTE	480
	CGCCCACCCC	CCGGGGTACA	GAGTCCGCTG	CONTROL COOL	Wacconnage:	COCCIOCON	540
	GGCTTGCCCG	CAGGITTICA	GCGGCCCCAC	CCACCAGGGC	ACCCCCCC AC	ATTACTOCOT	600
50	GGCCAACAAG	GTGTGCATCA	COGRETCAN	COMOTOTONO	MCCGGGCMAC	VIVACIOCOL	660
50	CCCCAACTCC	GACCAGGCGT	ACACCCGGGG	CTCCTTCCMG	TGCGGCCCGT	GCCMGCCCGG	720
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55		CCCAACTCAG					960
23							1020
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		CAGCGCAACA					1140
		AACGACGACC					1200
60	CGACGACATC	GACGGCGACC	GGATCCGCAA	CCAGGCCGAC	AACTGCCCTA	GOGTACCCAA	1200
00	CTCAGACCAG	AAGGACAGTG	ATGGCGATGG	TATAGGGGAT	GCCTGTGACA	ACTOTCCCCA	
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		CAGGATGGAG					1380
	TAACAGTGCC	CAGGAGGACT	CAGACCACGA	TGGCCAGGGT	GATGCCTGCG	ACGACGACGA	1440
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		AAGATCGACG					1620
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70	GGGTTACACT	GCCTTCAATG	GOGTGGACTT	CGAGGGCACG	TTCCATGTGA	ACACGGTCAC	1800
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	CATGTGGAAG	CAGATGGAGC	AAACGTATTG	GCAGGCGAAC	CCCTTCCGTG	CTGTGGCCGA	1920
	GCCTGGCATC	CAACTCAAGG	CTGTGAAGTC	TTCCACAGGC	CCCGGGGAAC	AGCTGCGGAA	1980
	CGCTCTGTGG	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCGCG	2040
	ARACGTGGGT	TGGAAGGACA	AGAAGTCCTA	TOGTTGGTTC	CTGCAGCACC	GGCCCCAAGT	2100
75	GGGCTACATC	AGGGTGCGAT	TCTATGAGGG	CCCTGAGCTG	GTGGCCGACA	GCAACGTGGT	2160
	CTTGGACACA	ACCATGCGGG	GTGGCCGCCT	GGGGGTCTTC	TGCTTCTCCC	AGGAGAACAT	2220
	CATCTGGGCC	AACCTGCGTT	ACCGCTGCAA	TGACACCATC	CCAGAGGACT	ATGAGACCCA	2280
	TCAGCTGCGG	CAAGCCTAGG	GACCAGGGTG	AGGACCOGCC	GGATGACAGC	CACCCTCACC	2340
	GCGGCTGGAT	GGGGGCTCTG	CACCCAGCCC	AAGGGGTGGC	CGTCCTGAGG	GGGAAGTGAG	2400
80	AAGGGCTCAG	AGAGGACAAA	ATAAAGTGTG	TGTGCAGGG			

Seq ID NO: 409 Protein sequence Protein Accession #: NP_000086.1



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10	PEGDAQIDPN	GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR	VCTMNSDPGL	AVGYTAFNGV APPGTOLKAV	DEEGTEHVNT KESTCOCROL	PNALMHTODT	540 600 660 720
15	Nucleic Aci	410 DNA sec id Accession mence: 67	a #: NM 001	565.1			
20	AGCACCATGA ATTCAAGGAG	11 TCAATTGCTT ATCAAACTGC TACCTCTCTC	GATTCTGATT TAGAACCGTA	TGCTGCCTTA	GCATCAGCAT	TCTAAGTGGC TAGTAATCAA	60 120 180 240
25	CGTGTTGAGA TCGAAGGCCA TAAAACCAGA CCTCTCCCAT	CAAGGTCTTT TCATTGCTAC TCAAGAATTT GGGGAGCAAA CACTTCCCTA	AATGAAAAG ACTGAAAGCA ATCGATGCAG CATGGAGTAT	AAGGGTGAGA GTTAGCAAGG TGCTTCCAAG ATGTCAAGCC	AGAGATGTCTAA GATGGACCAC ATAATTGTTC	GAATCCAGAA AAGATCTCCT ACAGAGGCTG TTAGTTTGCA	300 360 420 480
30	GCTCTACTGA ACCTTTCCCA	AAGGTGACCA CATCATCCTA GGTGCTATGT TCTTCCAAGG AAATAACTAA	AGCTATTCAG TCTTAGTGGA GTACTAAGGA	TAATAACTCT TGTTCTGACC ATCTTTCTGC	ACCCTGGCAC CTGCTTCAAA TTTGGGGTTT	TATTATGTAA TATTTCCCTC ATCAGAATTC	540 600 660 720 780
35	ACTTCATGGA CATACAATTC CTTATTTAAT TTTCAGTGTA TTTTAAAAAT	CTTCCACTGC CAAACACATA GAAAGACTGT CATGGAATAA ACAGATAGAT AAAATGAGGT	CATOCTCCCA CAGGAAGGTA ACAAAGTATA CATGTAATTA ATATGCTCTG	AGGGGCCCAA GAAATATCTG AGTCTTAGAT AGTACTATGT CATGTTAGAT	AAAATGTATG GTATATATTT ATCAATGAGT	TGGCTACCTA TGTAAGTATT CCTATATTGT AACAGGAAAA	840 900 960 1020 1080
40	Seq ID NO: Protein Ace	411 Protein	sequence				
		COBDION W	002550.0				
45	1 MNOTAILICC	11 LIFLTLSGIQ BKRCLNPESK	21 GVPLSRTVRC	31 TCISISNOPV KEMSKRSP	41 NPRSLBKLBI	51 , IPASQFCPRV	60
45 50	1 MNQTAILICC BIIATMKKKG Seq ID NO: Nucleic Ac:	11 	21 GVPLSRTVRC AIKNLLKAVS Quence #: XM_057	TCISISMOPV KEMSKRSP	1	ī '	60
	1 MNQTAILICC BILATMKKKG Seq ID NO: Nucleic Ac: Coding seq: 1 GGGAGGGAGA CGCGCGGAGA GGCTGCCCGG	11	21 GVPLSRTVRC AIRMLLKAVS guence 1 #: XM_057 874 21 GSTGAAAGGC ACCAGGTTCC CCATGGGACC	TCISISMOPV KEMSKRSP 014 31 GCATTGATGC TCTCCTCGGT CCAGGGCCCC	I NPRSLEKLEI 41 I ASCCTGCGGC CTCCTCCGCC	I IPASQFCPRV 51 GCCTCGGAG TCCAGCTCGG CCCAGCGGCT	60 120 180 240
50	1 MNQTAILICE BILATMENENG Seq ID No: Nucleic Ac: Coding seq: 1 GOGAGGGAGA GOCGGGGCGAG GOCGGGGCCGAG GOCGGGGCCGAGGGAGATGCCCGAGGGAATGGCTA GATTCCAGGAGAATTAT	11 LIFITLSGIQ EKKCLNPESK 412 DNA seid Accession dence: 143. 11 GAGGGGGGG CCAGACGCTG CAGCGGGGG CTGGTGGTGC AAGCAAAAG CMAGGCCAG GAGACGTTGAGG AAGCTTGAGG GAGACGTTGAGG GAGACGTTGAGG GGGATAGATC	21 GVPLSRTVRC AIRMLLKAVS THENCE 1 #: XM_057 874 21 GSTGAAAGGC CCATGCGAC TGCTGCTGCA CCAGGTTGC CAGGAGTGCC CAGGAGTGCC AGGCTCGAGTCGAG	TCISISMOPV KEMSKRSP 7014 31 GCATTGATGC CCAGGGCCCC GCTGCCCCGG GCAGAGGGAG TGGTCGAGACTAC ACCCAACTAC	41 AGCCTGCGGC CTCCTCCGCC GCGCCTCCC GCGCCTCCC GCGCCTCCC GCGCCCCC GCGCCCCC AAAGGAGAA AAAGCAGAAA AAGCAGTATA	51 GGCCTCGGAG TCCAGGTCCG GCAGCGGCT TCTATAATGG GGGCCAATGG AGGGGGAATG CATGAGTTC AAGAGCGTTC	60 120 180 240 300 360 420 480 540
50 55	1 MNOTAILICC EITATMCKKG Seg ID NO: Nucleic Ac. Coding seq:	11 LIFIGILES 10 EXECUTIVES 11 LIFIGILES 10 EXECUTIVES 12 EXECUTIVES 12 EXECUTIVES 14 EXECUTIVES 16 EXECUTIVES	21 GPPLSRTVRC ATKHLLKAVS TURENCE AT A #: XM_057 874 21 GGTGAAAGGC CCATGCGACC CCATGCGACC TCGCAGGTCC AGTCGACC TTGGGAAAAT TTGTCAGTGC CTTGGAAAAGC CTTTGGAAAAGC CTTTGGAAAAGC CTTTGGAAAAAGC CTTTGGAAAAAGC CTTTGGAAAAAGC CTTTGGAAAAAGC CTTTGGAAAAAGC CATTCAATGA	TCUSISMOPV KEMSKRSP TOLSISMOPV KEMSKRS TOLSISMOPV KEMSKRS	41 AGCTGGGGG CTGCTCGGC CGGGCGCGCGGGGGGGGGG	51 	60 120 180 240 300 360 420 480
50 55 60	1 MARGYALLICC EILATMERKS SEQ ID NO. NUCLEIC ACC COCING SEQ 1 GOGAGCOGAG COGCOCCAG COCCAG COGCOCCAG COGCOCCAG COGCOCCAG COGCOCCAG COGCOCCAG COGCOCCAG COGCOCCAG COGCOCCAG COGCOCCAG COGCOCCAG COGCOCCAG COGCOCCAG COG	11 1 1 1 1 1 1 1 1 1	21 GVPLSRTVRC ALTRILLERVS TURBLE B # 1 ML_057 B # 1 ML_057 B # 1 ML_057 B	TCISISNOPW KEMSKRSP TCISISNOPW KEMSKRSP TCISISNOPW KEMSKRSP TOLICA TCISISNOPW KEMSKRSP TCICCTOGAT CCACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	41	51 GGCCTCGGAG TCCAGCTCG CCCCGGAGG CCCCCGGAGG CCCCCATGA AGATCGGT AGATCGGT AGATCGGT TCCCATGA ATATTCACC TTACATGC AGATCGGT TCCCATGA ATATTCACC TTACATGCAT TCCCATGA ATATTCACC TTACATGCAT TCCACCCCT TTACATGCAT TCCACCCCT TTACATGCAT TCCACCCCT TTACATGCAT TCCACCCCT TTACATGCAT TCCACCCCT TTACATGCAT TCCACCCCT TCCACCCCT TCCACCCCT TCCACCCCT TCCACCCCCT TCCACCCCT TCCACCCCC TCCACCCCC TCCACCCCC TCCACCCCC TCCACCC TCCACCCC TCCACC TCCACCC TCCACCC TCCACCC T	60 120 180 240 360 360 420 480 660 660 720 780 900 900 900 1020 1080
50 55 60 65	1 MANDAILICE ETIATMENT SEG ID NO. Nucleic Act Coding seg Coding Codin	11 I I I I I I I I I	21 GVBLERTYRC ATRILLERIYS GVBLERTYRC ATRILLERIYS GVBLERIYSC SH XM_057 SH XM_057 GOTGALAGGC CCATCCCCCC CCATCCCCCC CCCATCCCCCC CCATCCCCCC CCATCCCCC CCATCCCCCC CCCATCCCCC CCATCCAT	TCUSISNOPW KEMSKRSP TOUSISNOPW KEMSKRSP TOUSISNOPM KEMSKRS T	41 AGCCTGCGGGC CTCCTCGGGCC CTCCTCGGGCC CTCCTCGGGCC CGTCCTCGGGCC CGTCCTCGGGCC CGTCCTCGGGCC CGTCCTCGGGCC CGTCTCGGGCC CGTCTCGGGCC CGGGAGCC CGGGAGCC CGGGAGCC CGGAGCC CGGAGCC CTCGGGCCT CCACCAATTA CGAATTCGGA AGCTCTCGACA AGCTCTCGACA CTCAGGCCT CCACCAATTA CGATTCGGA CTCGGGCT CTCACTCGGAC CTCGGGCT CTCACTCGGAC CTCGGGCT CTCATTCGGA AGCTTCGAT ATTATTGGA ATTATTGGA ATTATTGGA ATTATTGGA	51 TOUGHTOUGH TOUGHTOUGH TOUGHTOUGH COLLAGOGGET TOUGHT COLLAGOGGET TOUGHT	60 120 180 240 360 420 600 660 720 840 900 900 900 1020
50 55 60 65 70 75	1 MONTAILICE BILATMENS SEQ ID NO. Nucleic Act Coding sequipolic Coding Codicol Coding Codicol Co	11 FUTURE CONTROL	21 GYPLERTYRC AIRBILLANDS YUMEN CONTROL OF	TOTISISNOPY KENEKRSP 11 11 11 11 11 11 11 11 11	41 AGCCTGGGGG CTCGTCGGGG CGGGCTCCC CGGTGGAGG CGGGCTCCC CGGTGAGG CGGGCTCCC CGGTGAGGA CGGGTGAGGAGGAGA AGGCATACA AGCATACA TCAAAATGCA TCAAAATGCA TCAAATTCAA TTAAATTCAA TTAAATTCAA TTAAATTCAA TTAAATAAA	51 50 COCCOSIAN 51 COCCOSIAN TOGGOTOGO COCCAGOSOT COCCOSIAN TOTATAATOG GOSCOLATOG ANATOGOTO GARATOGOT GARATOGOT TOGATACO GARATOGOT TOGATACOC TTOGATACOC TTATATOTOC TACCAATOCT TTATTTCCAA	60 120 180 240 360 420 480 540 660 660 720 780 840 960 960 910 900 960 1020 1080 1140
50 55 60 65 70	1 MONTAILICE MONTAILICE SELLATMENTS SELLAT	11 L FUTURE CONTROL OF	21 ATTACAMANA TOTOCAMANA TOTOCAMA	TOTOSISMOPY KEMERRAP 1014 31 GCATTOATOC TOTOCTOGOT CCAGAGGCCC CCAGAGGCCA ACCTACACTAC ACCACACTAC ACCACAC ACCACACTAC ACCACACTAC ACCACACTAC ACCACACTAC ACCACACTAC ACCACAC ACCACACTAC ACCACACACTAC ACCACACTAC ACCACACTAC ACCACACTAC ACCACACTAC ACCACACTAC ACCA	41	1 PASQFCERV 51 GGCCTCGGAG GGCCTCGGAG CCACGGGCT TCAGGTCCG GGGCAATGG AGGGCAATGG AGGGCAATGG AGGGCAATGG AGGGCAATGG AGGGCAATGG AGGGCAATGG AGGGCAATGG AGGTTCCCAATGA ATGTTCCTACT TTTCTATTAGTT TTTTTTTAGTT TTTTTTTCCAA 51 MEMCLGGPAG MEMCL	60 120 180 240 360 420 480 540 660 660 720 780 840 960 960 910 900 960 1020 1080 1140

WO 02/086443 Seq ID NO: 414 DNA sequence Nucleic Acid Accession #: XM_084007 Coding sequence: 138..2405

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10	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCCTG	ACCTTTGCCC	180 240
10	TCTCTGTCAC	AAATCCCCTT GAATTGGGAA	CATGAACTAA	ANGUAGUTGU	GGCS ATTTCC	ACCACTGAGA	300
		ACAGCTTTTC					360
	TCAGAAAATT	ACTTCAAAAT	ATAGGCATAG	ATANGATTAA	ANGAATCCAT	ATACACCATG	420
	ACCACGACCA	TCACTCAGAC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCAGACCATG	480
15	AGCATCACTC	AGACCACGAG	CATCACTCTG	ACCATGATCA	TCACTCCCAC	CATAATCATG	540
	CTGCTTCTGG	TAAAAATAAG	CGALAAAGCTC	TTTGCCCAGA	CCATGACTCA	GATAGTTCAG	600 660
	GTAAAGATCC	TAGAAACAGC CAAGGACAGT	CAGGGGAAAG	GAGCTCACCG	CTCARCTCTC	TACAACACTG	720
		AACTCACTTT					780
20		AAGCAGCTCC					840
-	TGGCTGGTAG	GAAAACAAAT	GAATCTGTGA	GTGAGCCCCG	AAAAGGCTTT	ATGTATTOCA	900
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	CTCAACTTTC	AACAAATGAG	DATEMATER	ATACAGATGA	TOGRACTORA	GGCTATTTAC	1620
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35	AAGAGGTCAT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
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		TCATGACTAC					1860 1920
	TOGGGGGGGGA TO	CAGCCAGCGC GGTGATAATG	GOTGATGGCC	TOCACASTT	CAGCGATGGC	CTAGCAATTG	1980
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, ,	ATGAGTTGCC	TCATGAATTA	GGTGACTTTG	CTGTTCTACT	AAAGGCTGGC	ATGACCGTTA	2100
		CCTTTATAAT					2160
		TGGTCATTAT					2220
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73	COMMERCICATEG	TATGTTACTT	ATTTOCATAT	TTGABCATAL	ARTOGRATUT	COTATAAATT	2400
	TCTAGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAAGTTG	TCATAGTTTC	AGTAGGTCAT	2460
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	TAAACAAGAG	ATTTGGCATG CTAACACAGT	ACATGTTCTG	TATGTTTCAG	GGAAAAATGT	CITTAATGCT	2760
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55	AAAAATCACA	AAATTTGTTG	TAAATTAGAG	GGGAGAAATT	TAGAATTAAG	TATAAAAAGG	2940
	CAGAATTAGT	ATAGAGTACA	TTCATTAAAC	ATTTTTTTCA	GGATTATTTC	CCGTAAAAAC	3000
		CTCTCATATA					3060
		AATGAATTCA TTATATACCA					3120 3180
60	TATTOCICOLOGIC	TTATATATCA	CCANAGORCA	TATOMOTHOLI	TOTTOTAL	ACCTOCTTTA	3240
00	CARACTTATC	AGAGTAGTAA	AACTITGATA	TATATGAGGA	TATTAAAACT	ACACTAAGTA	3300
		CGATTCAGAA					3360
		CTTTATATAC				GCATTCTCTA	3420
65	GATGTTTCTT	TTTTACACAA	TARATTOCTT	ATATCAGCTT	g		
UJ	Com TD MO.	415 Protei	. compared				
		cession #: 1					
=-	1	11	21	31	41	51	
70	1	1	1	1	1	l	
	MARKLSVILI	LTFALSVINP	LHELKAAAFP	OTTEKISPNU	ESGINVDLAI	STROYHLOOL	60

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70)	1	1	1	1	1	1	
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		EHHSDHDHHS	EHNHAASGKN	KRKALCPDHD	SDSSGKDPRN	SQGKGAHRPE	HASGRRNVKD	180
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7:	5		FWYSRNTNEN					300
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_		REKVDTDDRT	EGYLRADSOE	PSHFDSQQPA	VLEEREVMIA	HAHPQEVYNE	YVPRGCKNKC	540
-80)	HSHFHDTLGO	SDDLIHHHHD	YHHI LUHHHH	ONHHPHSHSQ	RYSREELKDA	GVATLAMMVI	600
		MGDGLHNFSD	GLAIGAAFTE	GLSSGLSTSV	AVECHBLPHB	LGDPAVLLKA	GMTVKQAVLY	660
		NALSAMLAYL	GMATGIFIGH	YAENVSMWIF	ALTAGLEMYV	ALVEMVPEML	HNDASDHGCS	720
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Seq ID NO: 416 DNA sequence Nucleic Acid Accession #: NM_015419.1 Coding sequence: 1..8487

85

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	AATTTGGGGT	TTAATAGCAT	ACAGGCCCTG	TCAGAAACCT	CATTTGCAGG	ACTGACCAAG	240
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							960
20	AATATGACCG	ACGAGCACGG	GAACATGGTG	AACTTGGTCT	GTGACATCAA	GAAACCAATG	1020
							1080
	GTTGCCTTGG	ACTTTGAGTG ACAGTGAAGT	TCCAATGACC	CGAGAAAACT	ATGAAAAGCT	ATGGAAATTG	1140
	ATAGCATACT	ACAGTGAAGT	TCCCGTGAAG	CTACACAGAG	AGCTCATGCT	CAGCAAAGAC	1200 1260
25	CCCAGAGTCA	GCTACCAGTA AGATTCTTGC	CAGGCAGGAT	TOGOTCATOO	AGCCATCCAT	DGATATCCAG	1320
23	CTCAACCCAC	GTCAGAGTAC	GGCC23G23G	GTGCTACTTT	CCTACTACAC	CCAGTATTCT	1380
	CARACARTAT	CCACCAAAGA	TACAAGGCAG	GCTCGGGGGCA	GAAGCTGGGT	AATGATTGAG	1440
	CYTEGTOGEG	COCCOCCAGA	AGATCAGACT	GTCCTGGAAG	GGGGTCCATG	CCAGTTGAGC	1500
20	TGCAACGTGA	AAGCTTCTGA	GAGTCCATCT	ATCTTCT996	TGCTTCCAGA	TGGCTCCATC	1560
30	CTGAAAGCGC	CCATGGATGA	CCCAGACAGC	AAGTTCTCCA	TTCTCAGCAG	TGGCTGGCTG	1620 1680
	AGGATCAAGT	A COCCO MOCO	ATCTGACTCA	CHECKTOCKOT	AGIGCATIGC	TCAGCCAGCC	1740
	GAGARAGACA	CCATGGAGCC ACCGCATGGT CAGTGACAAT	TOGCAAGAAC	CCAGGGGAGT	CGGTGACATT	GCCTTGCAAT	1800
	GCTTTAGCAA	TACCCGAAGC	CCACCTTAGC	TGGATTCTTC	CAAACAGAAG	GATAATTAAT	1860
35	GATTTGGCTA	TACCCGAAGC ACACATCACA	TGTATACATG	TTGCCAAATG	GAACTCTTTC	CATCCCAAAG	1920
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	CATTTTACGG	TGGGAATCAC	AGTGACCAAG	AANGGGTCTG	ACATOCCATC	COUNTRACCO	2100
	GGCTCGGGCAG	GTGCAAAGGC TGGGAGATGA	AGAGAACACT	TCAAGGAGAC	TTCTGCATCC	AAAGGACCAA	2160
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	AGAAGAAAGC	TGAAACTCTG TGTTTGAATC	GAAGCATTCG	GAAAAAGAAC	CAGAGACCAA	TGTTGCAGAA	2280
	GGTCGCAGAG	TGTTTGAATC	TAGACGAAGG	ATAAACATGG	CAAACAAACA	GATTAATCCG	2340
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45	GTACCCCCGT	TGATTAAAAC TTTCTCCCCC	CACAAGICCI	CCATCCTIGA	CACTAGOOG	TGCTGAAGAA	2520
73	TOTOGRACIA	ATGTACCTCT GGCTAGAACA TGGAGGAAGT	ACTTGGTGAA	GAAGAGCACG	TTTTGGGTAC	CATTTCCTCA	2580
	GCCAGCATGG	GGCTAGAACA	CAACCACAAT	GGAGTTATTC	TTGTTGAACC	TGAAGTAACA	2640
	AGCACACCTC	TOGAGGAAGT	TGTTGATGAC	CTTTCTGAGA	AGACTGAGGA	GATAACTTCC	2700
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50	TCTCCTACTC	TGCACACATT GGTCTGCAGC	AGACACAGTC	TATGAAAAGC	CCACCCATGA ACCCCACATGA	CACTGAGGGG	2820 2880
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	GATTTGGAGA	CTAAGTCA CA CCCCCACCAT	ACCAGATGAG	GATAAGATGA	AAGAAGACAC	CTTTGCACAC	3000
	CTTACTCCAA	CCCCCACCAT	CTGGGTTAAT	GACTCCAGTA	CATCACAGTT	ATTTGAGGAT	3060
55							3120
	ATCCACCTTG	TGAAAAGTAG CTCAGACACT	TCTAAGCACT	CAAGACACCT	TACTGATTAA	AAAGGGTATG	3180 3240
	AAAGAGATGT	AGAGTGAGGG	CCA D CA CACCA	AATATGCTAG	CTTTGCCTGA	CTCCACACTG	3300
	GGTATAATGA	GCAGTATGTC	TCCAGTTAAG	AAGCCTGCGG	AAACCACAGT	TCCTACCCTC	3360
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	AAATTCOGCC	ACCGGCACAA CAACTCAAGC	GCAAACCCCA	CCCACAACTT	TTGCCCCATC	AGAGACTTTT	3540 3600
	TCTACTCAAC	CTTGGGTGGA	ACCTGACATT	AAGATTTCAA	ARCACTTOGA	DAADADADAAA	3660
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	CCAGAAAATA	AACATAGAAA	CATTGTTACT	COYNGTICAG	AAACTATACT	TTTGCCTAGA	3840
	ACTGTTTCTC	TGAAAACTGA	GGGCCCTTAT	GATTCCTTAG	ATTACATGAC	AACCACCAGA	3900
70	AAAATATATT	CATCTTACCC	TAAAGTCCAA	GAGACACTTC	CAGTCACATA	TARACCCACA	3960 4020
70	TCAGATGGAA	AASAAATTAA	AATTA CTAAT	COCATACCA	CTTCTCCCTC	CTTGGTCTCC	4080
	ACTATOGGAG	CTOGTGAATC	AGAATOCTCT	CCTGTAGGCT	TTCCAGGAAC	TCCAACCTGG	4140
							4200
-	GGGGAAAATC	TTACAGACCC CCTCTTTGAC CAAGCATAAA	TCCCCTTCTT	AAAGAGCTTG	AGGATGTGGA	TTTCACTTCC	4260
75	GAGTTTTTGT	CCTCTTTGAC	AGTCTCCACA	CCATTTCACC	AGGAAGAAGC	TGGTTCTTCC	4320 4380
	ACAACTCTCT	CAAGCATAAA	AGTOGAGGTG	GCTTCAAGTC	CTCABACTAG	ACCACACCTT	4440
	CACACCCCCTA	ATCTTGAAAC	CACTGIGGGI	CCAGCATCCT	CGTCCCCATC	CACAATTCTC	4500
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	GCAACCCCAG	TCAACAATGA ACCGGGATGC	AGGAACACAG	CATATGTCAG	GGCCAAATGA	ATTATCAACA	4680
	CCCTCTTCCG	ACCGGGATGC	ATTTAACTTG	TCTACAAAGC	TUGAATTUGA	AAAGCAAGTA	4740 4800
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85	CTACCTGARA	GGAGTCTACC AACTAACCAG TGTCCACACA	AAGCGCTTCC	AGATACTITG	TAACTTCCCA	GTCACCTCGT	4920
	CACTGGACCA	ACAAACCGGA	AATAACTACA	TATCCTTCTG	GGGCTTTGCC	AGAGAACAAA CATGTCCAAA	4980
	CAGTTTACAA	CTCCAAGATT	ATCAAGTACA	ACAATTCCTC	TCCCATTGCA	CATGTCCAAA	5040

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	CCCAGCATTC	CTAGTAAGTT	TACTGACCGA	AGAACTGACC	AATTCAATGG	TTACTCCAAA	5100
	GTGTTTGGAA	ATAACAACAT	CCCTGAGGCA	AGAAACCCAG	TTGGAAAGCC	TCCCAGTCCA TCTTTCTTTT AGTAATGAGA CTTCCATCTG	5160
	AGAATTCCTC	ATTATTCCAA	TGGAAGACTC	CCTTTCTTTA	CCAACAAGAC	TCTTTCTTTT	5220
5	CCACAGTTGG	GAGTCACCCG	GAGACCCCAG	ATACCCACTT	CTCCTGCCCC	AGTAATGAGA	5280
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	GACTTTGGCC	CTCCGGCACC	TCCGTTGTTG	CACACTCCGC	AGACCACGGG	ATCACCCTCA	5400
	ACTAACTTAC	AGAATATCCC	AACCOMPCONC	CACACCACA	CARACTTCIT	CTTTATACA TGCAGGAGGA CAAGTCCCCA AACAGGAAAA TCCGAATACC	5460
	COTCOTOCA	AGT CCT CAGG	MOCITOCAC	CNONGCHOCT	ANATOCTOR	CARCECCCCA	5520
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	CARCATOCAC	COCACTATAT	OTTO Character	ACCUACCTOC	accorderates	CAGGATGGTG	5820
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	TOGGTGCTCG	GGGACGGTAC	CUAGATCOGC	CCCTCGCAGT	TCCTCCMCGG	GAACTTGTTT CGGGCGCTAT GAACGTGCAG	6300
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	GACGGGAGTC	TGGTGAACTC	CTTCATGCAG	TCGGATGACA	GCGGTGGACG	CACCAAGCGC	6900
	TATGTCGTCT	TCAACAATGG	GACACTCTAC	TTTAACGAAG	TGGGGATGAG	GGAGGAAGGA	6960
	GACTACACCT	GCTTTGCTGA	AAATCAGGTC	GGGAAGGACG	AGATGAGAGT	CAGAGTCAAG	7020
35	GTGGTGACAG	CGCCCGCCAC	CATCOGGAAC	AAGACTTACT	TGGCGGTTCA	GGTGCCCTAT	7080
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	TTGTCCCCAA	CCAACAAGGT	GATCCCCCACC	TCCTCTGAGA	AGTATCAGAT	ATACCAMMAT	7200
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40	COCARACTOR	TTGACTGCAA	ACCTOR ACCC	ATCCCCACCC	CGAGGGTGTT	ATGGGCTTTT	7440
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	CGCAACGAGG	GAGGGGAGGC	GAGGTTGATC	GTGCAGCTCA	CTGTCCTGGA	GCCCATGGAG	7620
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	OCCICGGIGI	TIGACAGGGG	TACCIA:GIA	TOCHGONIGG	CONTRACTOR	CONCCCCTTCG	9220
	CCCCCCACCA	ACACCCGTGAT	COCCUATORCE	CALCULATION	ACTGCATGGC	CGAGCCCACC TATGGGGATT	8280
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-	GCTCGTCTGT	ATGGAAACAG	ATTTCTTCAC	CCCCAGGGAT	CACTGACCAT	CCAGCATGCC	8400
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	TTTCTTCTTT	TGCAAATGCC	ACTOGACTOC	CTTCATAAGC	GTCCATAGGA	TATCTGAGGA	8820
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75	CTGGCTTGTC	CATCTGGTCT	AAGGTGGCTG	CTTCTTCCCC	AGCCATGAGT	CAGTTTGTGC TAAGGTCAAT	9540
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	ATACTGTACA	TTTGATAATA	AAATAATATT	CTCCCAAAAA	AAAAA		
80		417 Protein					
00	Protein Ac	cession #: 1	NF_026234.1				

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		SVVLILLWGH					60
85		SETSFAGLTK					120
	OTLOGISMIM	RLHIDHNKIE	FIHPOAFNGL	TSLRLLHLEG	NLLHQLHPST	PSTFTFLDYF	180
	RESTURBLYE	AENMVRTLPA	SMLRNMPLLE	NLYLOCNPHT	CDCEMRNFLE	WDAKSRGILK	240

CKKDKAYBOG QLCAMCFSPK KLYKHEIHKL KDMTCLKPSI ESPLRQNRSR SIEBBQBQEE DOGSOLILEK POLPOWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHLNOT DPPDIDINAT 360 VALDFECPMT RENYEKLWKL IAYYSEVPVK LHREIMLSKD PRVSYQYRQD ADEBALYYTG VRACILARDE WVMOPSIDIO LWRROSTAKK VLLSYYTOYS QTISTKOTRO ARGRSWVMIE 400 5 PSGAVORDOT VLEGGPCOLS CHVKASESPS IFWVLPDGSI LKAPMDDPDS KFSILSSGNL 540 RIKSMEPSDS GLYQCIAQVE DEMDRMVYRV LVQSPSTQPA EKDTVTIGEN PGESVTLPCN 600 ALAIPEAHLS WILPHRRIIN DLANTSHVYM LPNGTLSIPK VQVSDSGYYR CVAVNQQGAD HPTWGITVTK KGSGLPSKRG RRPGAKALSR VREDIVEDEG GSGMGDEENT SRRLLHPKDQ 720 EVPLKTKDDA INGDKKAKKG RRKLKLWEHS EKEPETNVAE GRRVFESRRR INMANKQINP 700 10 ERNADILAKV ROKNLPKGTE VPPLIKTTSP PSLSLEVTPP FPAVSPPSAS FVQTVTSABE SSADVPLLGE EEHVLGTISS ASMGLEHNHN GVILVEPEVT STPLEEVVDD LSEKTEEITS 840 900 TEGOLKGTAA PILISEPYEP SPILHTLOTY YEKPIHEETA TEGNSAADVG SSPEPTSSEY
EPPIJAUGIA ESEPMOYPOP DIETKSOPDE DEMKEDTFAH LIPTPITHWW DSSTSQLFED 960 STIGERGYPG QSHLQGLTDN IHLVKSSLST QDTLLIKKGM KEMSQTLQGG NMLEGDPTHS 1080 15 SISSENGUES KSITLEDISTI GIMSSKSPVK KRABITYCTI IDENTITYTT TPROKVAPSS TMGTHESERE PAGRELEPN KPRIRIKOTP FTTFAPSSTF STOPTOAPDI KISSQUESSE VPTAWYDDITV NTPKOLEMEN NABETSKSTF REKKIRERINK HRYTESTUSS RASGKPSPS 1140 1200 PENKHRNIVT PSSETILLPR TYSLKTEGPY DSLDYMTTTR KIYSSYPKVQ ETLPVTYKPT 1320 1380 SDGKEIKDDV ATNUDKHKSD ILVTGESITN AIPTSRSLVS TWGEFKEESS PVGFPGTPTW 20 NPSRTAQPGR LQTDIPVTTS GENLTDPPLL KELEDVDFTS EFLSSLTVST PPHQEEAGSS 1440 TTLSSIKVEV ASSQAETTIL DODHLETTVA ILLSETRPON HTPTAARMKE PASSSPSTIL 1500 TISSIAVEV ASSQUITTI DOMINITA INVANIPETE ATPVINEGTO HASGENELST PSSDRDAPIL STRLELEKOV FORRSLPROP DSQRQDGRVH ASHQLTRVPA KPILPTATUR 1560 LPEMSTOSAS RYFYTSOSPR HWINKPEITT YPSGALPENK OFTTPRLSST TIPLFLHMSK 1680 25 PSIPSKFTDR RTDQPNGYSK VPGNKNIPEA ENPVGKPPSP RIPHYSNGRL PPPTNKTLSF PQLGVTRRPQ IPTSPAPVMR ERKVIPGSYN RIHSHSTFHL DPGPPAPPLL HTPQTTGSPS 1740 1800 THIONIPM'S STOSSISFIT SSVOSSOSFH QSSSKFFAGG PRASKMELG BEPOLITKSP QTVSVTAETD TVPPCBATCK PREVINTRY STGALMTHNI RIGREFULM GILVIRKUV QDBQQYHCTA SHLHGLDRM VLLBVTUQG QILABHQVD VVILGITLA ECLAKGTPAP 1860 1920 1980 30 QISWIFFDRR VWQTVSPVES RITLHENRTL SIKEASFSDR GVYKCVASNA AGADSLAIRL 2040 MANIFERRA HAMALPPUH (DEKLEHISIP PGISHHICT AKABLPSUR WULDDTQIR PSQFLHQMLF VPFNOTLYIR NLAFKOSQXY ECVANHLYGS ARRTYQLINVQ RARAMARITG TSPRRTDVRY GOTLKLIOSA SQDPMPRIM ELESKAMIDA LFSFDSRIKV FANGTUVKS VTINCAGDYL 2100 2160 2220 CVARNKYGDD YVVLKVDVVM KPAKIEHKEE NDHKVFYGGD LKVDCVATGL PNPEISHSLP 35 DGSLVNSFMQ SDDSGGRTKR YVVFNNGTLY FNEVGMREEG DYTCFAENQV GKDEMRVRVK 2340 VYTAPATIRN KTYLAVQVPY GDVVTVACBA KGEPMPKVTH LGPTNKVIPT SSEKYQIYQD GTLLIGKAQR SDSKNYTCLU RUSAGEBRIT VHIHVNYQFE KINGNPRIT TVREIAAGOS RKLIDCKABG IFTPRUNNAP PBGVUDAPY YGNRITVEN GBLDTELRK SDSVQLVCMA 2400 2460 RMEGGEARLI VOLTVLEPME KPIFHDPISE KITAMAGHTI SLNCSAAGTP TPSLVWVLPN 2580 GTDLQSQQLQ QRPYHADAM LHISCLSSVD AGARCVARN AGGREGAVS LEVGLKYDAN KQYHNLVSII NGETLKLPCT PPGAGQGRFS WTLPNGMHLE GPQTLGRVSL LDNGTLTVRE 40 2640 2700 ASVEDROTYV CRMETEYGPS VTSIPVIVIA YPPRITSEPT PVIVTRGUTY VKLKCHAKI PKADITHELP DKSHLKAGVQ ARLYGNRIH POGSLTIGHA TORDAGFYKC MAKNILGSDS 2760

Seq ID NO: 418 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1..5001

KTTVIHUP 45

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		CAAAACTAAC					60
	ACCTCTCAAG	AGGACGAATT	GGATGTACCT	GACGACATCA	GCGTCCGGGT	TATGTCATCT	120
	CAGTCTGTGC	TTGTGTCCTG	GGTGGATCCT	GTTCTGGAAA	AACAGAAGAA	AGTTGTTGCA	180
55	TCAAGACAGT	ACACCGTGCG	CTATCGAGAG	AAGGGGGAAT	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGGCGTGT	GCTGATTGAG	AACCTGATTC	CAGACACTGT	GTATGAATTT	300
	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAAATGGA	GTACGTCAGT	CTTCCAAAGA	360
	ACACCAGAAT	CTGCCCCTAC	CACAGCTCCT	GAAAACTTGA	ACCTCTGGCC	AGTCAATGGC	420
	AAACCTACAG	TIGTOGCTGC	ATCTTGGGAT	GCGCTACCAG	AGACTGAGGG	GAAAGTGAAA	480
60	GTCTGTCTGC	TGGACACAGG	ACTOTTTTCA	GTTTCCTCCT	TCCAACCATC	TGCCAAATCA	540
	TTTCAGAATA	CATTCTTTCA	TACGCCCCGG	CTCTCAAACC	ATTTOGAGCA	AAGTCCCTCA	600
	CCTATCCTGG	AGACACTACT	TCTGCCCTGG	TGGATGGTCT	GCAGCCTGGG	GAACGCTATC	660
	TTTTCAAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATTG	720
	TOGCTATGCC	AACAAGAATG	CAGCTGTACC	CAGAAGGATT	TCAGTTGTCT	AGCTTACCTG	780
65	ATCGATATCC	AAACCAAACA	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTOGA	840
	CCATGTTTTC	TTTTCTACTT	CCTCACATTT	ATCCTGGATA	TTGGCGGCTT	TTCCTTCATT	900
	ATGTGCTATG	AAGACCCANIN	TGTTTCTTCT	TTGACAGGCA	ATTCTTTAAA	ATCTGTTGCA	960
	GCCAGTAAGG	CGGATGTTCA	GCAGAACACG	GAGGACAATG	GGAAACCCCGA	AAAACCTGAG	1020
	CCTTCCTCAC	CTTCTCCCAG	AGCTCCAGCT	TCCTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
70	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAAAAT	ATTGGCTAAT	1140
	GGTGGGGGCGC	CCCGAAAACC	CCAGCTTCGC	GCCAAGAAGG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCACTGGGGA	GGAGGAGCTG	GGTTCCCGGG	AGGACTCGCC	CATGTCACCC	1260
	TCAGACACCC	AAGACCAGAA	ACGGACCCTG	AGGCCGCCAA	GTAGACACGG	CCACTCGGTG	1320
	GTTGCTCCCG	GCAGGACTGC	AGTGAGGGCC	CGGATGCCAG	OGCTGCCCCG	AAGGGAAGGC	1380
75	GTAGATAAGC	CTGGCTTTTC	CCTGGCCACG	CAGCCCCCCCC	CAGGGGCGCC	CCCCTCGGCT	1440
	TOGGCCTCTC	CIGCCCACCA	CGCGTCCACC	CAGGGCACCT	CTCATCGTCC	TTCCCTGCCT	1500
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		AGGGCGCCTT					1620
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	GCGCCATCAC	GGTCCACCAT	GTCCTCCTCC	GTCTCTTCTC	ATCTCTCGTC	CAGGACGCAG	1920
0.5	GTCTCTGAGG	GAGCOGAGGC	TTCTGATGGT	GAAAGCCACG	GTGACGGCGA	TAGGGAAGAC	1980
85	GGCGGAAGGC	AGGCGGAGGC	CACGGCCCAG	ACGCTGCGGG	CCCGGCCTGC	CTCTGGACAC	2040
	TTCCATTTGC	TCAGACACAA	ACCCTTTGCT	GCCAACGGGA	GGTCTCCAAG	CAGGTTCAGC	2100
	ATTGGGGGGG	GACCTCGGCT	GCAGCCCTCC	AGCTCCCCAC	AGTCGACTGT	GCCCTCCCCA	2160

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		/086443					
						AGGTATCCAT	
	GGAGACGAGG	AGGATGAGAA	GCCGCTTCCT	GCCACCGTTG	TCAATGACCA	CCTCCCTTCC	2280
	TCCTCCAGGC	AGCCCATCTC	CCGGGGCTGG	GAGGACTTAA	GGAGANGCCC	GCAGAGAGGG	2340
5	GCCAGCCTGC	ATCGGAAGGA	ACCCATCCCA	GAGAACCCCA	AATCCACAGG	GGCAGATACA	2400
3	CATCCTCAGG	GCAAGTACTC	CTCCCTGGCC	TCCAAGGCTC	AGGATGTTCA	ACAGAGCACA	2460
		CGGAGGGTCA					2520
	TCCCCTGCTC	GTCCTCCCGC	AGCACGGTCA	CAGCAGCATC	CCAGTGTTCC	CAGAAGGATG	2580 2640
	ACACCCGGCC	GGGCCCCAGA	ACAGCAGCCC	CCTCCTCCCG	TOGCCACGTC	CCAGCACCAC	2700
10	CCGGGACCCC	AGAGCAGAGA GGCCCCGCCC	COCCGCCTCGG	TCACCTTCCC	AGCCCAGGCT	CTCACTGACC	2760
10		CCAGAGGGAT					2820
		ACGACGACAG					2880
		CCAAGGAGGC					2940
		GGGCAGGTGG					3000
15	ACAGGGGGAG	GACCCGGCGG	OCHCCACAGG	0200000000	TOCCOOC	GGCMGCCCCCCC	3060
15	AGGCCCHGCC	AGCCTCCTTC	Chargesco	CHCTCCTCCA	AGTCCCAGCA	GTCGGTCTCA	3120
	CCCCACCACG	4004004004	CONCOCCC	TTTTTTAAAC	CCGGGGAAAGA	AGACCTTCTG	3180
		TGCCAAAGTG					3240
	CONTROL	CCANGGAAGA	GAGGGAGCCT	CCCATCGCGC	TTGCCCCTCG	CGGAGGGAGC	3300
20	CEGGCTCCTG	TGANGCGACC	TOTCCCCCCA	CCTCCAGGCA	GCTCCCCCAG	GGCCTCCCAC	3360
	GTCCCTTCCC	GACCGCCGCC	TOGCAGOGGT	GCCACCGEGA	GCCCCGTCGC	GGGCACCCAC	3420
	CCCTGGCCGC	GGTACACCAC	GCGCGCCCCV	CCTGGCCACT	TCTCCACCAC	CCCGATGCTG	3480
	TOOTTGOGGG	AGAGGATGAT	CCATCCCAGA	TTCCGTAACC	CTCTCTCCCCG	ACAGCCTGCC	3540
	AGACCCTCTT	ACAGACAAGG	TTATAATGGC	AGACCAAATG	TAGAAGGGAA	AGTCCTTCCT	3600
25	GGTAGTAATG	GAAAACCGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
	GITGTGGACC	TTGATCGTGG	GITAGTATTG	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
	CATGGAAATC	CTCTTCGGAT	TAAACTAGGA	GGAGATGGTC	GAACCATTGT	AGATCTGGAA	3780
	OGGACCCCCG	TGGTGAGTCC	TGACGGCCTC	CCACTCTTTG	GGCAGGGGGG	ACATGGCACA	3840
20	CCTCTGGCCA	ATGCCCAAGA	TAAGCCAATT	TTGAGTCITG	GAGGAAAGCC	GCTGGTGGGC	3900
30	TTGGAGGTCA	TCAAAAAAAC	CACCCATCCC	CCTACCACTA	CCATGCAGCC	CACCACTACT	3960
	ACGACGCCCC	TGCCTACCAC	TACAACCCCG	AGGCCCACCA	CTGCCACCAC	CATGCAGCCC	4020
	ACCACTACTA	CGACGCCCCT	GCCTACCACT	ACACCGAGGC	CCACCACTGC	CACCACCOGC	4080
	CGCACGACCA	CCAGGCGTCC	AACAACCACA	GTCCGAACCA	CTACGCGGAC	AACCACCACC	4140
35	ACCACCCCCA	AACCCACCAC	TCCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAACGGCAC	4260
23	GACGATGATG	GCAACCTGAT	AATGAGCTCC	AATGGGATCC	CAGAGTGCTA	OGCTGAAGAA	4320
	GATGAGTTCT	CAUGCTTUGA	GACTGACACT	GCAGTACCTA	COGNAGAGGC	CTACGTTATA	
	TATGATGAAG	ATTATGAATT	TUAGACUTCA	AGGCCACCAA	CCACCACTGA	TCCTGAAGAA	4440
	ACTGCTACCA	CACCUAGGGT	GATCCCAGAG	CHARGOCOCCA	1CAGTICCTT	CCTAAATAAA	4500
40	GAATTTGATC	accessments	DOMA COMPAT	GETGCTCCTT	ACCTORCOIN	GGACAGCCTG	4560
70						TGCTCCCCGC	
	PACAMONICA	macmacacam	CC10MMGRAG	CACTCATTTO	TOATTOTOGA	TTGGGACAAA	4680
	GCCA CCCCAG	GAGATTTGGT	CACAGGTTAT	TEGGETTACA	GTGCATCCTA	TODAGATTTC	4740
		AGTITTCCAC					4800
45	ARGCCCCARCA	CGAGGTATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTACGGACCT	4860
	ATCAGCCCTT	CGGTCTCATT	TOTCACCGAA	TCAGATAATC	CTCTGCTTGT	TOTGAGGCCC	4920
	CCAGGGGGTG	AGCTATCTGG	ATCCCATTCG	CTTTCAAACA	TGATCCCAGC	TACACGGACT	4980
	GCCATGGACG	GCAATATGTG	AAGCGCACGT	GGTATCGAAA	GTTCGTGGGA	GTTGTTCTTT	5040
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50	TIGGAGACAG	CTGGGGAAGA	GGTGAAGACC	ATTGCCAATT	TGTGGATTCA	CACCTTGATG	5160
	GAAGAACAGG	GCCTCAGTCC	TATGTAGAAG	CCCTCCCTAC	TATTCAAGGC	TACTATCGCC	5220
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	TGGGCTGGTA	CGAGTGTGGG	GTCTCCATCC	CTGGAAAGTG	GTAATCACAG	GACCGTCATG	5340
	CTGCAAGCTT	GCCCTGCCCA	GCCCCACCAA	CTAAGTCGCA	CTAGGGGGCTG	TGAGCAAAGA	5400
55	CAGCCAGCAT	GCTCAGCCCC	GCTGCCCTAG	GTGCCAGGAA	GGTCACAGAT	GGACACTGGC	5460
	CATTCTGGTC	ATCTCAGTCT	GGAACTCAGT	CCCACTTCTT	GGCCTGGACA	ATGAACAGGA	5520
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00	TGCTACATGC	TITCZGTTTT	TUTCATTITG	GATTTCTCCA	MACTAACTG	CAAAATTAAGCT	5760 5820
	TUAGGTCCCT	TTGTATGCAG TGAAATTTAC	THUMANGGAA	TIMITAAAAA	TACCACCAGE	CENTRALITA	5880
	ALATUUTACT	ATTCTCAATT	TOTATOGACT	TATOTATATA	TOCATATACA	TATCCACACT	5940
	TOTALLIGIAN	ALICICAMIT	ANALYTY	AATTTTTACT	TOTTCACCA	AAAAAAAAA	6000
65	AAAAAAA						

Seq ID NO: 419 Protein sequence

	Protein Acc	ession #: 1	Sos sequence	9			
70	1	11	21 	31 	41 	51 	
	MPGTKLTRTG	APADYRVILK	TSQEDELDVF	DDISVRVMSS	QSVINSWVDP	VLEKOKKVVA	60
	SROYTURYRE	KGBLARWDYK	QIANRRVLIE	NLIPDTVYBF	AVRISQUERD	GKNSTSVFQR	120
	TPESAPITAP	ENLINVUPVNG	KPTVVAASWD	ALPETECKVK	VCLLDTGLFS	VSSFQPSAKS	180
75	FONTFFHTPR	LSNHLEQSPS	PILETLLLPW	WMVCSLGNAI	PSKSGPQTGE	AWDLTPKPSL	240
		QKDFSCLAYL					300
		TGNSLKSVAA					360
	QGRNAKDLLL	DLKNKILANG	GAPRKPQLRA	KKAEELDLQS	TEITGEEELG	SREDSPMSPS	420
	DTQDQKRTLR	PPSRHGHSVV	APGRTAVRAR	MPALPRREGV	DKPGFSLATQ	PRPGAPPSAS	480
80	ASPAHHASTO	GTSHRPSLPA	SLNDNDLVDS	DEDERAVGSL	HPKGAFAQPR	PALSPSRQSP	540
	SSVLRDRSSV	HPGAKPASPA	RRTPHSGAAE	EDSSASAPPS	RLSPPHCGSS	RLLPTOPHLS	600
		EDAPATNSNA					660
		LRARPASCHF					720
		HPKLSSGIRG					780
85	SLHRKEPIPE	NPKSTGADTH	POGKYSSLAS	KAQDVQQSTD	ADTECHSPKA	QPGSTDRHAS	840
	PARPPAARSQ	QHPSVPRRMT	PGRAPEQQPP	PPVATSQHHP	GPQSRDAGRS	PSQPRLSLTQ	900
	AGRPRPTSQG	RSHSSSDPYT	ASSEGMLPTA	LQNQDEDAQG	SYDDDSTEVE	AQDVRAPAHA	960

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5	WPRYTTRAPP SNGKPNGQRI TPVVSPDGLP TPLPTTTPR	IALAPROGSL GHFSTTPMLS INGPOGTKKV LFGQGRHGTP PTTATTMOPT		RNPLSRQPAR ABGRYLQDSH SLGGKPLVGL PRPTTATTRR	PSKPPPKSAR PSYRQGYNGR GNPLRIKLOG EVIKKTTHPP TTTRRPTTTV	PNVEGKVLPG DGRTIVDLEG TTIMQPTTTT RTTTRTTTTTT	1020 1080 1140 1200 1260 1320 1380 1440
10	DEDYEFETSR PSAPCSLTDA TPGOLVTGYL	PPTTTEPSTT LDHFQVDSLD VYSASYEDFI	ATTPRVIPEE EIIPNDLKKS RNKFSTQASS GGELSGSHSL	GAISSPPEEE DLPPQHAPRN VTHLPIENLK	FDLAGRKRFV ITVVAVEGCE PMTRYYFKVQ	APYVTYLNKD SFVIVDWDKA	1500 1560 1620
15	Seq ID NO: Nucleic Aci Coding sequ	420 DNA sec d Accession ence: 128	puence 1 #: NM_022 1237	743			
20	TCTCTGCTGC AAAGCTGATG	AACACCCCTA CGATGCTCTC CCAGACCACA	CCCTCCTTCT CTGTTCTCCG AGTGCCGCGT AGCGGGAATG	TGTATTGGCT CGCCAAATAC CAAATGCCTT	TTTCTGGGCA TGTAGTGCTA AAAAGCTGCA	AGTGTCAGAA AACCCAGATA	60 120 180 240
25	TCCTCCAGAC TTCAGAATCA TGAAGATAAG AGAAATACAG	TCCGTTCGAC GAGAAGCTTT AAAGAGGGCC GATGCCTCTC	TTCTTGGCAG ACTCATTTTA TCAGGCAACT AGCTGCCACC CCATCTGTAA	TGATCTGGAG CGTAATGACA TGCCTTTGAC	TCAAATATTA TTTCAACATT CTTTTTGAAG	ACAAACTGAC TCATGAGAGA CCTTTGCAAA	300 360 420 480 540
30	ATATCCCAGT TGGGCCCCAC CTGCTACCTG CTGCTTTGAA TGGTGATGAG	ATCTCTTTGC CTCTTACTGC GATATGCTGA TGTGACTGTT CAAGTATGGA	TCAATCACAG GAGCAGTCCG TGACCAGTGA TCCGTTGCCA AGGAAGTTCA	CTGTGACCCC AGACATCGAG GGAGCGCCGG AACCCAGGAC AGAATCCCTG	AACTGTTOGA GTGGGAGAGG AAGCAGCTGA AAGGATGCTG AAAAAAATTG	TTGTGTTCAA AGCTCACCAT GGGACCAGTA ATATGCTAAC AAGAACTGAA	600 660 720 780 840
35	GGCACACTGG TGAACGGCIT CIGCATCAAC ATACAGGATT	AAGTGGGAGC CCCGATATCA CTCGGCCTGT TTTTTCCCAG	AGGTTCTGGC ACATCTACCA TGGAGGAAGC GAAGCCATCC GCATGTTTCC	CATGTGCCAG GCTGAAGGTG CTTGTTCTAT CGTCAGAGGG CCAAGCAATG	GCGATCATAA CTOGACTGCG GGTACTCGGA GTTCAAGTGA AAGAATCTGA	GCAGCAATTC CCATGGATGC CCATGGAGCC TGAAAGTTGG GACTGGCTTT	900 960 1020 1080 1140
40	TGATATTATG TTTAGAAGAA CGGCGTGTGT CTGAACCTCT	AGAGTGACAC TGCGACGCCA CITTGTTGAA CTTATTGGAA	ATGGCAGAGA ACATCAGAGC TGCCTTATTG ATTCTGTTCC CATTAGTTGT	ACACAGCCTG ATCCTAAGGG AGGTCACACA GTGTTTGTGT	AACGCAGTCA CTCTATGCTT AGGTAAATAA	GAGGGAAATA TGTTAGCTGT AGGCAGACAT	1200 1260 1320 1380 1440
45	ATTTOGTTGA	GGATGCCAAA 421 Protei	AAAAAAAAA sequence	AAAAAA			
			_				
50	MRCSQCRVAK	11 CSAKOOKKA	21 WPDHKRECKC KKEGLRQLVM	31 LKSCKPRYPP	DSVRLLGRVV	51 PKLMDGAPSE DLPFAPAKVI	60 120
55	CNSFTICNAE LDMLMTSEER WKWEOVLAMC	MQEVGVGLYP RKQLRDQYCF OATTSSNSER	SISLLMHSCD ECDCFRCQTQ LPDINIYQLK QLHQGMFPQA	PNCSIVFNGP DKDADMLTGD VLDCAMDACI	HLLLRAVRDI EQVWKEVQES NLGLLEEALF	LKKIEELKAH YGTRTMEPYR	180 240 300 360
60	Nucleic Ac:	422 DNA sei id Accession mence: 238.	n #: NM_0030	014.2			
	1	11	21	31	41	51	
	1	11	ī-	i	i	1	
65	COGAGCTCCC AAACTCTCCT COCAGGAAGA	CGCCCCGAAG CGGCCCGACC GCGCCCCAGA	GCTGAGAGCT CCGCGGCCCC AGATTTCTTC	GGCGCTGCTC GCTTTGCTGC CTCGGCGAAG GGGGTCGCAG	GTGCCCTGTG CGACTGGAGT GGACAGCGAA CGCGAGAGGG	TGCCAGACGG TTGGGGGAAG AGATGAGGGT CAGTGCCATG	60 120 180 240
65 70	CGGAGCTCCG AAACTCTCCT GGCAGGAAGA TTCCTCTCCA GCGCCCTGCG ATGCCCAACC GAGGAGCTGG GCGCCCATTT	CGCCCGGAAG CGGCCGCACA GAAGGCGCTT TCCTAGTGGC AGGCGGTGCC ACCTGCACCA TGGACGTGAA	GCTGAGAGCT CCGCGGGCCCC AGATTTCTTC TCTGTCTGCC GCTGTGCCTG CATCCCTATG CAGCACGCAG CTGCAGCGCC GTTGCAGCGCC	93CSCTGCTC GCTTTGCTGC CTCGCGAAG GGGTTGCAG TGGCTGCAC TGCCGGCACA GAGAACGCA GTGCTGCGCT GACCCTATCA	OTGCCTGTG CGACTGGAGT GGACAGCGAA CGCGAGAGGG TGCCCTGGG TGCCCTGGAA TCCTTGCCCT TCTTCTTCT AGCCGTGCAA	TGCCAGACGG TTGGGGGAAG AGATGAGGGT CAGTGCCATG CGTGCGCGGC CATCACGCGG CGAGCAGTAC TGCCATGTAC GTCCGTGTGCC	120 180 240 300 360 420 480 540
	COGRAGETCOS ARACTETCOT GGCRGGARGA TTCCTCTCCA GGGCCTGCG ATGCCCAACC GAGGAGCTGG GCGCCCATTT CAACGGGGGC AGCCTGGCCT ATCGTCAGG CAGGGAACGG CAGGGAACGG	CGCCCCGAAG CGGCCCCAGA GAGGCGCTT TCCTAGTGGC AGGCGTCCCACA ACTICACCA GCACCCTGGA GCACCCTGGA GCACCACCACACACACACACACACACACACACACAC	GCTGAGAGCT CCGCGGGCCCC AGATTTCTTC CCTCTCTCCCC CCTCTGCCTG CATCCCTATG CAGCAGCAG CTGCAGCGCC GTTCCTGCAC GGAGCCCTC GCCTCTCTAT GGATGTTAAA	GGGGGTGGTG GCTTTGGTGG CTCGCGGAAG GGGTTGGAG TGGCTGCACC TGCCGCACA GAGAACGCCA ATGAAGATGT GACCCTATCA ATGAAGATG GACCTATGA GCGATAGAC GGCTAAGCC	GTGCCTIGTG GGACAGCGA GGACAGCGA GGCACAGCGG TGCCTGGAA TCCTGGCCAT ACACCACAG TGTGCTCTC TCACACCAGA CCACTGCATTC TCACACCAGA CCACTGCATTC TCACACCACAGA CCACTGCATTC TCACACCACAGA CCACTGCATTC TCACACCACAGA CCACTGCATTC TCACACCACAGA CCACTGATTC TCACACCACAGA CCACTGATTC TCACACCACAGA CCACTGATTC TCACACCACAGA CCACTGATTC TCACACCACAGA CCACTCATTC TCACACCAGA CCACTGATTC TCACACCACAGA CCACTGATTC TCACACCACAC	TGCCAGACGG TTGGCGGAAG AGATGAGGGT CAGTGCCATG CGTGCGGGGC CAT CACGCGG CGACCAGTAC TGCCATGTAC GTCCGTGTGC CTGGCCGGAAGCC CATGATGTAC CAGTGTACATACTACATGTAC TATTCATGCC	120 180 240 300 360 420 480 540 600 720 780 840
70	GGAGCTCGG AAACTCTCTT GGCAGGAKGA TTCCTCTCCA AGGCCTGGC ATGCCCAACC GAGGAGCTGG GGCCCATTT CAACGGGGC AGCTGGCT ATCGTCAGGG AGCTGGCT ATCGTCAGGG AAGGTTGAGGC AAAGTTAAAAG GAGATCTTCA ACTGTCAGGG AAATTAAAAG AGGTTAAAAG AGGTTAAAAAG AGGTTAAAAG AGGTTAAAAAG AGGTTAAAAAAG AGGTTAAAAAAG AGGTTAAAAAG AGGTTAAAAAG AGGTTAAAAAG AGGTTAAAAAG AGGTTAAAAAAG AGGTTAAAAAG AGGTTAAAAAAAA	CGCCCGAAG CGGCCCCAAG CGGCCCCAGA GGGCCCCAGA AGGGGGTGTGC AGGGGGTGAA CCTCCACCTGGA GCACGACTGAACTTGACTGAACTTGACTGATGACT CAACTTTGATTGGC CTGTGCAGAG GTCCACACATTGAACTTGAACTTTGGA	GCTGAGAGCT GCGGGGGCCC AGATTTCTC TCTGTCTGC GCTGTGCCT CATCCCTATS CAGCAGCAG CTGCAGCAGC GTTCCTGCAC GCTGTCTTA GGATGTAAA AACGTATACC AGGTGGCTGC ACCCATCCCT	I GSCCTGCTC GCTTTGCTGC GCTTTGCTGC CTCGGCGACA TGGCTGCACC TGCCGGCACA ATGAGGATGCCA ATGAGGATGACCTATCA ATGAGGATGACC ATGCTGGGCT GACCCTATCA ATGAGGATGACC AACAGAGACC AACAGAGC AACAGAGC AACAGAGC CGAACACTCAGC CGAACACTCAGC CGAACACTCAG	GTGCCTGTG GTGCCTGTG GGACTGGAGT GGACACCAA. GGCAGAGGGG TGCCCTGGA TCTTCTTCTG AGCCTGCAA ACAACCACAG TGTGCATTC TCACACCAGA CCGATGCTATGT CACACCAGT CACACCAGT TCACACCAGT CACACCAGT TCACACCAGT TCACACCAGT TCACACCAGT TCACACCAGT TCACACT	TGCCAGACGG TTGGGGGAAG AGATGAGGGT CAGTGCCATG CGTGCGCGGC CATCACGGG CATCACGGG CTCACTGTGC CTGGCCGAA GCCTGAAGCC CATGATGTAC CATGATGTATATATATGTATGCC GGATGTAAAA TATCAATGCC GGATGTAAAA TATCAATGCT TTAGGAGTGGAAGTTT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020
70 75	GGGAGTCOG AAACTCTCT GGCAGGAAGA TTCCTCTCCA GGCCCTGCG ATGCCCAACC AGGGAGTGG CGAGCAGCTGG AGCAGCTGG AGCAGCTGG AGCAGCTGG AGCAGCTGG AGCATTT CAACCGGGCC AGCAGAAAGAGAG AAGTAAAAA GAGATCTCA TCTTGCCAATC CTTCAAGGA AAAAAAAAAA	COCCOSAAG COCCOSAAG COCCOSAAG COCCOSACA COCCOS	GCTGAGAGCT GCGGGGGCCC AGATTTCTTC CCTGCTGCCTG GCTGTGGCCTG CATCCCTATG CAGCACCCAG GTTCCTGCAC CGAGCCCCTC GCCTCTCTAT GGATGTTAAA AACGTATATCTC GAGTGGCTGC ACTCATCCCT	9300CTGCTC 937TT3GTNG CTC00CGAM 030GTCGCM TGGCTGCAC TGGCTGCAC AGGAACGCCA ATGAGGTTGAC ACCATTGAGCT ACCATTGAGCA ACGACTAGAG CGCTTAGAG CGCTTAGAG CGCTTAGAG CGCATAGAG CGACTTAGAG CAGAACACC CGACTCAGAG CAGAACACC ATGAAAACT ATTGAAA	OTGCCCTGTG CSRCTGGAGT GSACAGCGAA CGCGAGAGGG TGGCCCTGGAA TCCTGGCCAT TCTTCTTCTG AGCCGTGCAA ACAACCACAG TGTGCATTC CAACACAGA CCGATACGCTGT CAACACGAGA CCGATCGCTA TCACACGGAGACAGT TCACACGGAGAGACAGT TCATCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	TGCCAGACGG TTGGCGAGACGG TTGGCGGAGAGGAGAG	120 180 240 300 360 420 480 540 660 720 780 840 900

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	GETTTTCTTT	GTARGCCATC	ACAAGCCATA	GTGGTAGGTT	TGCCCTTTGG	TACAGAAGGT	1500
	GAGTTAAAGC	TGGTGGAAAA	GGCTTATTGC	ATTGCATTCA	GAGTAACCTG	TGTGCATACT	1560
	CTAGAAGAGT	AGGGAAAATA	ATGCTTGTTA	CAATTCGACC	TARTATGTGC	ATTGTAAAAT	1620
5	AAATGCCATA	TTTCAAACAA	AACACGTAAT	TTTTTTACAG	TATGTTTTAT	TACCTTTTGA	1680
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			TTTTTGAAAA				1860
			TTCAGTTTCT				1920
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			ATGATGCTTC				2040
			ATTAGGAGTT				2100
			GTATGTCACT				2160
			AATGGCCTTC				2220
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			AAATGAGAAT				2340
			ATTTTATCAA				2400
			TTATTGGCCT				2460
			ACGCCCAAAG				2520
20			ATTAGTATTT				2580
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			TTATATTCCA				2760
	TATTGGATAC	TTAGGTGGTT	TCTTCACTGA	CARTACTGAA	TAXACATCTC	ACCGGAATTC	
25							
		423 Protei					
	Protein Acc	cession #: 1	NP_003005.1				
	1	11	21	31	41	51	
30	ī	ī	Ĩ.	Ī .	i	1	
••	METATTWATE	TATALOVE	GAPCEAVRIP	MCRHMPWNIT	RMPNHLHHST	OENAILAIEO	60
			YAPICTLEFL				120

	1	11	21	31	41	51	
30	Ī	Ī	Ī	1	1	1	
	MFLSILVALC	LWLHLALGVR	GAPCEAVRIP	MCRHMPWNIT	RMPNHLHHST	QENAILAIEQ	60
		AVLRFFFCAM					120
		YDRGVCISPE					180
	KKVKPTLATY	LSKNYSYVIH	AKIKAVORSG	CNEVTTVVDV	KEIFKSSSPI	PRTQUPLITN	240
35	SECOCPHILP	HODVLINCYE	WRSRMMLLEN	CLVEKNRDQL	SKRSIQWEER	LQEQRRTVQD	300
	XXXTACDTSD	SMEDKBACKE	DA DK DA SPKK	NIKTRSACKE	TNPKRV		

Seq ID NO: 424 DNA sequence Nucleic Acid Accession #: BC010423 Coding sequence: 248..1780

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	1	11	21	31	41	21	
	1		1	!	1	1	60
45	CACAGCGTGG	GAAGCAGCTC	TGGGGGAGCT	CGGAGCTCCC	GATCACGGCT	TCTTGGGGGT	120
43	AGCTACGGCT	AGGCAAGAAC	AACGGGGCCC	GGGCTGGGGC	TOGGTCCCCT	AUTGUAGACC	180
	CAAGTGCGAG	AGGCAAGAAC	TCTGCAGCTT	CUIGCUITUI	GOGTCAGTTC	CITATICANG	240
	TCTGCAGCCG	GCTCCCAGGG	AGATCTCGGT	GGAACTTCAG	MMCGCTGGG	CAGTCTGCCT	300
	TTCAACCATG	CCCCTGTCCC	TGGGAGCCGA	GATGTGGGGG	CCTGAGGCCT	GGCTGCTGCT	360
50	GCTGCTACTG	CTGGCATCAT	TTACAGGCCG	GTGCCCCGCG	GGTGAGCTGG	AGACCTCAGA	420
50	CCTGGTAACT	GTGGTGCTGG	GCCAGGACGC	AAAACIGCCC	TGCTTCTACC	GAGGGGACTC	480
	CGGCGAGCAA	GTGGGGGAAG	TGGCATGGGC	TOGGGTGGAC	GCGGGCGAAG	GOGCCCNGGA	
	ACTAGOGCTA	CTGCACTCCA	AATACGGGCT	TCATGTGAGC	CCGGCTTACG	ACCCCCCCT	540 600
	GGAGCAGCCG	COOCCCCCAC	GCAACCCCCT	GGACGGCTCA	Greereeree	GCAACGCAGT	660
	GCAGGCOGAT	GAGOGCGAGT	ACGAGTGCCG	GGTCAGCACC	TTCCCCCCCC	GCAGCITCCA	720
55	GGCGCGGCTG	CGGCTCCGAG	TGCTGGTGCC	TCCCCTGCCC	TCACTGAATC	CIGGICCAGC	
	ACTAGAAGAG	GGCCAGGGCC	TGACCCTGGC	AGCCTCCTGC	ACAGCTGAGG	GCAGCCCAGC	780
	CCCCAGCGTG	ACCTGGGACA	CGGAGGTCAA	AGGCACAACG	TCCAGCCGTT	CCTTCAAGCA	840
	CTCCCGCTCT	GCTGCCGTCA	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGG	900
	GCAGCCACTG	ACTTGTGTGG	TGTCCCATCC	TGGCCTGCTC	CAGGACCAAA	GGATCACCCA	960
60	CATCCTCCAC	GTGTCCTTCC	TTGCTGAGGC	CTCTGTGAGG	GGCCTTGAAG	ACCAAAATCT	1020
	GTGGCACATT	GGCAGAGAAG	GAGCTATGCT	CAAGTGCCTG	AGTGAAGGGC	AGCCCCCTCC	1080
	CTCATACAAC	TGGACACGGC	TGGATGGGCC	TCTGCCCAGT	GGGGTACGAG	TGGATGGGGA	1140
	CACTTTGGGC	TTTCCCCCAC	TGACCACTGA	GCACAGCGGC	ATCTACGTCT	GCCATGTCAG	1200
	CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACTGTGGAT	GTTCTTGACC	CCCAGGAAGA	1260
65	CTCTGGGAAG	CAGGTGGACC	TAGTGTCAGC	CTCGGTGGTG	GTGGTGGGTG	TGATCGCCGC	1320
	ACTOTTCTTC	TGCCTTCTGG	TGGTGGTGGT	GGTGCTCATG	TCCCGATACC	ATCGGCGCAA	1380
	GGCCCAGCAG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCAGGG	AGAACTCCAT	1440
	CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
	GAGAGCCGAG	GGCCACCCTG	ATAGTCTCAA	GGACAACAGT	AGCTGCTCTG	TGATGAGTGA	1560
70	AGAGCCCGAG	GGCCGCAGTT	ACT CCACGCT	GACCACGGTG	AGGGAGATAG	AAACACAGAC	1620
	TGAACTGCTG	TCTCCAGGCT	CTGGGCGGGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGCCAT	1680
	CAAACAGGCC	ATGAACCATT	TTGTTCAGGA	GAATGGGACC	CTACGGGCCA	AGCCCACGGG	1740
	CAATGGCATC	TACATCAATG	GGCGGGGACA	CCTGGTCTGA	CCCAGGCCTG	CCTCCCTTCC	1800
	CTAGGCCTGG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCTTAA	1860
75	ACACCCCCAT	TTCTTGCGGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACCTCC	1920
	AACCCTTCTG	TTCATCGGGA	GGGCTCCACC	AATTGAGTCT	CTCCCACCAT	GCATGCAGGT	1980
	CACTGTGTGT	GTGCATGTGT	GCCTGTGTGA	GTCTTGACTG	ACTGTGTGTG	TCTGGAGGGG	2040
	TGACTGTCCG	TGGAGGGGTG	ACTOTOTOCO	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
	AAGTGAACTG	TOGTGTATGT	CCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACTGTCAGG	2160
80	CTTTGGCGTG	TGTGTCATGT	GGCTGTGTGT	GACCTCTGCC	TGAAAAAGCA	GGTATTTTCT	2220
	CACACCCCAC	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
	CAGACCCAGG	TCTGCGGGCA	TAGCTGGAGC	TGGAATCTGC	CYCCCGCTGTG	AGGGAACCTG	2340
	TOTOTACCA	CTTCGGAGCC	ATGGGGGGCAA	GTGTGAAGCA	CCCMCTCCCT	GOGTCAGCCA	2400
	CACCCTTGAA	CTGTTACAGA	ACCCCTCTCC	CCTCTY3CTGG	CCTCTGGGGCC	TGCTGCATGT	2460
85	ACATATTTTC	TOTALATATA	CATGOGCCGG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
0.5	ACTIVITATION	TTTTTCTTT	TTTTTTTTTT	CCCTTTCCAT	TAGETGTATE	TTTTATTTAT	2580
	TTTTATTTT	ATTTTTTTT	AGACTTTGAG	TOCAGOCTIGG	ACCATATACC	CAGACCCTGT	2640

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Seq ID NO: 425 Protein sequence

5	Protein Ac	cession # : /	AH10423				
	1	11	21	31	41	51	
	1	1	1	1	1	1	
		GPEAKLLLLL					60
		DAGEGAQELA					120
10		TFPAGSFQAR					180
		TSSRSFKHSR					240
		RGLEDQNLWH					300
		GIYVCHVSNE					360
		MSRYHRRKAQ					420
15	EGHPDSLKON	SSCSVMSEEP	EGRSYSTLTT	VREIETOTEL	LSPGSGRAEE	EEDQDEGIKQ	480
	AMNHEVQENG	TLRAKPTGNG	IYINGRGHLV				

	AMNHEVQENG	TLRAKPTGNG	IYINGRGHLV				
	Seq ID NO:	426 DNA sec	nence				
20		d Accession sence: 373		474.2			
20	Course sequ	Jence: 37	1036				
	1	11	21	31	41	51	
	CACTAACGCT	CTTCCTAGTC	CCCGGGCCAA	CTCGGACAGT	TTGCTCATTT	ATTGCAACGG	60
25	TCAAGGCTGG	CTTGTGCCAG	AACGGCGCGC	GCGCGACGCA	CGCACACACA	CGGGGGGAAA	120
	CTTTTTTAAA	AATGAAAGGC	TAGAAGAGCT	CAGCGGGGGC	GCGGGCCGTG	CGCGAGGGCT	180 240
	CCGGAGCTGA	CTCGCCGAGG GATGGTGCAG	CAGGAAATCC	CTCCCGGTCGC	ACCOCCCCCC	CECCOCTOGGC	300
	GOGACCATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCCCCCCC	GCCCCCTCCT	GCTCGCCCTG	
30	GCCGGTGCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATOGAA	CGAAGGAAGA	420
	GCTGATGAAG	TTGTCAGTGC	CTCTCTTCGG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC AAGCAAAGAA	480
	TTCGACTCCA	AGAATCATCC	AGAAGTGCTG	AATATTOGAC	GCAGTTTCAC	GGAAACCCAC	600
	TATCTOCARG	ACCOUNT ACTORA	TOTOTOTOTO	CCTCGAAATT	ACACCCTAAT	TCTGGGTCAC	660
35	TGTTACTACC	ATGGACATGT	ACGGGGGATAT	TCTGATTCAG	CAGTCAGTCT	CAGCACGTGT	720
	TCTGGTCTCA	GGGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGTCTTAGA	ACCAATGAAA	780
	AGTIGCAACCA TOTOCATCAC	ACAGATACAA	ACTOTTOGGA	GCGAAGAAGC	ATGTGTTTTCC	CCGGGGATCA ACCACCCTCT	900
40	GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
	CAGOGATTAA	TAGAGATTGC	TAATCACGIT	GACAAGTTTT	ACAGACCACT	GAACATTCGG AAGTCAGGAC	1080
	CCATTCACCA	GCCTCCATGA	AGTGTGGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAAA	
	TCCCATGACA	ATGCGCAGCT	TGTCAGTGGG	GTTTATTTCC	AAGGGACCAC	CATCGGCATG	1260
45	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTOTCAT	GGACCATTCA	1320
	GACAATCCCC	TTGGTGCAGC	CGTGACCCTG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG AGGAGGCTGC	1380
	ATCATGAACG	CTTCCACCGG	GTACCCATTT	CCCATGGTGT	TCAGCAGTTG	CAGCAGGAAG	1500
	GACTTGGAGA	CCAGCCTGGA	GAAAGGAATG	GGGGTGTGCC	TGTTTAACCT	GCCGGAAGTC	1560
50	AGGGAGTCTT	TOGGGGGCCA	GAAGTGTGGG	AACAGATTTG	TGGAAGAAGG	AGAGGAGTGT	1620
	BACTGTGGGG	AGUCAGAGGA	ACATGGGCTG	TOCTOTORAG	ACTRICCACCAC	CTGTACCCTG GAAGCCTGCA	1740
	GGAACAGCGT	GCAGGGACTC	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800
55	AGCCCTCACT	GCCCAGCCAA	CCTCTACCTG	CACGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
22	GGCTACTGCT	ACANTGGCAT	CTGCCAGACT	CACGAGCAGC	AGTGTGTCAC	ACTOTOGGGA	1920 1980
	TATGGCAACT	GTGGCAAAGT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
	AAATGTGGAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCCGGC	CAGTCATTGG	TACCAATGCC	2040 2100
60	GTTTCCATAG	AAACAAACAT TGGGCGATGA	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
00	CACGIGIACI	TGGGCGATGA	CATGCCGGAC	TOTCASARTA	TEAGRICAGE	TGGGGTTCAC	
	GAGTGTGCAA	TGCAGTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
	GAGGCCCACT	GGGCACCTCC	CTTCTGTGAC	AAGTTTGGCT	TTGGAGGAAG	CACAGACAGC	2400
65	GGCCCCATCC	GGCAAGCAGA	TAACCAAGGT	TTAACCATAG	GAATTCTGGT	ACCATCCTG ACGACTGCTG	2520
05	TTTACAAATA	AGAAGACCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
	COTGGCTTCC	AACOCTGTCA	GGCTCACCTC	CCCCACCTTG	GANAAGGCCT	GATGAGGAAG	2640
	CCGCCAGATT	CCTACCCACC	GAAGGACAAT	CCCAGGAGAT	TGCTGCAGTG	TCAGAATGTT TCAGCGAGTG	2700 2760
70	GACATCAGCA	TOCHCOORGE	COCCACCAGOCA	CCTRCCCTCAGC	COCHETCIONC	CCTGCCAGCC	
70	AAGCCTGCAC	TTAGGCAGGC	CCAGGGGACC	TCTAACCCAA	ACCCCCCTCA	GAAGCCTCTG	2880
	CCTGCAGATC	CTCTGGCCAG	AACAACTCGG	CTCACTCATG	CCTTGGCCAG	GACCCCAGGA	2940
	CAATGOGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000 3060
75	TGAAGACAGA	ACTUTOCACAC	ATCTTTCAGC	TOCAGTTIGGA	GTTTTTGTA	CCAACTITTA	3120
, ,	GGATTTTTTT	TAATGTTTAA	AACATCATTA	CTATAAGAAC	TTTGAGCTAC	TGCCGTCAGT	3180
	GCTGTGCTGT	GCTATGGTGC	TCTGTCTACT	TGCACAGGTA	CTTCTAAATT	ATTAATTTAT	3240
	GCAGAATGTT	GATTACAGTG	CAGTGCGCTG	TAGTAGGCAT	TTTTACCATC	ACTGAGTTTT ATCCTGCTTG	3300 3360
80						AAGCAGTCCC	
	CCAACTACCC	CCAGCTGTGC	TTATGGTACC	AGATGCAGCT	CAAGAGATCC	CAMSTAGAAT	3480
	CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC GCTCCCAGGG	3540
	ACACCTOCCA	CARATCTCCC	TTCTGGCCAG	GAAGCTTTOO	TGAGAACCTYC	GGTTGCAGAC	3660
85	AGGAATCTTA	AGGTGTAGCC	ACACCAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
	TGACCCTGAG	CTGACCAGCC	GTGAGCATGT	TTGGAAGGGG	TCTCTAGTGT	CACTCAAGGC	3780
	GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTCGCTG	TCCTTTCTAG	AGCACTGCCA	3840

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	CYCLABACYC	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTAATA	3960
	CANTICATION	GTATTCAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAACTA	TTTTCAGATG	4020
	TCAACCATTA	ACCAGATCTA	GTCAATCAAG	TOTOTTTACT	GCRAGGTTCA	ACTTATTAAC	4080
5	3 SWEACCCAC	ACTCTTTATG	CTTCCARRE	CTACAACCAA	TOGRATISTICA	TGTTCATGGG	4140
	WHITE COMMON	GTCTGCTATC	APPADROOM	CATATTOCAC	DANGARCOTT	CTCTATGGGG	4200
	TATAGTTCAL	TTCCAACTTG	ATTAITCOIN	MUNITED AND	AMCCOMMUNE A	CACACTCTCA	4260
	CATCCTCTT	TAAACACTTG	GCTGCAGGAA	CONTRACTOR	ACCOUNTED	ATTACCATAT	4320
	ACCYATTICE	ATCAACTTCC	CHACCIACCI	GIIGNOCKIC	MCHONNIGIO	MINOCOMPOSITE	4380
10	CAACTTGCTT	TTCAAATGCC	TAAATATTAT	GAGATGTGGC	TTOGGCAGCA	TCCCCTTOOM	4440
10	CICTICACIC	TTCAAATGCC	TGACTAGGGA	GCCATGTTTC	ACANGGICII	DOMEST ONC!	4500
	AATGGCATGA	GAAATACAAA	AATACTCAGA	TANGGTAAAA	TGCCATGATG	CCTCTGTCTT	4560
	CTGGACTGGT	TTTCACATTA	GAAGACAATT	GACAACAGTT	ACATAATICA	CICIGAGIGI	4620
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTTCCTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGGTTT	GOCTTCCAGA	AAACAAAACT	GCATTTCACT	Trecessier	
15	TCCCCACTGT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
	AAACACACAC	AAAAGGGAAC	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
	TTATTCTATA	GTTATTAAGT	TCTTTAAAAT	GTAAAGCCAT	GCTGGAAAAT	AATACTGCTG	4860
	ACATACATAC	AGAATTACTG	TAACTGATTA	CACTTGGTAA	TIGTACTAAA	GCCAAACATA	4920
	TATATACTAT	TAAAAAGGTT	TACAGAATTT	TATGGTGCAT	TACGTGGGCA	TIGICITITI	4980
20	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCCT	CCAATTATAA	GAGGATATGA	5040
	ACCAAAAAAA	AAAAAAAAA	AA				
	Sea ID NO:	427 Protein	sequence				
		ession #: 1					
25							
	1	11	21	31	41	51	
	ī	ī	ī	1	1	1	
	MAAD DT. DIZED	ARALLLALAG	ALLAPCEARG	VSLANDGRAD	EVVSASVRSG	DLWIPVKSFD	60
	CHARLEST VOI	RLORESKELI	INTERNEGLE	ASSFTETHYL	ODGTDVSLAR	NYTVILGHCY	120
30	Andrianadaeu	SAVSLSTCSG	LEGITVEENE	SYVLEPMKSA	THRYKLPPAK	KLKSVRGSCG	180
20	OUR PROPERTY AND A PARTY OF THE	KNVFPPPSQT	MADDUKDETT.	KATKYVELUT	VADNEEFORO	GKDLEKVKOR	240
	SUBSTITUTE	PYRPLNIRIV	THOMBROOM	DAGGROUDDE	TOT.UBBI.DUD	KMKLLDRKSH	300
	DIBINGTON	FOGTTIGMAP	THENOMEDIC	CCTUMDUCDM	PLCAAUTLAH	RT-CHN POMPH	360
	DELAGENSOVI	MAVEKGGCIM	NA OTCVDEDM	UPOCCOPENT.	ETST-EKGMGV	CLENTPEVEE	420
35	DIEDRGCSCQ	FVEEGEECDC	CONSTRUCTOR	CHARMONT VD	DAYCARCICC	PDCOLX PAGE	480
33	BEGGGRCGMR	LPEFCTGASP	UGDANIUME	CHALLCIDAL	CANALCOARS	OOCUTI-WORK	540
	ACKDSSNSCD	RVNSAGDPYG	HCPANVILIND	GHOCODARGI	CINGICCIND	DRUTOTNAMO	600
	AKPAPGICFE	GRILCRGTHV	NCGKVSKSSF	AKCEMICIANC	OKIQCQOMS	MA CAMOUNDS	660
	IETNIPLOQG	NNRKNCHCEA	ILGUDRPDPG	DVLAGIACAD	OKICHNIQUE	TOTTUMTLOT	720
40	AMOCHGROVC	RKTLIRLLFT	HKAPPFCDKF	GFGGSTDSGP	TROMONOGUT	IGIDALIDOD	780
40	LAAGFVVYLK	RKTLIRLLFT	NKKTTLEKLE	CVRPSRPPRG	POPCONIDGE	DONGLINKEP	840
	DSYPPKDNPR	RLLQCQNVDI	SRPLNGLNVP	QPQSTQRVLP	PLHKAPKAPS	VPARPLPARP	900
		PNPPQKPLPA	DPLARTTRLT	HALARTPGQW	ELGUKUMPUK	PAPQIPHQVP	900
	RSTHTAYIK						
10							
45		428 DNA se					
		id Accession		714			
	Coding sequ	ience: 135.	.1043				
	1	11	21	31	41	51	
50	1	i	1	1	1	1	
	GAGGAGGAGG	GAAAAGGCGA	GCAAAAAGGA	AGAGT@3GAG	GAGGAGGGGA	AGOGGCGAAG	60
	GAGGAAGAGG	AGGAGGAGGA	AGAGGGGAGC	ACAAAGGATC	CAGGTCTCCC	GACGGGAGGT	120
	TAATACCAAG	AACCATGTGT	GCCGAGCGGC	TOGGCCAGTT	CATGACCCTG	GCTTTGGTGT	180
	TOGGCCACCTT	TGACCCGGCG	CGGGGGGACCG	ACGCCACCAA	CCCACCCGAG	GGTCCCCAAG	240
55	ACAGGAGCTC	CCAGCAGAAA	GGCCGCCTGT	CCCTGCAGAA	TACAGCGGAG	ATCCAGCACT	300

CCAGTAGGTT ATTTAGCTTG GGAAAGGTGG TGTTTCTGTA AGAAACCTAC TGCCCAGGCA 3900

GAGGAGGAGG	GAAAAGGCGA	GCAAAAAGGA	AGAGTGGGAG	GAGGAGGGGA	AGOGGCGAAG	60	
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TAATACCAAG	AACCATGTGT	GCCGAGCGGC	TOGGCCAGTT	CATGACCCTG	GCTTTGGTGT	180	
TGGCCACCTT	TGACCCGGCG	CGGGGGACCG	ACGCCACCAA	CCCACCCGAG	GGTCCCCAAG	240	
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AGTGTGAGCA	GAACTGGGGA	AGCCTGTGCT	CCATCTTGAG	CTTCTGCACC	TCGGCCATCC	780	
AGAAGCCTCC	CACGGCGCCC	CCCGAGCGCC	AGCCCCAGGT	GGACAGAACC	AAGCTCTCCA	840	
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TGTCTGGGCT	GGGGGGGACA	CTGTCCAAGG	GAGTGGCCCC	TATGAGTTTA	TATTTTAACC	1740	
ACTGCTTCAA	ATCTCGATTT	CACTITITIT	ATTTATCCAG	TTATATCTAC	ATATCTCTCA	1800	
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TAAAAAAAAA	AAAACCAGCC	CATCCTTTGA	GGCTGATTTT	TCTTTTTTTT	AAGTTCTATT	1920	
TEAAAAGCTA	TCAAACAGCG	ACATAGCCAT	ACATCTGACT	GCCTGACATG	GACTCCTGCC	1980	
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WO 02/086443 AAATCAAGGA GACIGCIGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAA 2280 TITAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA 2340 GGGAGAGGAA GAAAAGAGAG AGAGAAAAGA GCCTCGTGCC Sec ID NO: 429 Protein sequence Protein Accession #: NP_003705 31 41 51 10 MCAERICORM TIAINIATED PARCEDATED PERPODESSO OKURISIONE ARTOHOLINA GDVGCGVFEC PENNSCEIRG LHGICMTFLH NAGKFDAQGK SFIKDALKCK AHALRHRPGC 120 ISRKCPAIRE MYSOLORECY LKHOLCAAAQ ENTRYIVEMI HFKOLLLHEP YVOLVNLLLT 180 CGEEVKEAIT HSVQVQCEQN WGSLCSILSP CTSAIQKPPT APPERQPQVD RTKLSRAHHG EAGHHLPEPS SRETGRGAKG ERGSKSHPNA HARGRVOGLG AQGPSGSSEW EDEQSEYSDI 300 15 Sec ID NO: 430 DNA sequence Nucleic Acid Accession #: NM_005940 Coding sequence: 23..1489 20 AAGCCCAGCA GCCCCGGGGC GGATGGCTCC GGCCGCCTGG CTCCGCAGCG CGGCCGCGGG CHCCTCCTG CCCCCGATGC TGCTGCTGCT GCTCCAGCCG CCGCCGCTGC TGGCCCGGGC 120 25 TOTGCCGCCG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180 AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACGCAG GAAGCCCCCC GGCCTGCCAG CAGCCTCAGG CCTCCCCGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA 200 CCGACAGAAG AGGTTCGTGC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 260 CONTAINED AUGITEUTS TITTUIGIGG GEGETSONS ANGAGGGE TEACHAGG GATCHITEG TITCAIGGE AGITGGTGCA GGGCAGGTG COGCAGACGA TGGCAGAGGC CTTAAAGGTA TGGACGATG TGACGCCACT CACCITIACT GAGGTGCACG AGGGCGTGC 420 30 400 TGACATCATG ATCCACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCGT TTGATGGGCC TOGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACIT CCACTATGAT GAGACCTOGA CTATCGGGGGA TGACCAGGGC ACAGACCTGC TGCAGGTGGC 660 AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCCTGAT 720 35 CHECOCOTTE TACACCTTTC OCTACCTACT GAGTCTCACC CCAGATGACT GCAGGGGGGCT 780 TCAACACCTA TATGGCCAGC CCTGGCCCAC TGTCACCTCC AGGACCCCAG CCCTGGGCCC 840 CCAGGCTGGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC CGCCAGATGC CTGTGAGGCC TCCTTTGAGG CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960 GOSCTTTGTG TGGCOCCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTGGCCTC 1020 TOGOCACTGG CAGGGACTGC CCAGCCCTGT GGACGCTGCC TTCGAGGATG CCCAGGGCCA 1080 CATTIGGITC TICCAAGGIG CICAGIACIG GGIGTACGAC GGIGAAAAGC CAGICCIGGG 1140 CCCCGCACCC CTCACCGAGC TGGGCCTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCCACCC 1260 CAGCACCCGG COTOTAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGGCC CTCTGAGATC GAAGCTGCCT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGCCGGGCC CCTCTACTG AAGTTGACC CTGTGAAGG GAAGGCTGTG GAAGCTTCC CCGTCTCCT 1220 1380 1440 GOSTOCTGAC TTCTTTGGCT GTGCCGAGCC TGCCAACACT TTCCTCTGAC CATGGCTTGG ATGCCCTCAG GGGTGCTGAC CCCTGCCAGG CCACGAATAT CAGGCTAGAG ACCCATGGCC 1560 ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGTCTCCTGC AGGCGGAATGG 1620 50 COMPANIES ASSESSED ASSESSEDA ASSESSED ASSESSED ASSESSED ASSESSED ASSESSED ASSESSED ASSESSEDA ASSESSED ASSESSED ASSESSED ASSESSED ASSESSED ASSESSED ASSESSED 1680 AGCGACTOTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740 GGGACCCGCT ATGCAGGTCC TGGCAAACCT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG GTAGCACCAT GGCAGGACTG GGGGAACTGG AGTGTCCTTG CTGTATCCCT GTTGTGAGGT 1860 TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920 55 TGAGCAACTG GGCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC 1980 ATCTGTCTGC CTTCTGGCTG ACAATCCTGG AAATCTGTTC TCCAGAATCC AGGCCAAAAA 2040 GITCACAGEC AAATGGGGAG GGGTATTCFT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG CARCHTACOT CAATOCTOTC CORGGOOGGA TECTOOTGAA GECCTTTTOG CAGCACTOCT ATCCTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTT 2160 2220 60 TITTTAAACT GAGGATTGTC ATTAAACACA GTTGTTTTCT Sec ID NO: 431 Protein seque Protein Accession #: NP_005931 65 21 21 41 51 MAPAAWLRSA AARALLPPML LILLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA PAPATQEAPR PASSLRPPRC GVPDPSDGLS ARNRQKRFVL SGGRWEKTDL TYRILRFPWQ 120 LVOEOVROTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYNHGDDLPF DGPGGILAHA 180 70 PFPKTHREGD VKFDYDSTWT IGDDCGTDLL QVAAHEFGEW LGLQHTTAAK ALMSAFYTFR YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 240 VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA QYWYYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS 420 PVPRRATOWR GVPSEIDAAF QDADGYAYPL RGRLYWKFDP VEVKALEGFP RLVGPDFFGC 490 75 APPANTEL Seq ID NO: 432 DNA sequence Nucleic Acid Accession #: NM 024022 Coding sequence: 202..1563 80 31 41 ACCOGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTCATGCCC GTGTGAGCCA GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG 120 85 CONTINUENT TITTOGGAT COGGANTAT GAGGERGAGE TOGAGGCOGA CCCCGATOTE AGAGGTCCTO ANATOTICAC CHOGGGGAA ANTGATCOGC CHICAGTGT ACCCCTTTC CCTTGATAT TIGAAAATAA GTCCTGTTOG ACCAGTGCA 180

	WO 02/	086443					
	GATGCTGTTG	CTGCACAGAT TTGCATTGAT	CCTGTCACTG	CTGCCATTGA	AGTITITICC	AATCATCGTC	360 420
	TCAGGGATCA	ACAGATGTCG	CTCATCCTT	AAGTGTATCG	AGCTGATAGC	TOGATGTGAC	480
	GGAGTCTCGG	ATTGCAAAGA	CGGGGAGGAC	GAGTACCGCT	GTGTCCGGGT	GGCTGGTCAG	540
5	AATGCCGTGC	TCCAGGTGTT	CACAGCTGCT	TCGTGGAAGA	CCATGTGCTC TCCCAAGCTA	CGATGACTGG	600
	CARRACOTOR	ACGCAAATGT GAGTGAGCTC	OCTOONGOOD.	CAGPECCOOG	AGGAGTTTGT	GTCCATCGAT	720
	CACCTCTTGC	CAGATGACAA	GGTGACTGCA	TTACACCACT	CAGTATATGT	GAGGGAGGGA	780
	TGTGCCTCTG	CAGATGACAA GCCACGTGGT TCGTGGGTGG	TACCTTGCAG	TGCACAGCCT	GTGGTCATAG	AAGGGGCTAC	840
10	AGCTCACGCA	TCGTGGGTGG	AAACATGTCC	TTGCTCTCGC	AGTGGCCCTG	GCAGGCCAGC	900 960
	CTTCAGTTCC	AGGGCTACCA ACTGTGTTTA	TEACTIVETAC	CTCCCCAAGE	CATGGACCAT	CLEGGEGGE	1020
	CTAGTTTCCC	TGTTGGACAA	TCCAGCCCCA	TCCCACTTGG	TGGAGAAGAT	TGTCTACCAC	1080
10	AGCAAGTACA	AGCCAAAGAG	GCTGGGCAAT	GACATCGCCC	TTATGAAGCT	GGCCGGGCCA	1140
15	CTCACGTTCA	ATGAAATGAT TGTGCTGGAC	CCAGCCTGTG	TGCCTGCCCA	ACTCTGAAGA	GAACTTCCCC	1200
	GATGGAAAAG	ACCACGCGGC	COTCAGGATGG	DETTCCARCA	MGGATGGAGG	CCACAGGGAC	1320
	GTGTACGGTG	GCATCATCTC	CCCCTCCATG	CTCTGCGCGC	GCTACCTGAC	GGGTGGCGTG	1380
	GACAGCTGCC	AGGGGGACAG	CGGGGGGGCCC	CTGGTGTGTC	AAGAGAGGAG	GCTGTGGAAG	1440
20	TTAGTGGGAG	CGACCAGCTT	TOGCATCGGC	TGCGCAGAGG	TGAACAAGCC	TGGGGTGTAC	1500
	ACCOGTGTCA	CCTCCTTCCT	AGCCACCTGA	CAUGAGUAGA	TOGACIACIA	AGCCCGATCC	1620
	TCCCCCTGGAC	TCCCCGTGTAG	GAACCTGCAC	ACGAGCAGAC	ACCCTTGGAG	CTCTGAGTTC	1680
	CGGCACCAGT	AGCAGGCCCG	AAAGAGGCAC	CCTTCCATCT	GATTCCAGCA	CAACCTTCAA	1740
25	GCTGCTTTTT	GTTTTTTGTT	TTTTTGAGGT	GGAGTCTCGC	TCTGTTGCCC	AGGCTGGAGT	1800
	GCAGTGGCGA	AATCCCTGCT	CACTGCAGCC	CTCCCCCCC	CCACACCCAA	CTAATTTTTC	1920
	TATTTTTAGT	AGAGACAGGG	TTTCACCATG	TTGGCCAGGC	TGCTCTCAAA	CCCCTGACCT	1980
	CAAATGATGT	GCCTGCTTCA	CCCTCCCACA	GTGCTGGGAT	TACAGGCATG	GGCCACCACG	2040
30	CCTAGCCTCA	COCTOCTTTC	TGATCTTCAC	TAAGAACAAA	AGAAGCAGCA	ACTTGCAAGG	2100
	GCGGCCTTTC	CCACTGGTCC	ATCTGGTTTT	ACCCACCAGGG	ACCUPACION .	ATTCCTGACG	2220
	CCAGCCCAGA	AGTGCAGAAC	TGCAGTCACT	GCACGTTTTC	ATCTCTAGGG	ACCAGAACCA	2280
	ARCCCACCCT	TTCTACTTCC	AAGACTTATT	TTCACATGTG	GGGAGGTTAA	TCTAGGAATG	2340
35	ACTOSTITAA	GGCCTATTTT	CATGATTTCT	TTGTAGCATT	TGGTGCTTGA	CGTATTATTG	2400
	AAAAA	CCAAATAATA	TOTTTCCTTC	CCTCADDOGA	MANAGORANON	ACCOUNT OUT	2460
40	Seq ID NO:	433 Protein	n sequence				
40	FIOLEIN AC	Session #1	_				
	1	11	21	3.1	41	51	
		7-	7"	-	1	1	
	MORNIDABAUE	N DECEMBEL DO	1	Ī	Lettpikeep	TTVTGTTALT	60
45	LALAIGLGIH	APFSFRSLFG PDCSGKYRCR	 LDDLKISPVA SSFKCIELIA	PDADAVAAQI RCDGVSDCKD	GEDEYRCVRV	GGQNAVLQVF	60 120
45	LALAIGLGIH	PDCSGKYRCR	 LDDLKISPVA SSFKCIELIA ACAOLGEPSY	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS	LEGOFREEFV	SIDHLLPDDK	120 180
45	LALAIGLGIH TAASWKTMCS VTALHESVYV	PDCSGKYRCR DDWKGHYANV REGCASGHVV	 LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACGHR	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG	GEDEYRCVRV LEGGFREEFV NNSLLSQWPW	GGQNAVLQVF SIDHLLPDDK QASLQFQGYH	120 180 240
	LALAIGLGIH TAASWKTMCS VTALHESVYV LCOGSVITPL	PDCSGKYRCR DDWKGHYANV REGCASGHVV WIITAAHCVY	LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN	GEDEYRCVRV LEGGFREEFV NMSLLSQWPW PAPSHLVEKI	GGQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPKR	120 180
45 50	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCOGSVITPL LGNDTALMKL	PDCSGKYRCR DDWKGHYANV RESCASSEVV WIITAAHCVY AGPLTFNEMI	LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI OPYCLPNSEE	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN NFPDGKVCWT	GEDEYRCVRV LEGGFREEFV NMSLLSGWPW PAPSHLVEKI SGWGATEDGG	GGQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300
	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCGGSVITPL LGNDIALMKL VPLISNKICN	PDCSGKYRCR DDWKGHYANV REGCASGHVV WIITAAHCVY	LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI QPVCLPNSEE PSMLCAGYLT	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN NFPDGKVCWT GGVDSCQGDS	GEDEYRCVRV LEGGFREEFV NMSLLSGWPW PAPSHLVEKI SGWGATEDGG	GGQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
	LALAIGLGIH TAASWKINCS VTALHHSVYV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP	PDCSGKYRCR DDNKGHYANV REGCASGHVV WIITAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL	LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSNTI QPVCLPNSEE PSNLCAGYLT DWIHEQMERD	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN NFPDGKVCWT GGVDSCQGDS	GEDEYRCVRV LEGGFREEFV NMSLLSGWPW PAPSHLVEKI SGWGATEDGG	GGQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
50	LALAIGLGIH TAASMKTMCS VTALHESVYV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic Ac:	FDC9GKYRCR DDMKGHYANV RESCASGHVV WIITAAHCVY AGPLIFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA se- id Accessio	LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSNTI QPVCLPNSEE PSNLCAGYLT DWIHEQMERD QUENCE D#: NM 000	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN NFPDGKVCWT GGVDSCQGDS LKT	GEDEYRCVRV LEGGFREEFV NMSLLSGWPW PAPSHLVEKI SGWGATEDGG	GGQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
	LALAIGLGIH TAASMKTMCS VTALHESVYV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic Ac:	PDCSGKYRCR DDWGHYANV RESCASGHVV WIITAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA se	LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSNTI QPVCLPNSEE PSNLCAGYLT DWIHEQMERD QUENCE D#: NM 000	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN NFPDGKVCWT GGVDSCQGDS LKT	GEDEYRCVRV LEGGFREEFV NMSLLSGWPW PAPSHLVEKI SGWGATEDGG	GGQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
50	LALAIGLGIH TAASMKIMCS VTALEHSVYV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic Ac. Coding seq	PDOSCKYRCR DDMKGHYANV RESCASGHVV WIITAAHCVY AGFLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA second Accession Lence: 97	LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI QVCLPNGEE PSMLCAGYLT DWIHEQMERD Quence n #: NM_000 2139	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN NFPDGKVCWT GGVDSCQGDS LKT	GEDEYRCVRV LEGGFREEFV NMSLLSGWPW PAPSHLVEKI SGWGATEDGG	GGQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
50	LALATGLGIH TAASWKTMCS VTALHESVYV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic Ac: Coding sequ	FDCSGKYRCR DDWKGHYANV REGCASGHVW WIITAAHCVY AGPLIFNEMI HRDVYGGIIS GUYTRVTSFL 434 DNA sei id Accession lence: 97	LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSNTI QPVCLPNSEE PSMLCACVLT DWIHEQMERD Quence n #: NM_000 2139	PDADAVAAQI PDADAVAAQI PCOOVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN NFPDGKVCWT GGVDSCQGDS LKT	GEDEYRCVRV LEOQFREEFV MMSLLSOMPM PAPSHLVEKI SGNGATEDOG GGPLVCQERR	GGQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPFKR DASPVLNHAA LWKLVGATSP	120 180 240 300 360 420
50	LALATGLOTH TAASMKTMCS VTALHESYTV LCOGGVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID MO: Nucleic Ac: Coding sequ	PDCSGKYECR DDMRGHYANV REGCASGHVV WITTAHHCYY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA seid Accession Lence: 97	LDDLKISPVA SSFKCIELIA ACAQUSFBSY TLQCTACSHR DLYLPKSNTI QPVCLPNEEB PSMLCAGYLIT DWIHEQMERD quence n #: NM_000 2139 21 1 TGGGCAGAGG	PDADAVAAQI PDADAVAAQI PDADAVAAQI PSEDNLRVSS RGYSSRTVGG QVGLVSLLDN NFPDGKVCWT GGVDSCQGDS LKT	GEDEYRCVRV LEOOFREEFV INSLLSOMPW PAPBHLVEKI SGNGATEDOS GGPLVCQERR	GGOMAVIQUE SIDHLLEPDK QASLQFQGYH VYHSKYKPKR DASPVLNEAA LMKLVGATSF	120 180 240 300 360 420
50	LALATGLOIH TAASMKINGS VTALHESYYV LOOGSVITPL LOOGINIPL LONDIAIMML VPLISMKICN GIGCAEVMKP Seq ID NO: Nucleic Ac: Coding sequence 1 CACCITCIGC CCAGGAACTC	FDCSGKYRCE DDNKGHYARV REGCASGHVW WITTAAHCUY AGPLTFNHH HRDVYGGIIS GVYTRVTSFL 434 DNA sei id Accessio ience: 97	LDDLKISPVA SSFKCIELIA ACAQLIFPSY TLQCTACOGHR DLYLPKSNTI QPYCLPMSEE PSMLCACYLT DWHHEQMERD Quence n #: NM_000 2139 21 1 TGGGCAGAGG GAATCCATCT	PDADAVAAQI PDADAVAAQI PCOGVSDCKD VSSDNLRVSS RGYSSRIVOG QVGLVSLLDN NFPDGKVCWT GGVDSOQGDS LKT	GEDEYRCVRV LEOOPREEPV NMSLLSQWPW PAPSHLVEKI SGNGATEOG GGPLVCQERR 41 AAGCTGCCAA	GGOMAVLOVE SIDHLLEPDK QASLQPQGYH VYHSKYKPKR DASFVLMHAA LMKLVGATSF 51 GGCACCATCT ACCCTTTTTG	120 180 240 300 360 420
50	LALATGLOTH TABSHKIMCS VTALHESVYV LCOGSVITPL LGONDIALMML VPLISHKICN GIGCAEVHKP Seq ID MO: Nucloic Ac: Coding sequ 1 CACCITCIGC CCAGGACTEC TOGGIAGTATA	PDCSGKYECR DDWKGHYANV REGCASGHVV REGCASGHVV WITTAHHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA seid Accessio Lence: 97 11 ACTGCTCATC CCACGAGGAG CCTTSAACTT	LDDLKISPVA SSFKCIELIA ACAGLGFBSY TLQCTACGHR DLYLPKSNTI QPVCLPNSEE PSMLCAGYLT DWIHEQMERD Quence n #: NM_000 2139 21 1 TGGGCAGAGG GAATCCATCT GGGTCATGGA	PDADAVAAQI PDADAVAAQI PCOOVSDCKD VSSDNLRVSS RGYSSRIVG GVGLVSLLDN NFPDGKVCH GGVDSCQGDS LKT 493.2	GEDEYRCVRV LEGOPREBPV NMSLLSQWPW PAPBILVEKI SGNGATEDOG GGPLVCQERR 41 AAGCTGCCAA TGCCACAAAT TGCCACAAAT TGTTCATTGC	GGONAVIGUE SIDHLLEPDK QASLQPQGYH VYHSKYKPKR DASEVLMEAA LMKLVGATSF S1 GGCACCATCT ACCCTITTIG CCAAATGCCC CTRCACCCATA	120 180 240 300 360 420
50	LALATGLOTH TAASMKTMCS VTALHESVYV LOOSEVITPL LONDIALMKL VPLISKKICN GIGCAEVHKP Seq ID NO: Nucleic Ac: Coding sequ 1 CACCITICNC CCAGGAACTC CTGCTAGTATA ACAGGCATAAAA	PDCSGKYRCE DDMKGHYANV REGCASGHVW WIITAAHCVY WIITAHCVY WIITAHCVY WIITAHCVY WIITAHCV W	LDDLKISPVA SSFKCIELIA ACAGLGFSSY TLQCTACOHR DLYLDFSSTI OPVCLPNSEE FSMLCACVLT DWIHEQMEND QUENCE n #: NM_000 2139 21 TGGGCAGAGG GAATCATCT GGTTCATGGA ACCCAACAC	PDADAVAAQI PDADAVAAQI PCOOVSDCKD VSSDNLKVSS RGYSSRIVOG OVGLUSLLDN NFPDGKUCHT GGVDSCQGDS LKT 1493.2 31 1 AAGCTTCAGA GAGAATATGC TGTGTTTTACG AAGACACAGT	GEDEYRCVRV LEGOPREEPV NMSLLSOMPM PAPSHLVEKI SGNGATEDG GGPLVCQERR 41	GGONAVIGUE SIDHILEPDK QASLOPQGYH VYBBKYKER DASPVLNEAA LMKLVGATSF 51 	120 180 240 300 360 420 60 120 180 240 300
50 55 60	LALATGLOTH TAASMKIMCS VTALHESYYV LCOGSVITPL LGNDIALMKL VPLISNKICN Seq ID NO: Nucleic Ac: Coding sequ CACCITCIGC CCAGGAACTC CTGCTAGTAT TACAGGGATAA AAGAGTAAAA GGACTTCGAG	PDCSGXYRCM DDMSGHYANV REGCASGHVV WITTAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA sei id Accessio Lence: 97 11 ACTGCTCATC CCAGCACGCA CCTTGAACTT AAGGCCGACT GGGACCGACG GGGACCACGA	LDDLKISPVA SSFKCIELIA ACAQLGFPSY TLQCTACOSHR DLYLDFSSNTI DLYLDFSSNTI DLYLDFSSNTI DLYLDFSSNTI DLYLDFSSNTI DLYLDFSSNTI TQUENCE DSHLCACYLT DWHHEQMEND TQUENCE TGUENCACYLT TGUENCE GAATCATCAT AGAGGAGAG AGAGGAGAGG AGAGGAGGAGGA	PDADAVAAQI PDADAVAAQI PDADAVAAQI PDADAVAAQI PSEDAVAAQI PSEDAVAAQI PSESSAVAAQI	GEDEYRCVRV LEGOPREBEV NMSLLSQWPW PAPSHLVBKI SGMGATEDOG GGPLVCQERR 41 AAGCTGCCAAAT TGTGACACATA TCTTCATTCC TGGTCCAC TGGTCCAC AACCAGGCTA AACCAGGCTA	GGONAVIGUE SIDHILEPDIX QASIGPQQYH VYHSKYKPKR DASPVIAHAA LMKLVGATSP 51 GGCACCATCT ACCCTTTTG CCHAATGCCC CTACACCATA AGGCCTGCT AGGCCTGCT GGGAAGTCCT	120 180 240 360 420 60 120 180 240 300 360
50	LALATGLOTH TAASMKIMCS VTALHESVYV LCOGSVITPL LGNDITALMKL VPLISRKICH Seq ID NO: Nucleic Ac: Coding sequ CACCITCIGC CCAGGAACTC CTGCTAGTAT ACAGGAACTC CTGCTAGTAT ACAGGAACTC AGGACTCAGGAACTC AGGACTCAGAACTC CTGCTAGTAT ACAGGAACTC AGGACTCAGA GGACTCAAG	PDCSGKYRCE PDCSGKYRCE PDNSGHYANV REGCASGHVW WIITAAHCVY WIITAAHCVY WIITAHCVY WIITAHCVY WIITAHCVY WIITAHCVY WIITAHCVY WIITAHCVY WIITAHCV WII	LDDLKISPVA SSFKCIELLA SSFKCIELLA ACAQLISPEY TLQCTACSHR DLYLPKSHT OPVCLPNSEE PSHLCAGYLT OWNIECHMEN Quence n #: NM_000 2139 21 I TOGGCCAGAGG GAATCCATCT GGTTCATGGA ACCCAACAC AAGAGGAGGC TCCTTCTGGA	PDADAVAAOI RCDGVSDCKD VSSDNLRVSS VSSDNLRVSS VSSDNLRVSS GYSSRTVGG QVGLVSLLDN NFPDGNVCUM GGVDSCQGDS LKT 1493.2 31 AAGCTTCAGA GAGAAATATGC GAGGTACTC CCACCAGGAA CCACGGGAA CCACCGGGAA	GEDEYRCVRV LEGOPREEPV NNSLLSOMPN PAPSHLVESE SGNGATEDGG GGPLVCQERR 41	GGONAVIGUE SIDHILIPDIX QASIQPQQYH VYHBKYKPKR DASPVINEAA LMKLVGATSF S1 	120 180 240 300 360 420 60 120 180 240 300 360 420
50 55 60	LALATGLOTH TAASMKIMCS VTALHESYYV LCOGSVITPL LCONDIALMKL VPLISNKICN Seq ID NO: Nucleic Ac. CACCITCIGC CACCITCIGC CCAGGAACTC CTGCTAGTAT TACAGGCATAA AAGACTAAAA GGACTTCAGG GGACTCCAG GGACTCCAC GCAC G	PDCSGKYRCE PDCSGKYRCE PDMEGHYARV REGCASGHVW MITTAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA seid Accessio ience: 97 11 ACTGCTCATC CCMGCACGCA CCTTGAACTT AAGGCCCACT GGCACCGACG GGCACCACG GGCACCGAGG GAGGCCAGG GGACCCAGG	LDDLKISPVA SSFKCISLIA SSFKCISLIA SSFKCISLIA SSFKCISLIA SSFKCISLIA SSFKCISLIA TÜÇTRÖJİR DIYLEKSMTİ DIYLEKSMTİ DIYLEKSMTİ DIYLEKSMTİ DIYLEKSMTİ DIYLEKSMTİ DIYLEKSMTİ TÜĞÜCAĞÜĞÜ GANTCCATÇ AĞĞAĞĞĞĞ TÖĞCAĞĞĞ TÜĞÜCAĞĞĞ TÜĞÜCAĞĞĞ	PDADAVAQI RCDGVSDCVO VSSDNLRVSS RCYSSRTVOG GYUSCYSLDN MPPDGWCVFT GGUDSOQDS LKT 1493.2 31 AAGCTTCMGA GAGAATATCC GTGTTTTTACG AAGCACCAGG CCACCAGGGA CCACCAGGGA CCACCAGGGA CCACCAGGGA CCACCAGGGA CCACCAGGGA CCACCAGGGA CCACCAGGGA	GEDEYRCURV LEGGPREEPV INSELISOMEN PAPSHLUSE SGNGATEDGG GGPLVCQERR 41	SGONAVIGUE SIDELLEPDIX QASIG/FQSYH VYHSKYKPKR DASEVIAHAA LMKLVGATSF 51 	120 180 240 360 420 60 120 180 240 300 360
50 55 60	LALATGLOIM TAASMKIMCS VTALESVYU LCOGSVITPL LCOGSVITPL LGNDIALMKI VPLISHKICN GIGCAEVHKP Seq ID NO: CACGITCIOC CCAGGGACTC GCAGGGACTC GCGAGGACTC GTGGTAGTAT ACAGGGATAA AAGAGTAAAA GGACTCCAAG GGACTCCAAG GGACTCCAGG GGACTCCAG	FDCSGKYRCR DDMKGHYANY RESCASGHVW RESCASGHVW MITTARICVY AGRITYSHMI HARDYYGGIS GVYTRYTSFI 11 ACTGCTCATC CCAGCAGGA CCAGCAGGA GCAGCAGG GGAGCCAGG GGAGCCAGG GGAGCCAGG GGAGCCAGG GGAGCCAGG GGAGCCAGG GGAGCCAGG GGAGCCAGG GGAGCCAGG	LDDLRISPVA SSFKCIELIA SSFKCIELIA SSFKCIELIA SSFKCIELIA SSFKCIELIA LODLRISPVA TLQCTA GGBR TLQCTA GGBR TLQCTA GGBR TLQCTA GGBR TLQCTA GGBR TLQCTA GGBR TLQCTA GGBR TLQCTA GGBR TLQCTA GGBR TLQCTA GGBR TLQCTA GGBR TLCTA GGBR	PADDAVAAQI RCDGVSBCKD VSBDILEVSB RGVSBCLVO VGULVSLLDI NPPDGKVCHT GGULVSLDI ANGCTTCMA GGAGATATIC ANGCACAG CCACCAGGA CCACCAGGA GGCCACCAG	GEDETRICTAY LECOPPEEPU MISLISONEN PAPSHILVERI SONGATEDOS GUPLVOGER 41 AAGCTGCCAAAT TCCCACAAT TCTCAATCCAT TCTTCATTCC CATCAGCTT CATCAGCTT CATCAGCTG CATCAGCTG GACCACCTG GACCCACCTG	GGONAVLOVE SIDELLEPDK QASLOPQGYH VYHSKYNFKR DASEVLNEAA LMKLVGATSF SI GGCACCATCT ACCCTITTIG CCHAATGCCC CTHACACCATA AGGCCCAGA AAAGGGAAACCA AAAAGGAAACA AAAAGGAAACA AAAAGAAACAAAAAGAAAAAAAA	120 180 240 360 420 60 120 240 300 420 480 540 600
50 55 60 65	LALATGIOTH TAASMKHNOS VTALMESYVV LOOGSVITHL LOODITAIMML VPLISHRICH GIGCAEVHKE Seq ID NO: Nucleic Ac. Coding sequ 1 1 CACCITCIGC CCAGGAACTC CTGCITATATA ACAGGAACTG CTGCITAGATA ACAGGAACTG GGACTCCAGG GGACTCCAGG GGTTCCAGG GGTTCCAGG CCGGTTGGAA CCGCTTGGAC CCGCTGGAAC CCGCTGAAC CCCTCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCGCTGAAC CCCTCTGAAC CCCTCTGAAC CCCTCTGAAC CCCTCTGAAC	FDCSGKYRCR DDNKGHYANY RECCASGHVW RECCASGHVW RECCASGHVW AFFLTRIENI HERDYSGGLIS GVYTRVISFL 434 DNN secid Accessio- Lence: 97 11 ACGGCTCATC CCMCGCAGCA CCCTTGAACTT AAGGCCACT GGCACCAGCA GCACCCACT GGCACCAGCA CCTTGAACTT TTCTGGAGA TTCCTGGAGC TTTCTGTGCC TTTCTGTGCC	LDDLKISPVA SSFKCIBLIA SSFKCIBLIA SSFKCIBLIA SSFKCIBLIA SSFKCIBLIA DIVLESMIT TÜÇÜTÄ GĞİR DIVLESMIT DIVLESMI	PADAWAQI RCDGVSDCIO VSSINLEVSS RGYSSRIVOG VGLIVSLLIN RPDGVICVT AGGUSCOGIS LICT 19 3.1 1 AGCTTCM2A AGGATATICC CAGGATATICC CAGGATATICC CAGGATACIC GAGGACACA GAGACACAG GAGACACAG GAGACACAG GAGACACAG GAGACACAG GAGACACAG GAGACACAG GAGACACAG GAGACACAG GAGACACAG GAGACACAG CACCAGGAT CACCAGAT CACCAGGAT CACCAGGAT CACCAGGAT CACCAGGAT CACCAGGAT CACCAGGAT CA	GEDETRICTRY LEOOPREEPU NISLISONEN APPSHLIVERI SONGATEDOS GGPLVCOERR 41 AAGCTOCCAA TGGCACAAAT TCTTCATTCC CTGAACCATTA TCTTCATTCC CATTATGGAC GACCACTGG GACCACCAG GACCACCAGG	GOQNAVLOVP SIDELLEPON OASIC/POSTH VYBEKYERE DASPVLMHAA LIKELVGATSP 51 GCCACCATCT ACCCTITTEG CCHARTECC CTRACCCATA AGGCCTGC CGRAATCCC GGRAATCCC GGRAATCCC GGRAATCCC ARAGGAGAT AANGCAGAGA AANCCCTGGA AANCCCCAGA AANCCCCAGA ACCCCAGA	120 180 240 360 420 180 240 360 420 360 420 540 660
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10	AACAAACCTT	TACCASTCTT	AGTGAGCAGC	AACGTAAAAA AAGGTTTTCT	CCRATATTAA	AAAATATCAC	2400
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35	GPYGPKGDVG	PAGLPGPRGP	PGPPGIPGPA	GISVPGKPGQ TGPSGPPGVG	QGPTGAPGPR	GFPGEKGAPG	180 240
	CRMCPTCPPC	POGPPGERGP	EGICKPGAAG	APGOPGIPGT	KGLPGAPGIA	GPPGPPGFGK	300
	DOLDGL/CER	GPAGL/PGGPG	AKCEOGPAGL	PGKPGLTGPP	GRIMGPOGPKG	IPGSHGLPGP	360 420
40	KGETGPAGPA	GYPGAKGERG	SPGSDGKPGY	PGKPGLDGPK RGPIGPPGIP	GNPGLPGPKG	CECEPTOR	480
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	ATCANA A COC	PACABGGTCCG	CATCGAAGGC	TCCCTGTGGT	GGACCTACAC	AAGCAGCATC	420
5	TTCTTCCGGG	TCATCTTCGA	AGCCGCCTTC	ATGTACGTCT	TCTATGTCAT	GTACGACGGC	480 540
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30	CACCGAGCGC	TGGTCGCCGC	TCTCCTTCCG	GTGAGTCCCA	GCCCCGAGTT	GGCTCTGGCG	120 180
30	CLOSTOCATO	CGCCAGTGCC	AGATOTOTOG	AGCCTTGGTG	TTCTTTCCTA	TGAATTTTTA	240
	GTTGGGAAGC	CTCCTTTTGA	GGCAAACGAA	GTCCATGTAA	GCAAAGAAAC	CATCGGGAAG	300
	ATTTCAGCTG	CCAGCAAAAT ACAGCGTCGG	GATGTGGTGC	TOGGCTGCAG	TOGACATCAT	TOCCATCACA	360 420
35	CHCHCHCLCC	CTCTGGACAT	CAGCCCCCGAG	AGGGTCAGAG	TOGGGAGCATT	CCAGTTCAGT	480
	TOTACTOTTC	ATCTGGAATT GGATGGTTTT	CCCCTTGGAT	TCATTTTCAA	CCCAACAGGA	AGTGAAGGCA	540 600
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	GCCGTGCGGG	CAGAGCTGGA ATCTGTTCAA	GGAGATCACA	GGCAGCCCAA	AGCATUTGAT GGLAGCTGTG	CAGCCGGCAG	1560 1620
55	COCCCACCO	GCCCGGLCLCL	AGCCCTGGAC	CTOGTCTTCA	TGTTGGACAC	CTCTGCCTCA	1680
	GTAGGGCCCG	AGAATTTTGC CTGACGTGAC	TCAGATGCAG	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	1740 1800
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C 0	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	1920 1980
60	GGGAGAGGGG	AGAGGGGTGC CAGAGGATGC	AGCCGTTCCT	GCCCAGAAGC	TGAGGAACAA	TGGCATCTCT	2040
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70	GTCTGTGCCC	CAGGTCCTTA	G				
70	Pog ID NO.	441 Protei	n geometre				
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	1	11	21	31	41	51	
75	ī	ī	Ī	Ĭ.	Ĭ.	Ī	
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	DOSNEWSKOS	PERSKHEATT	VCDGLDISPE	RVRVGAFOFS	STPHLEFPLD	SFSTQQEVKA	180
80	RIKRMVFKGG	RTETELALKY	LLHRGLPGGR	NASVPQILII	VTDGKSQGDV	ALPSKQLKER	240 300
80						CALKLSLECK	360
	VDLLFLLDSS	AGTTLDGFLR	AKVFVKRFVR	AVLSEDSRAR	VGVATYSREL	LVAVPVGBYQ	420
	DVPDLVWSLD	GIPFRGGPTL	TGSALRQAAE	RGFGSATRTG	DPODLFNOIP	LTESHSEDEV	480 540
85							600
	APGURTEPP	AAML RATSOA	PYLOGVGSAG	TALLHIYDKV	MTVQRGARFG	VPKAVVVLTG ADLRYHQDVL	660 720
	SKIGAEDAAVP	MUKLIKNNGIS	APARCAGRAT	- OF GREWINGS	ouanvAMI	,	, 20

WO 02/086443 PCT/US02/12476 TEWLOGBARQ PVNLCKPSPC MNBGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ 780 GWILETPLER WAPPQBGSSR TPPSNYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 442 DNA sequence Nucleic Acid Accession #: Bos sequence

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	AAGTCCCAGG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACTGTG	540
20	TTTGCTGTGG	GGGTCAGGTT	TCCCAGGTGG GGCTGAGCAG	GAGGAGCIGC	CCACCAGGG	CAGUGAGUUT	600 660
20	ACCCTCACCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
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30	CAGGATGTGC	CTGACCTGGT	CTGGAGCCTC GCAGGCGGCA	GATGGCATTC	CCTTCCCTCC	TOGCCCCACC	1260 1320
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	GCTGGGAGG	GCCCCCACTG	GCCCCTGAGG	GAGTGGAGCT	CTTGCTCTGT	ATGTGTGAGC	2280 2340
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	Protein Acc	cession #:	Eos sequenc	•			
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60	MANAGEMENT	PPINALAOPP	ROQHVLLAEQ	URDATMCLES	TLESSATOS	ATPOCRVEAN	240
00	PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSNK	RVFLTHPATC	YRTTCPGPCD	300
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	RAKVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	ODALDPAR	DGIPFRGGPT	420
65			GQDRPRRVVV SDPQDLFNQI				480 540
O)	ENVIOLEDEE!	OSEVERCALO	FEVNPDVTQV	GLVVYG90VO	TAPGLDTEPT	RAMERAISO	600
	APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDAAV	PAOKLRINGI	660
	SVLVVGVGPV	LSEGLERLAG	PRDSLIHVAA	YADLRYHODV	LIEWLCGEAK	QPVNLCKPSP	720
70			GWEGPHCENR	EMSSCSACAS	QGWILETPLR	HMADVQEGSS	780
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Seq ID NO: 444 DNA sequence Mucleic Acid Accession #: Eos sequence Coding sequence: 89..2356

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80		TTTTCCAGAG					180
		GGGAAGATTT					240
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	ACTTGCTCTG	AAATACCTTC	TGCACAGAGG	GTTGCCTGGA	GGCAGAAATG	CTTCTGTGCC	540
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PCT/US02/12476

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		ACCAACGCCC					780
		TGCAGGGTCG					840
5		GGCAATGCCC					900
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		TGCCCAGGCC					1020
		CTGGACGGCT					1080
10		AAGCTGAGCC					1140
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		GTGCCTGTGG					1320
		TTCCGTGGTG					1380
		GGGAGCGCCA					1440
15		TCACACTCCG					1500
		CTGCTGGGTG					1560
		AAGCATGTGA					1620
		GGGAAGCTGT					1680
••		ATGTTGGACA					1740
20		AGAAGCTGTG					1800
		TATGGCAGCC					1860
		CTGCGGGCCA					1920
		CTGCACATCT					1980
~ ~		GCTGTGGTGG					2040
25		CTGAGGAACA					2100
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		CTCTGCAAAC					2280
20		CGCTGCAAGT					2340
30		CCCTGAGGCA					2400
		GAGAAGGCCT					2460
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		TAGCGGCCTG				AGAATGTTGT	2760
	TGACACAGTA	ATGCCCAGCA	GAGGCCTTTA	CTAGAGCATC	CTTTGGACGG		
40		445 Protein					
	Procett Wo	cenaton #: 1	oo ocquence	•			
	1	11	21	31	41	51	

	1	11	21	31	41	51	
	ī	î	ĩ	ĩ.	í	Ĩ.	
		CVFLFSRVPP					60
45		KHFAITVCDG					120
	MVFKGGRTET	ELALKYLLHR	GLPGGRNASV	PQILIIVTDG	KSQGDVALPS	KQLKERGVTV	180
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	LTGSALROAA	ERGFGSATRT	GODRPRRVVV	LLTESHSEDE	VACPARHARA	RELLLLGVGS	480
	EAVRAELEEI	TGSPKHVMVY	SDPQDLFNQI	PELQGKLCSR	QRPGCRTQAL	DLVFMLDTSA	540
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55	SATAAGAGAA	LSEGLRRLAG	PRDSL IHVAA	YADLRYHQDV	LIEWLCGEAK	QPVNLCKPSP	720
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	CCGATCTGGG	CACCOGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCGCAGAA	AGATCTCAGA	180
	GTAAAGAAGA	ACTTAAAGAA	ATTCAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTOGTCA	240
	TCCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAACAC	GAGGCTGCAG	300
	TCAGTTCGGG	AAGGCTGTAG	GACCCGCAGC	CAGTGCAGGC	ACTOTOGACO	TCTCAGGGTG	360
70	GCGATGAAGT	TTCCAGCGCG	GAGTA CCAGG	GGAGCAACCA	ACAAAAAAGC	AGAGTCCCGC	420
	CAGCCCTCAG	AGAATTCTGT	GACTGATTCC	AACTCCGATT	CAGAAGATGA	AAGTGGAATG	480
	AATTTTTTTGG	AGAAAAGGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAAACTC	540
	ATGTCTGAAT	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGGAA	GACATCCCCT	CCCAGGCTCC	600
	GACTCACAAT	CARGGAGACC	GCGAAGGCGT	ACATTCCCGG	GTGTTGCTTC	CAGGAGAAAC	660
75	CCTGAACGGA	GAGCTCGTCC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCCTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
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		CGCATATAAT					900
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85		ATTTGCTGCC					1320
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	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440

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	TOTALTICON	TATTTTATTT	ACTIGGIGIT	GARATAGCCC	TCATAAAACC	TAAGCACTTG	1620
	CARACACAAT	ATTACTACTA	ACTRACTAGA	TCTATTGAAT	TTCAGAGAAG	AGCCTTCTAA	1680
5	CTTGTTTACA	CAAAAACGAG	TATGATTTAG	CACTCATACT	AGTTGAAATT	TTTAATAGAA	1740
	TCAAGGCACA	AAAGTCTTAA	AACCATGTGG	CARCETTAGG	TAATTATTGC	GACTTANTTT	1860
	CTCCTAATTT	CTTCTGCCCG	AAGGGTAAGT	GGTGCGTCCA	GCTTA CACGA	TCATAATTCA	1920
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10	ATGAGTAAGC	TGATTTGAAT TCACATGTAA	TTTCAGTATA	AAACTTTAGT	ATAATTGTAG	TTTGCAAAGT	2040
	TTATTTCAGT	AAACTAGTCT	GTGGTTCTTT	GCAGTTTCTT	GTAAATTTAT	AAACCAGGCA	2160
	CARCOTTCAR	GTTTAGATTT	TRACCACTTT	TATAACAATG	ATAAGTGCCT	TTTTGGAGAT	2220
1.5	CTEACTTTA	OCAGETTOTT.	AACCTGACAT	CTCTGCCAGT	CTAGTTTCTG	GGCAGGTTTC	2280 2340
15	CTGTGTCAGT	ATTCCCCCTC ATGTCCAATT	CTCTTTGCAT	TAATCAAGGT	ATTTGGTAGA	GGTGGAATCT	2340
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	TATACAAAAG	TTTATTTTAA	TAATAAAATG	TTTGTTCTAA	ллалалала		
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	IIOCOIN NOC						
	1	11	21	31	41	51	
25	MUNDERSOAD	LRVKKNLKKF	DYUKT, TAMET	SSSSDDSCDS	PASDNFANTE	LOSVREGCRT	60
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	GGGCCCTGTC	TCTCAGGCTC GTGTGGTGGG	TOGGTUTCC	CTGCACTGTC	ATTCTTGGCC	TTGGCAGGTC	660
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	GEOGRACICAGG	AGGGTGACAG	TGGTGGGCCC	CTGATGTACC	AATCTGACCA	GTGGCATGTG	1200
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60	AAGGTCTCAG	CCTATCTCAA	CIGGATCTAC	AATGTCTGGA	AGGCTGAGCT	GTAA	
	Sea ID NO:	449 Protei	n semience				
	Protein Acc	cession #:	NP_0639	47.1			
65	1	11	21	31	41	51	
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	MLQDPDSDQP	LNSLDVKPLR	KPRIPMETFR	KVGIPIIIAL	LSLASIIIVV	VLIKVILDKY	60
	YFLOGOPLHF	IPRKQLCDGE FTEALAETAC	LDCPLGEDEE	HCVKSPPEGP	AVAVRLSKOR	STLQVLDSAT	120 180
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20	ATGATGGACA	ATAGGATCTG	GGGCCCTGGC	GGCTTGGACC	ATAGCGGAAG	GACCCTCCCT	1560
	ATAGGCCAGA	ATTTTCCAAT	TAGAGGAATT	CAGTTATATG	ATGGCCCCAT	CAACATCCAA	1620 1680
	COCCTGAATA	ATGCCTGGCA	GAGCTGCCCC	CATAACAACG	TGACCOGCAT	TOCCTTTGAG	1740
	GACGTTCCGA	TTACTTCCAG	AGTGTTCTTC	GGAGAGCCTG	GGCCCTGGTT	CAACCAGCTG	1800
25	GACATGGATG	GGGATAAGAC	ATCTGTGTTC	CATGACGTCG	ACGGCTCCGT	GTCCGAGTAC	1860
	CCTGGCTCCT	ACCTCACGAA GGAGAGGGGC	GAATGACAAC	TGGCTGGTCC	GGCACCCAGA	CIGCATCAAT	1920
		GTAACCTGCG					2040
	TACCTGGAGG	GGGGGCTCAC	CAGGAGCACC	CATTACCAGC	AATACCAACC	GGTTGTCACC	2100
30	CTGCAGAAGG	GCTACACCAT	CCACTGGGAC	CAGACGGCCC	CCGCCGAACT	CGCCATCTGG	2160
	CTCATCAACT	TCAACAAGGG	CGACTGGATC	CGAGTGGGGC	TCTGCTACCC	GCGAGGCACC	2220
		TOCTCTOGGA GGACCTTGCA					2280
	TACTACTGGG	ACGAGGACTC	AGGGCTGTTG	TTCCTGAAGC	TGAAAGCTCA	GAACGAGAGA	2400
35	GAGAAGTTTG	CTTTCTGCTC	CATGAAAGGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
	CCAAAGAACG	CAGGCGTCAG	TGACTGCACA	GCCACAGCTT	ACCCCAAGTT	CACCGAGAGG	2520
		ACGTGCCGAT AGGTGAAGAT					2580 2640
	TTCGCTTACA	TTGAAGTGGA	TGGGAAGAAG	TACCCCAGTT	CGGAGGATGG	CATCCAGGTG	2700
40	GTGGTGATTG	ACGGGAACCA	AGGGCGCGTG	GTGAGCCACA	CGAGCTTCAG	GAACTCCATT	2760
		TACCATGGCA					2820
	STGCTTATGG	CATCAAAGGG CAGACAGGGG	AAGATACGTC	TCCAGAGGCC	CATGGACCAG	AGTGCTGGAA	2880 2940
	GGCAGCTTCC	GGCCCATCTG	GGTGACACTG	GACACTGAGG	ATCACABAGC	CAAAATCTTC	3000
45	CAAGTTGTGC	CCATCCCTGT	GGTGAAGAAG	AAGAAGTTGT	GAGGACAGCT	GCCGCCCGGT	3060
	GCCACCTCGT	GGTAGACTAT	GACGGTGACT	CTTGGCAGCA	GACCAGTGGG	GGATGGCTGG	3120
	GTCCCCCAGC	CCCTGCCAGC	TGGTGCTGC	GAAGGCCGTG	ACTCARGCCCT	GATOGGCCAA	3180 3240
	CCCCTGGGGC	GGTGCTGGCC	AATGCTGGAA	ACATTCACTT	TCCTGCAGCC	TCTTGGGTGC	3300
50	TTCTCTCCTA	TCTGTGCCTC	TTCAGTGGGG	GTTTGGGGAC	CATATCAGGA	GACCTGGGTT	3360
	GTGCTGACAG	CAAAGATCCA	CTTTGGCAGG	AGCCCTGACC	CAGCTAGGAG	GTAGTCTGGA	3420
	GGGCTGGTCA	CTTGGCCTTA	CCCATGGTCT	TCAGCAGACA	AGTGAGGGTG	GTAAATGTAG	3480 3540
	GATTAGGAGC	TOGGGGTAGAA	CTGGCTATCC	TTGGGGGAAGA	GGCAAGCCCT	GCCTCTGGGC	3600
55	GTGTCCACCT	TTCAGGAGAC	TTTGAGTGGC	AGGTTTGGAC	TTGGACTAGA	TGACTCTCAA	3660
		agitctgaga			TCACATGGTA		3720
	AACAGTTCAT	GGATATCCAC AACTAATGCC	TGATATCCAT	GATGCTGGGT	CCAGTAGGGC	ACACGGGATG	3780 3840
	GTCCATGTGC	ACTGCAATGC	CAGGTTGAGG	AATCACAGAG	ACCTABANTO	GAGGCCAGTCAG	3900
60	CCATTTCAGA	GOGGAGGCTC	AGGAAGGCTT	CTTGCTTACA	GGAATGAAGG	CTGGGGGCAT	3960
	TTTGCTGGGG	GGAGATGAGG	CAGCCTCTGG	AATGGCTCAG	GGATTCAGCC	CTCCCTGCCG	4020
	CTGCCTGCTG	AAGCTGGTGA AGTGTGGTCA	CIACGGGGTC	GCCCTTTGCT	CACGTCTCTC	TGGCCCACTC	4080 4140
	ATTICACTOR	CAGGCAGCCC	TGCCTCTGAC	TOCALGAGG	TGBAGTCCAC	AGARGTGAGG	4200
65	TCCTGCCTTA	GGGCCTCATT	TGCTCTTCAT	CCAGGGAACT	GAGCACAGGG	GGCCTCCAGG	4260
	AGACCCTAGA	TGTGCTCGTA	CTCCCTCGGC	CTGGGATTTC	AGAGCTGGAA	ATATAGAAAA	4320
	TATCTAGCCC	AAAGCCTTCA CTAAGGGAGG	TTTTAACAGA	TGGGGAAAGT	GAGCCCCCAA	GATGGGAAAG	4380
		AACCOGCCCC					4440 4500
70	GACAAGTCCC	CTCGAAGGAA	AGGAAATGAC	TAGAGTAGAA	TGACAGCTAG	CAGATCTCTT	4560
	CCCTCCTGCT	CCCAGCGCAC	ACAAACCCCGC	CCTCCCCTTG	GTGTTGGCGG	TCCCTGTGGC	4620
	CTTCACTTTG	TTCACTACCT	GTCAGCCCAG	CCTGGGTGCA	CAGTAGCTGC	AACTCCCCAT	4680
		TGTTTCTGGT					4740 4800
75		AGTOUCTTTC					4860
	ATAGAGAGCC	CAAAGAGCTC	CTGTAAGAGG	GAGAACTCTA	TCTGTGGTTT	ATAATCTTGC	4920
	ACGAGGCACC	AGAGTCTCCC	TGGGTCTTGT	GATGAACTAC	ATTTATCCCC	TTTOCTGCCC	4980
		CTCTTTCCTT GTCCAAGAGT			CCCTCCACCC		5040 5100
80	CCACCAAACA	TCTTTCAGCT	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATOG	5160
	CIGCITCAAA	GGCCAGAGTC	ACAGGAAGGA	CTTCTTCCAG	GGAGATTAGT	GGTGATGGAG	5220
		AAATGACCTC			TTTGTTGAGT		5280
	CIAATGCAAG	GTCTTTGGCT	TUTGAACCAC	TIAGGATGTG	ATCACTTTCA TCTATTTGAA	AGTTCTCAC*	5340 5400
85	GTTGTACATA	TGTTTCACAG	TACAGGATCT	GTACATAAAA	GTTTCTTTCC	TAAACCATTC	5460
	ACCAAGAGCC	AATATCTAGG	CATTTTCTTG	GTAGCACAAA	TTTTCTTATT	GCTTAGAAAA	5520
	TTGTCCTCCT	TGTTATTTCT	GTTTGTAAGA	CTTAAGTGAG	TTAGGTCTTT	AAGGAAAGCA	5580

WO 02/086443 ACCICCTCT GAMATGCTTG TCTTTTTCT GTTGCCGAAA TAGCTGGTCC TTTTTCGGGA 5640
GTTAGATGTA TAGAGTGTTT GTATGTAAAC ATTTCTTGTA GGCATCACCA TGAACAAAGA 5700

TATATTTTCT ATTTATTAT TATATGTCCA CTTCAAGAAG TCACTGTCAG AGAAATAAAG

Sec ID NO: 451 Protein seque Protein Accession #: XP 051860.2

10 MICHAELSTEU VYKKOODYRF ACYDRORACH SYRVRFLOSK PURPKLTUTI DINVISTILM LEDNVOSHKP GDTLVIASTD YSMYQAEEPQ VLPCRSCAPN QVKVAGKPMY LHIGEEIDGV DMRAEVGILS RNIIVMGEME DKCYPYRNHI CNFFDFDTFG GHIKFALGFK AAHLEGTELK 180 15 HMGQQLVGQY PIHPHLAGDV DERGGYDPPT YIRDLSIHHT FSRCVTVHGS NGLLIKDVVG 240 YNSLGHCPPT EDGPEERNTF DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300 DCHAVSTFWM ANPANNLING AMAGSEETGF WFIFHHVPTG PSVGMYSPGY SEHIPLGKFY 360 NNRAHSNYRA GMIIDNGUKT TEASAKDKRP FLSIISARYS PHODADPLKP REPAIIRHFI 420 AYKNODHGAN LRGGDVWLDS CRFADNGIGL TLASGGTPPY DDGSKQEIKN SLFVGESGNV 20 GTEMMENRIW GPGGLDHSGR TLPIGQNFPI RGIQLYDGPI NIQNCTFRKF VALBGRHTSA 540 LAFRIANAWQ SCPHRIVTGI AFEDVPITSR VFFGEPGPWF NQLDMDGDKT SVFHDVDGSV SEYPGSYLTK HDNNLVRHPD CHNVPDWRGA ICSGCYAOMY IOAYKTSWLR MKIIKNDPPS 600 660 HPLYLEGALT RSTHYGOYOP VVTLOKGYTI HWDOTAPABL AIWLINFNKG DWIRVGLCYP 720 RGTTPSILSD VHNRLLKOTS KTGVPVRTLO MDKVBOSYPG RSHYYWDEDS GLLPLKLKAQ 780 25 NEREKFAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLFGSQLK 840 TKDHFLEVKM ESSKOHFFHL WNDFAYIEVD GKKYPSSEDG IQVVVIDGNQ GRVVSHTSFR 900 960 NSILOGIPWO LENYVATIPD NSIVLMASKG RYVSRGPWTR VLEKLGADRG LKLKEQMAFV GENGREBOTH WILDTERNEY KIROVURIPU WKKKKI.

31

30 Seq ID NO: 452 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 261..2861

35 GAGCTAGOGC TCAAGCAGAG CCCAGCGCGG TGCTATCGGA CAGAGCCTGG CGAGCGCAAG COGCCCCGGG ACCCAGCGGG GCTGAGCGCG GCCAGGGTCT GAACCCAGAT TTCCCAGACT 120 ACCURACY COCCURACY ACCURAGE ACCURAGE CULTURAL CACCURACY 180 ACCITICAGGO CICCITAGGOT COTOGCOCGO GAGGOGIGAC ACTOTOTOGO CIACAGACCO 40 AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCCTC TTCAAGGCCA TGCTGACCAT CAGCTGGCTC ACTCTGACCT GCTTCCCTGG GGCCACATCC ACAGTGGCTG 360 CTGGGTGCCC TGACCAGAGC CCTGAGTTGC AACCCTGGAA CCCTGGCCAT GACCAAGACC ACCATGTGCA TATCGGCCAG GGCAAGACAC TGCTGCTCAC CTCTTCTGCC ACGGTCTATT 420 480 CCATCCACAT CTCRGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT TGCGAACCCG GCACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGCCCTCT 600 GCCCTTTCCA GGCCAATTTC ACCATCATTT TGTATGGAAG GGCTGATGAA GGTATTCAGC --CGGATCCTTA CTATGGTCTG AAGTACATTG GGGTTGGTAA AGGAGGCGCT CTTGAGTTGC 720 ATGGACAGAA AAAGCTCTCC TGGACATTC TGAACAAGAC CCTTCACCCA GGTGGCATGG CAGAAGGAGG CTATTTTTT GAAAGGACCT GGGGCCCCCU TGGAGTTATT GTTCATGTCA 780 50 TCGACCCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA 900 AAGAGAGTGA ACGTCTGGTC CAGTATTTGA ACGCGGTGCC CGATGGCAGG ATCCTTTCTG 960 TTGCAGTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA 1020 ARTTOGRAM CALACTTC CTGCACCTTG CATTTAGACA CCCTTGGAGT TTTCTAACTG 1080 TGAAAGGAAA TCCATCATCT TCAGTGGAAG ACCATATTGA ATATCATGGA CATCGAGGCT 1140 55 CTGCTGCTGC CCGGGTATTC AAATTGTTCC AGACAGAGCA TGGCGAATAT TTCAATGTTT 1200 CTTTTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTCGAT CATGATAAAG 1260 TATCTCAGAC TAMAGGTGGG GAGAMANTT CAGACCTCTG GAMAGCTCAC CCAGGAMAMA 1320 TATGCAATGG TCCCATTGAT ATACAGGCCA CTACAATGGA TGGAGTTAAC CTCAGCACGG AGGTTGTCTA CAAAAAAGGC CAGGATTATA GGTTTGCTTG CTACGACGG GGCAGAGCCT 1380 60 GCCGGAGCTA COSTUTACIOS TECENTETES GGAAGCCTGT GAGGCCCAAA CECACAGTCA CCATEGACA CAATGTGAACA AGCACCATTC TGAACTTGGA GGATAATGTA CAGTCATGGA 1500 1560 AACCTGGAGA TACCCTGGTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAGAGT 1620 TCCROSTGCT TCCCTGCAGA TCCTGCGCC CCAACCAGGT CAAAGTGGCA GGGAAACCAA
TGTACTGCA CATCGGGAG GAGATAGAGG GCGTGGACAT GCGGGGGGAG GTTGGGCTTC 1680 65 TGAGCCGGAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800 1860 ACATCTGCAA TTTCTTTGAC TTCGATACCT TTGGGGGGCCA CATCAAGTTT GCTCTGGGAT TERROGERGE RESETTINGED ORGANISATION TO BE RESETTED ORGANISATION CTROTTENED 1920 AGTACCCGAT TCACTTCCAC CTGGCCGGTG ATGTAGACGA AAGGGGAGGT TATGACCCAC 1980 CCACATACAT CAGGGACCTC TCCATCCATC ATACATTCTC TCGCTGCGTC ACAGTCCATG 2040 70 GCTCCSATGG CTTGTTGATC AAGGACGTTG TGGGCTATAA CTCTTTGGGC CACTGCTTCT 2100 TCACOGAAGA TGOGCCOGAG GAACGCAACA CTTTTGACCA CTGTCTTGGC CTCCTTGTCA AGTITIGAAC COTOCTOCCO TOGGACOGTG ACAGCAAGAT GTGCAAGATG ATCACAGAGG 2220 ACTOCTACCO AGGGTACATO COCAAGOCCA GGCAAGACTG CAATGCTGTG TOCACCTTCT GGATGGCCAA TOCCAACAAC AACCTCATCA ACTGTGCCGC TGCAGGATCT GAGGAAACTG 2280 GATTITIGGTT TATTITITICAC CACGITACCAA COGGCCCCTC CGTGGGAATG TACTCCCCCAG 2400 GTTATTCAGA GCACATTCCA CTGGGAAAAT TCTATAACAA CGGAGCACAT TCCAACTACC GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCACCGA GGCCTCTGCC AAGGACAAGC 2460 2620 GGCCSTTCCT CTCAATCATC TCTGCCAGAT ACAGCCCTCA CCAGGACGCC GACCCGCTGA 2580 AGCCCTCGGA GCTGGCCATC ATCAGACACT TCATTGCCTA CAAGAACCAG GACCACGGGG 2640 80 CCTGGCTGCG CGGCGGGGAT GTGTGGCTGG ACAGCTGCCA TTTCAGAGGG GAGGCTCAGG AAGGCTTCTT GCTTACAGGA ATGAAGGCTG GGGGCATTTT GCTGGGGGGA GATGAGGCAG 2760 CCTCTGGAAT GGCTCAGGGA TTCAGCCCTC CCTGCCGCTG CCTGCTGAAG CTGGTGACTA 2820 COGGOTONIC CHINGCICAL GUCUCTONO CUCACTUANG ANGRAGAST GUGGTUAGAG 2880 OGGAGCAATG GGCTTTGCTG CTTATGAGCA CAGAGGAATT CAGTCCCCAG GCAGCCCTGC 2940 85 CTCTGACTCC AAGAGGGTGA AGTCCACAGA AGTGAGCTCC TGCCTTAGGG CCTCATTTGC 3000 TCTTCATCCA GGGAACTGAG CACAGGGGGC CTCCAGGAGA CCCTAGATGT GCTCGTACTC 3060 CCTCGOCCTG GGATTTCAGA GCTGGAAATA TAGAAAATAT CTAGCCCAAA GCCTTCATTT 3120

PCT/US02/1	2470

	WO 02/	086443					
	TARCAGATOG	GGAAAGTGAG	CCCCCAAGAT	GGGAAAGAAC	CACACAGCTA	AGGGAGGGCC	3180
	TGGGGAGCCC	CACCCTAGCC	CTTGCTGCCA	CACCACATTG	CCTCAACAAC	CGGCCCCAGA	3240
	GTGCCCAGGC	ACTCCTGAGG	TAGCTTCTGG	AAATGOOGAC	AAGTCCCCTC	GAAGGAAAGG	3300
5	AAATGACTAG	agtagaatga	CAGCTAGCAG	ATCTCTTCCC	TCCTGCTCCC	AGCGCACACA	3360
2	AACCCGCCCT	CCCCTTGGTG	TTGGCGGTCC	CTGTGGCCTT	CACTTTGTTC	ACTACCTOTC	3420
	AGCCCAGCCT	GGGTGCACAG	TAGCTGCAAC	TCCCCATTGG	TGCTACCTGG	CTCTCCTGTC	3480
	TCTGCAGCTC	TACAGGTGAG	OCCCAGCAGA	GGGAGTAGGG	CIUGUCATUI	COCCUMENTO	3600
	CCAATTTGGC	TGATCTTGGG TGCCCTGCTC	TGTCTGAACA	GCIATIOGGI	CCMCCCCMGI	acacemormo	3660
10	TUCTUCTON	AACTCTATCT	CECCETTATA	PECCENCELLAIN	AGGCACCAGA	anciverna	3720
10	CECTODOGAG	GAACTACATT	MARCOCCUTTY	CCTCCCCCAA	CCACAAACTC	TTTCCTTCAA	3780
	AGAGGGGGGGG	CCTGGCTCCC	TUCCOCCIA	THEACTCATE	AGACTCGGTC	CARGAGTCCA	3840
	TTCCCCCACCT	GGGAGCCAAC	TOTTCAGGGAG	GTCTTTCCCA	CCAAACATCT	TTCAGCTGCT	3900
	GGGAGGTGAC	CATAGGGCTC	TGCTTTTAAA	GATATGGCTG	CTTCAAAGGC	CAGAGTCACA	3960
15	CONTROVERCE	CTTVVCACCCA	CATTACTYCE	CATRODAGAGO	ASSETTIONS.	TGACCTCATG	4020
	TCCTTCTTGT	CCACGGTTTT GGATGTGATC	GTTGAGTTTT	CACTOTTOTA	ATGCAAGGGT	CTCACACTGT	4080
	GAACCACTTA	GGATGTGATC	ACTITICAGGT	GGCCAGGAAT	GTTGAATGTC	TTTGGCTCAG	4140
	TTCATTTAAA	AAAGATATCT	ATTTGAAAGT	TCTCAGAGTT	GTACATATGT	TTCACAGTAC	4200
••	AGGATCTGTA	CATAAAAGTT	TCTTTCCTAA	ACCATTCACC	AAGAGCCAAT	ATCTAGGCAT	4260
20	TTTCTTGGTA	CCACAAATTT	TOTTATTGCT	TAGAAAATTG	TCCTCCTTGT	TATTTCTGTT	4320
	TGTAAGACTT	AAGTGAGTTA	GGTCTTTAAG	GAAAGCAACG	CTCCTCTGAA	ATGCTTGTCT	4380
	TTTTTCTGTT	GCCGAAATAG	CTGGTCCTTT	TTCGGGAGTT	AGATGTATAG	AGTGTTTGTA	4440
	TGTAAACATT	TCTTGTAGGC	ATCACCATGA	ACAAAGATAT	ATTTTCTATT	TATTTATTAT	4500
25	ATGTGCACTT	CARGAAGTCA	CTGTCAGAGA	AATAAAGAAT	TGTCTTAAAT	GTCATGATTG	4560 4620
25	GAGATGTCCT	TTGCATTGCT	TGGAAGGGGT	GTACCTAGAG	CCAAGGAAAT	TGGCTCTGGT	4620
		TTTGCTGTTA		CATACAAAGG	ATGTCAMAN	MANAGAMAN	4000
	AAAAAAAAA	AAAAAAAAA	AA				
	C TD NO.	453 Protein					
30	Protein Ace	ession #: 1	Los semenos				
50	PIOCEIN NO	egeton #+ 1	soa sequenci	•			
	1	11	21	31	41	51	
	Ī	Ī-	ī	Î.	1	1	
	MGAAGRODFL	PKAMLTISWL	TLTCFPGATS	TVAAGCPDQS	PELQPWNPGH	DODHHVHIGO	60
35	GKTLLLTSSA	TVYSIHISEG	GKLVIKDHDE	PIVLRTRHIL	IDNGGELHAG	SALCPFOGNE	120
	TITLYCODADE	GEODDDVVGI.	KYTGUGKGGA	LELHGOKKLS	WIFINKTINE	GGMAEGGYFF	180
	ERSWGHRGVI	VHVIDPKSGT	VIHSDRFDTY	RSKKESERLV	QYLNAVPDGR	ILSVAVNDEG	240
	SRNLDDMARK	VHVIDPKSGT AMTKLGSKHF	LHLGFRHPWS	FLTVKGNPSS	SVEDHIEVHG	HRGSAAARVF	300
	KLFOTEHGEY	FNVSLSSEWV	ODVENTENED	HDKVSOTKGG	EKISDLWKAH	PCKICNRPID	360
40	10ATTMDGVN	LSTEVVYKKG QSWKPGDTLV	QDYRFACYDR	GRACKSYRVR	FLCGKPVRPK	LTVTIDTNVN	420
	STILNLEDNV	QSWKPGDTLV	IASTDYSMYQ	AEEFQVLPCR	SCAPNOVKVA	GKPMYLHIGE	480
	BIDGVDMRAB	VGLLSRNIIV	MGEMEDICYP	YRNHICNFFD	PDTFGGHIKF	ALGFKAAHLE	540
							600
	GIBTKHMOOO	PAGGISTULU	PYCDADPECO	IDPFITIRDE	PIUNITANCA		
10	KDVVGYNSLG	HCFFTEDGPE	ERNTFDHCLG	YDPPTYIRDL LLVK9GTLLP	SDRDSKMCKM	ITEDSYPGYI	660
45	PKPRODCNAV	HCFFTEDGPE	NLINCAAAGS	BETGFWFIFH	HVPTGPSVGM	YSPGYSEHIP	660 720
45	PKPRQDCNAV LGKPYHNRAH	STPHMANPHN SNYRAGMIID	NLINCAAAGS NGVKTTEASA	BETGFWFIFH KDKRPFLSII	HVPTGPSVGM SARYSPHODA	YSPGYSEHIP DPLKPREPAI	560 720 780
45	PKPRQDCNAV LGKFYHNRAH IRHFIAYKNO	STPWMANPNN SNYRAGMIID DHGAWLRGGD	NLINCAAAGS NGVKTTEASA VWLDSCHFRG	BETGFWFIFH KDKRPFLSII	HVPTGPSVGM SARYSPHODA	YSPGYSEHIP DPLKPREPAI	660 720
45	PKPRQDCNAV LGKFYHNRAH IRHFIAYKNO	STPHMANPHN SNYRAGMIID	NLINCAAAGS NGVKTTEASA VWLDSCHFRG	BETGFWFIFH KDKRPFLSII	HVPTGPSVGM SARYSPHODA	YSPGYSEHIP DPLKPREPAI	560 720 780
	KDVVGYNSLG PKPRQDCNAV LGKFYHNRAH IRHFIAYKNQ FSPPCRCLLK	HCPFTEDGPE STPWMANPNN SNYRAGMIID DHGAWLRGGD LVTTGSPFAH	ERNTFDHCLG NLINCAAAGS NGVKTTEASA VWLDSCHFRG VSLAHS	BETGFWFIFH KDKRPFLSII	HVPTGPSVGM SARYSPHODA	YSPGYSEHIP DPLKPREPAI	560 720 780
45	KDVVGYNSLG PKPRQDCNAV LGKFYNNRAH IRHFIAYKNQ FSPPCRCLLK	HCPFTEDGPE STFWMANPKN SNYRAGMIID DHGAWLRGGD LVTTGSPFAH 454 DNA 88:	ERNTFDHCLG NLINCAAAGS NGVKTTEASA VWLDSCHFRG VSLAHS	ELVKSGTLLP BETGFWFIPH KDKRPFLSII EAQEGFLLTG	HVPTGPSVGM SARYSPHODA	YSPGYSEHIP DPLKPREPAI	560 720 780
	KDVVGYNSLG PKPRQDCNAV LGKFYNNRAH IRHFIAYKNQ FSPPCRCLLK Seq ID NO: Nucleic Ac:	HCPFTEDGPE STFMMANPKN SNYRAGMIID DHGAWLRGGD LVTTGSPFAH 454 DNA 80: id Accession	ERNTFDHCLG NLINCAAAGS NGVKTTEASA VWLDSCHFRG VSLAHS Quence ##: NM_013	ELVKSGTLLP BETGFWFIPH KDKRPFLSII EAQEGFLLTG	HVPTGPSVGM SARYSPHODA	YSPGYSEHIP DPLKPREPAI	560 720 780
	KDVVGYNSLG PKPRQDCNAV LGKFYNNRAH IRHFIAYKNQ FSPPCRCLLK Seq ID NO: Nucleic Ac:	HCPFTEDGPE STFWMANPKN SNYRAGMIID DHGAWLRGGD LVTTGSPFAH 454 DNA 88:	ERNTFDHCLG NLINCAAAGS NGVKTTEASA VWLDSCHFRG VSLAHS Quence ##: NM_013	ELVKSGTLLP BETGFWFIPH KDKRPFLSII EAQEGFLLTG	HVPTGPSVGM SARYSPHODA	YSPGYSEHIP DPLKPREPAI	560 720 780
50	KDVVGYNSLG PKPRQDCNAV LGKFYNNRAH IRHFIAYKNQ FSPPCRCLLK Seq ID NO: Nucleic Ac:	HCPFTEDGPE STFMMANPKN SNYRAGMIID DHGAWLRGGD LVTTGSPFAH 454 DNA 80: id Accession	ERNTFDHCLG NLINCAAAGS NGVKTTEASA VWLDSCHFRG VSLAHS Quence ##: NM_013	ELVKSGTLLP BETGFWFIPH KDKRPFLSII EAQEGFLLTG	HVPTGPSVGM SARYSPHODA	YSPGYSEHIP DPLKPREPAI	560 720 780
	KDVGYNSLG PKPRQDCNAV PKPRQDCNAV LGKPYNNRAH IRHFIAYKNQ FSPPCRCLLK Seq ID NO: Nucleic Ac: Coding sequence	HCFFTEDGPE STPHMANPNN SNYRAGMIID DHGAWLRGGD LVTTGSPFAH 454 DNA sei id Accession sence: 85	ERNTFDHCLG NLINCAAAGS NUVKTTEASA VWLDSCHFRG VSLAHS Quence 1 #: NM_01: 2466	LLVKSGTLLP BETGFWFIFH KDKRPFLSII EAQEGFLLTG 282.2	SDRDSKMCKM HVPTGPSVGM SARYSPHQDA MKAGGILLOG	TYBGYSEHIP YSPGYSEHIP DPLKPREPAI DEAASGNAQG	660 720 780 840
50	MDVGYMSLG PKPRQDCNAV LGKPYMNRAH IRHFIAYKNQ FSPPCRCLLK Seq ID NO: Nucleic Ac: Coding seq	HCFFTEDGPE STPHMANPHN SNYRAGMIID DHGAWLRGGD LVTTGSPFAH 454 DNA sei id Accession lence: 85	ERNTFDHCLG NLINCAAAGS NGVKTTEASA VWLDSCHFRG VSLAHS QUENCE 1 #: NM_01: 2466 21 TGGCTCAGAG	LLVKSGTLLE BETGPWIPH KDKRPFLSII EAQEGFLLTG 282.2	SDRDSKMCKM HVPTGPSVGM SARYSPHQDA MKAGGILLOG 41 AACTGATGGG	TYBEGSFAUT YSPGYSEHIP DPLKPREPAI DEAASGNAQG 51 1 GGTTTTTGCT	660 720 780 840
50	KDWOYNELG PKPRODCNAV LGKFYNNAH IRHFIAYKNQ FSPPCRCLLK Seq ID NO: Nucleic Ac: Coding sequ	HCPFTEDOPE STPHMANPHN SNYRAGMID DHGAWLRGGD LVTTGSPFAH 454 DNA sei id Accession Lence: 85 11] GAGGATGGGA TCAGGGCGGA	ERNTFDHCLG NLINCAAAGS NGVKTTEASA VWLDSCHFRG VSLAHS Quence 1 #: NM_01: 2466 21 TGGCTCAGAG CACCATGTGG	LLYRSTLLP EETGFWFIFH KDKRPFLSII EAQEGFLLTG 282.2 31 GTGCTGGTAA	SDROSKMCKM HVPTGPSVGM SARYSPNGDA MKAGGILLOG 41 AACTGATGGG AGGACCATGGA	TYBGYSEHIP TYBGYSEHIP DPLKPREPAI DEAASGNAQS 51 GGTTTTTGCT CGGGAGGCAG	60 720 780 840
50	KDWOYNELG PKPRODCNAV LGKFYNNAH IRHFIAYKNO FSPPCRCLLK Seq ID NO: Nucleic Ac: Coding seq 1 CGACTCCTTA GTCCTCCCCCC	HCPFTEDGPE STFMMANPAN SNYRAGMIID DHGAWLRGGD LVTTGSPFAH 454 DNA section of the control idence: 85 11] GAGCATGGCA TCAGGGCGGA	ERNTFDHCLG NGVKTTEASA NGVKTTEASA WULDSCHERG VSLAHS QUENCE 1 #: NM_01: 2466 21	LLYRSTLP EETGFWIFLF KDERFFLSII EAQEGFLLTG 282.2 31 	SDROSKMCKM BYPTGPSVGM SARYSPHQDA MKAGGILLOG 41 	S1 	600 720 780 840 600 1200 180
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50 55 60 65 70 75	ROYOUTHERD PERFORMANCE AND PER	IGEPTERORIE STPHENAPIE DISANLERGE DISANLERGE LITTGEFFAI 454 DNA sec di Accessio GOOGNOTOR GOOGNOTOR TOCHOCONO GOOGNOTOR ACCESSIO GOOCNOTOR ACCESSIO GOOGNOTOR ACCESSIO GOOGNOTOR ACCESSIO GOOGNOTOR ACCESSIO GOOGNOTOR ACCESSIO GOOGNOTOR ACCESSIO GOOGNOTOR ACCESSI	EMPTPOLICUS INTERCANOS	LIVINGS TEAT ENGINEERS TEAT ENGINEERS TEAT 11 1 1 1 1 1 1 1 1 1	41 I I I I I I I I I	13 PATENTIAL TO PA	600 1200 180 240 360 420 360 420 480 540 900 1020 1020 1020 1140 1200 1320 1320 1320 1330 1340 1340 1350 1360 1360 1360 1360 1370 1370 1370 1370 1370 1370 1370 137
50 55 60 65 70 75	REPURPHEND SERVICE SER	SCEPPEDORIS SCEPPE	EMPTPOLICUS INTERPOLICUS INT	LIMINES SITE IN LIMINES SITE SITE IN LIMINES SITE IN LIMINES SITE IN LIMINES SITE IN LIMINES S	SIDIOS MAGNETICA SERVICIA SERV	19 PANY SERVICE OF THE PAN	660 720 780 840 120 180 240 360 360 360 600 720 960 1020 1140 11320 11320 11320 11320 11320 11320 11320 11320 11320 11320 11320
50 55 60 65 70 75	REPURCHISESS PROPERTIES AND PROPERTI	SCEPTEDOSPIN SCEPT	EMPTPOLICUS EMPTPO	LEVISOR TEAT IN THE PROPERTY OF THE PROPERTY O	41 AT THE PROPERTY OF THE PRO	15 PANY SERIE IN 15 PAN	600 1200 180 240 360 420 360 420 480 540 900 1020 1020 1020 1140 1200 1320 1320 1320 1330 1340 1340 1350 1360 1360 1360 1360 1370 1370 1370 1370 1370 1370 1370 137
50 55 60 65 70 75	REPURSIES SERVICE SERV	SCHEPTERORES SCHEROLISE SCHEROLIS	EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT EMPLEME	LEMENSHIEL IN LE	41 AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOCA AACTOATOGO GOACOTOCA AACTO	150-000-000-000-000-000-000-000-000-000-	660 720 780 840 60 120 180 240 360 420 480 560 660 660 660 720 780 900 1140 900 1240 1320 1380 1410 1380 1410 1500 1500 1500 1500 1500 1500 150
50 55 60 65 70 75	REPURSIES SERVICE SERV	SCHEPTERORES SCHEROLISE SCHEROLIS	EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT EMPLEME	LINESPHET IN LINES	41 AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOCA AACTOATOGO GOACOTOCA AACTO	150-000-000-000-000-000-000-000-000-000-	600 1200 180 240 360 360 360 600 720 960 960 1200 1200 1200 1200 1200 1200 1200 12
50 55 60 65 70 75	REPURSIES SERVICE SERV	SCEPTEDOSPIN SCEPT	EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT DELLOS EMPLEMENT EMPLEME	LINESPHET IN LINES	41 AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOATOGO GOACOTOCA AACTOCA AACTOATOGO GOACOTOCA AACTO	150-000-000-000-000-000-000-000-000-000-	600 120 120 120 120 130 360 420 480 540 600 720 960 1020 1020 1020 1020 1030 1020 1030 1040 1020 1030 1040 1050 1050 1050 1050 1050 1050 105

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	CAGGAGGGG	CCAACCGAGA	CCCCAGGAGA	GGCAAGGCA	AGAGGGAGGA	GAAGTCGGCA	2040
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5	CCCTACAGTC	TCACGGCCCA	GCAGAGCAGC	CTCATCAGAG	AGGACANGAG	CAACGCCAAG	2160
3	TTGTTCCTGA	GTALAGTGGA	GGAGACGTTC	CAGTGTATCT	GCTGTCAGGA	CCCGTTCCAG	2220
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10							2500
	CCTAAAAAGG	TTTGTCTTCC	TTTTTTTTA	TTTTTATTT	TCAAATCTAT	ACATTITCAG TCTTTGAAAA GGAATCAGAA	2640
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15	ACTACGTGGT	GTGGAGGCTG	TIGATGTTTC	TGGTGTCAAG	TTCTCAGAAG	TTGCTGCCAC	2820
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	AGCAAGCATC	TTCCTGACAG	CATTTTGTCA	TCTAAAGTCC	AGTGACATGG	TTCCCCGTGG	2940 3000
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20	TGCTTAGCGT	CTGAGATCCG	CGTGAAAAGT	CCTCTGCCCA	CGAGAGCAGG	GAGTTGGGGC	3120
							3180
	TGTCCGACGA	AGGCGGCCAC	GGACGGACGC AGACGACAGT	CAGCACACGA	AGTCACGTGC	AAGTGCCTTT	3240
							3360
25	OCA & OCCUPANT	CACCOTTATA	CARCATTRAC	ATT OR STITT	TOTALCTCAG	CARCTCACAA	3420
	CTTACAAGAG	GGTTTTTTTT	TAATTTTTTT	TTCTCTTAAT	GAACACATTT	TCTAAATGAA	3480
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	TTGCAGCCTA	TACCTCARTA	AAACAGGGAT	ATTTTAAATC	ACATACCTGC	AGACAAACTG	3660
30	CAGCAATGTT	ATTTTTALAC	CONTRACTOR	ACCTOCATAT	TCTTAGATTA	TTAATGTATT	3720
	AGGGAAGAAT	GAGACAATTT	TGTGTAGGCT	TTTTCTAAAG	TCCAGTACTT	TGTCCAGATT	3780
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33	Protein Acc	ession #: 1	dP_037414.2				
	1	11	21	31	41	51	
	MILTOURISMOG	POTHEWNST.S	DITEURRIDO	KIORLEHVED	GLOBI-PYRGE	QMEDGHTLFD	60
40	YEVRLNDTIO	LLVROSLVLP	HSTKERDSEL	SDTDSGCCLG	QSESDKSSTH	GEAAAETDSR	120
							180
	DAIAHAKADD	Abengaadous	SRDVRARART LGDDSLNDCR	IIKWQDLEVG	QVVMLNYNPD	NPKERGFWYD	240 300
	SCKHCKDDUN	BICBUCACHL	CGGRODPDKO	LMCDECDMAF	HIYCLDPPLS	SVPSEDEWYC	360
45	PECRNDASEV	VLAGERLRES	KKKAKMASAT	SSSORDWGKG	MACVGRTKEC	SVPSEDEWYC TIVPSNHYGP DHGNFFTYTG	420
	IPGIPVGTMW	RFRVQVSESG	VHRPHVAGIH	GRSNDGAYSL	VLAGGYEDDV	DHGNFFTYTG	480
	SGGRDLSGNK	RTAEQSCDQK	LTNTNRALAL VVKYWPEKGK	NCFAPINDQE	GAEAKDWRSG	KPVRVVRNVK	540 600
	LGLTMOYPEG	YLEALANRER	EKENSKREEE	BOOBGGFASP	RTGKGKWKRK	SAGGGPSRAG	660
50	SPRRTSKKTK	VEPYSLTAGO	SSLIREDKSN	AKLWMEVLAS	LKDRPASGSP	FOLFLSKVEE	720
	TFQCICCQEL	VFRPITTVCQ	HNVCKDCLDR	SFRAQVESCP	ACRYDLGRSY	AMQVNQPLQT	
	Seq ID NO:	456 DNA sec	quence				
55	Nucleic Act	ld Accession lence: 325.	1 #: NM_001	200.1			
	course orde						
	1	11	21	31	41	51 	
~	GGGGACTTCT	TGAACTTGCA	GGGAGAATAA	CITGCGCACC	CCACTTTGCG	COGGTGCCTT	60
60	TGCCCCAGCG	GAGCCTGCTT	CGCCATCTCC	GAGCCCCACC	GCCCCTCCAC	TCCTCGGCCT	120 180
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	CTGCGGTCTC	CTAAAGGTCG	ACCATGGTGG	CCGGGACCCG	CTGTCTTCTA	OCCUTTGCTGC	360
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70							720 780
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7.5	ACACCAGGTT	GGTGAATCAG	AATGCAAGCA	GG TGGGAAAG	TTTTGATGTC	ACCCCCGCTG GTGGCCCACT	960
75	TGATGCGGTG	GACTGCACAG	GGA CACGCCA	ACCATGGATT	CGTGGTGGAA	GTGGCCCACT	1020
	TGGAGGAGAA	ACAAGGTGTC	TOUANGAGAC	TGCTAGTAGC	TTTTGGCC27	TTGCACCAAG GATGGAAAAG	1140
	GGCATCCTCT	CCACAAAAGA	GAAAAACGTC	AAGCCAAACA	CAAACAGCGG	GATGGAAAAG AAACGCCTTA	1200
00	AGTOCAGCTG	TARGAGACAC	CCTTTGTACG	TGGACTTCAG	TGACGTGGGG	TOGAATGACT	1260
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	TOGCTGATCA	TOTGRACTOO	ACTAATCATG TGCTGTGTCC	CCATIGTTCA	CACTGCTATC	TCGATGC197	1380
	ACCTTGACGA	GAATGAAAAG	GTTGTATTAA	AGAACTATCA	GGACATGGTT	GTGGAOGGTT	
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85							

Seq ID NO: 457 Protein sequence Protein Accession #: NP_001191.1 WO 02/086443 PCT/US02/12476

5	1 MVAGTRCLLA	11 LLLPQVLLGG RDAVVPPYML	21 AAGLVPELGR	31 RKPAAASSGR	41 PSSQPSDEVL	51 SEFELRILSM	60 120
,	LPETSGKTTR TANSKFPVTR	RFFFNLSSIP LLDT	TEEFITSAEL	QVFREQMQDA	LGNNSSFHHR	INIYEIIKPA	180
10	Nucleic Ac	458 DNA sec id Accession sence: 18	#: NM_001 736				
	1	11	21 l	31 l	41	51	
15	ATGGGGAGAA	GACGGAGGCT	GTGTCTCCAG	CICTACTTCC	TGTGGCTGGG	CTGTGTGGTG	60 120
	CAGCOGCOGC	AGGGCACGGC CGCAACAGGT	TCGGTCCGCT	ACAGCAGGCT	CTGAAGGCGG	GTTTCTAGCG	180
							240 300
20	TOGARGACGC	GAGGGCCCAA TCCCTGGAGG	AAACCAGIGC	ATTGTCCCGA	TTTGTAGAAA	TAGTTGTGGA	360
	тотосьтськ	GTTCCCGTCC AATCAATTCA	GCAGTGCAGT	GTGAGATGCA	TGAATGGTGG	GACCTGTGCA	420 480
	GATGACCACT	GCCAGTGCCA GTCAGAATGG	GAAAGGATAT	ATTGGAACTT	ATTOTOGACA	ACCIGICIGI	540
25	CAAAATGGAT	GTCAGAATGG CACAGTGTGA	AAGAGATTAC	ACCACAGGCC	CGTGTGTCTCAC	TCAGGTCAAC	600 660
	AACCAGATGT	GCCAAGGGCA GGGCGTGGGG	GCTGACAGGC	ATTGTCTGCA	CGAAGACTCT	GTGCTGTGCC	720 780
	CGACGGGGTT	TCATCCCCAA	CATCCGCACT	GGAGCTTGCC	AAGATGTTGA	TGAATGCCAG	840
30	GCTATCCCAG	GGATATGCCA CTGGTCACAA	AGGAGGAAAC	TGTATCAATA	CAGTOGGCTC	TTTTGAATGC	900 960
50	TGCAGCATCA	TTCCTGGGAT	ATGTGAAACT	GGTGAATGTT	CCAACACOGT	GGGAAGCTAT	1020
	TTTTGTGTTT	GTCCACGTGG TGTGTTTCTC	ATATGTAACC	TCAACAGATG	GCTCTCGATG	CATCGATCAG	1080 1140
25	ACDATICACIA	DEDGEORGE	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	COGRACCATT	1200
35	CCAATGGGAG	GTCCTGTCAG GAATTCCAGG	GAGTGCTGGT	TCCAGACCTG	GAGGCACTOG	GGGAAATGGC	1260 1320
	TTTGCCCCAA	GTGGCAATGG	CAATGGCTAT	GGCCCAGGAG	GGACAGGCTT	CATCCCCATC	1380
	CCACCTATCA	ATGGCTTTTC TCACTGGACT	BACKSTTCTC	AACCACACAA	TAGATATOTG	TARGCATCAT	1440 1500
40	GCTAACCTTT	GTTTAAATGG ATAAGCAGGA	ACGCTGTATA	CCAACTGTCT	CAAGCTACCG	ATGTGAATGC	1560 1620
	A RECOMMODA	OTTA STOCKOL	THOTOTOTA & C.	ACA COTOGOTO	COTATTATTO	TARATOTCAT	1680
	GCTGGATTCC	AGAGGACTCC TTTGTAAAAA	TACCAAGCAA	GCATGCATTG	ATATTGATGA	GTGCATCCAG	1740 1800
45	TGCAATGCCG	CCTTTGAATT	AACTACAGAT	GGAAAAAACT	GTGTTGATCA	TGATGAATGT	1860
	ACAACTACCA	ACATGTGTTT CAGGATTTGT	GAATGGAATG	TGCATCAATG	AAGATGGCAG	TGTTGATGAA	1920
	TOCCADACCC	CAGGAATCTG	CATGALTGGG	CACTGCATCA	ACAGTGAAGG	GTCCTTCCGC	2040
50	TGTGACTGTC	CCCCAGGCCT	AGGAATCAAG	ANAGGAGTGT	GTGTGTGTGT	TGATACTCAC	2100 2160
• •	GCAGTGACCA	AGTCCGAATG	CTGCTGTGCC	AATCCAGACT	ATGGTTTTGG	AGAACCCTGC	2220
	ATCACTGTGG	CTGCAAAAAA ATGGAAGAGA AAAACTTACG	TATCAGCTGAA	TGTGCTTTGG	ATCCTGATAT	ATGTGCCAAT	2340
55	GGGATTTGTG	AAAACTTACG GAAGAAACTG	TOGTAGTTAC	COTTOTAATT	GCAACAGTGG	CTATGAACCA	2400 2460
55	CATABOOGAT	тотоссозаа	CACCCAGGA	AGTTACAGCT	GTACGTGCCC	ACCAGGGTAT	2520
	GTGTTCAGGA	CTGAGACAGA CCTGCAGAAA	GACCTGTGAA	GATATAAATG	AATGTGAAAG	CARCCCATGT	2580 2640
	AAACTCAGCT	CCACAGGATT GCGGCTGTGA	GATCTGTATT	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC	2700
60	ATCCAGGACA	GCCGCTGTGA GAGCCGCCTG	GGTGAATATT	AATGGAGCCA TOTGAGCGGT	CTCTGAAATC	TGAATGCTGT	2760 2820
	CCAAGAGGGC	TTGCCAGGAT	TAAAGGTGTT	ACCTGTGAAG	ATGTTAATGA	GTGTGAGGTG	2880
	TECCETGAAG	TTTGTCCAAA GCCTTACGTT	TGGACGCTGT	GCCCGTGTAT	AGGGATCTTT	TCATTGCGAG	2940 3000
65	CAGTGTTACT	TGAAGTGGGA	TGAAGATGAA	TGCATCCACC	CCGTTCCTGG	AAAGTTCCGC	3060
	AAACCTGGCA	GCTGCTGTGC CCAAGGAATA	CGAGACACTG	TGCCCCCCGCG	GGGCTGGCTT	TGCTAACCGA	3120 3180
	GGGGATGTTC	TTACTGGGGG CTTATGGGAA	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCATTTCCT	3240
70	AGTGGCTTTG	CTCTAGACAT	GGAGGAAAGA	AACTGCACGG	ACATOGAGGA	GTGCAGGATT	3360
	TOTOCTGACO	TCTGTGGCAG GCTATGAAAG	TGGAATCTGC	GTCAATACAC	CGGGCAGCTT	TGAGTGCGAG	3420 3480
	TOTOLACOTA	ACCOMMON	TTGTAGGGGT	GGCACCTGTG	TGAACACTGA	GGGCAGCTTT	3540
75	CAGTGTGACT	GCCCACTGGG	ACACGAGCTG	TCACCATCCC	GTGAGGACTG	TGTGGATATT CATGATTGGA	3600 3660
, ,	ACCTATCAGE	GCTCTTGCAA	TCCTGGATAT	CAGGCTA CGC	CAGACCGCCA	GGGCTGTACA	3720
	GGAAGCTACG	AATGTATGAT	CAGTGAGGGT	TATGCCCTGA	TGCCAGATGG	GAGATOGTGT	3780 3840
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80	ACATGCATTG	AGTATOGCTG ATGTCAATGA	ATGTGACCTA	AATTCAAATA	TCTGCATGTT	TGGGGAATGT	3960 4020
	CDCDDCACAC	DOCCUPACION TO COMPANY	CATTTGCCCAC	TOTOLOGOTOG	GTTACTCAGT	CAAGAAGGGG	4080
	GCCTCATGTC	GTACAGATGT TGAATATCCC	AGGAAGCTTC	AAGTGTAGCT	GCAGAGAAGG	CTGGATTGGA	4140 4200
85							4260 4320
	GGTGATGGCT	GTGTAAATAC TTACCTGCTC	AGATGTTGAT	GAGTGTGCAG	AAAACATAAA	CCTCTGTGAG	4380

AACGGACAGT GCCTTAATGT CCCGGGTGCA TATCGCTGCG AGTGTGAGAT GGGCTTCACT 4440 CCAGCCTCAG ACAGCAGATC CTGCCAAGAT ATTGATGAAT GCTCCTTCCA AAACATTTGT 4500 GTCTCTGGAA CATGTAATAA CCTGCCTGGA ATGTTTCATT GCATCTGCGA TGATGGTTAT 4560 GAATTGGACA GAACAGGAGG GAACTGTACA GATATTGATG AGTGTGCAGA TCCTATAAAC 4620 5 TGTGTCAATG GCCTATGTGT CAACACGCCT GGTCGCTATG AGTGTAACTG CCCACCCGAT 4680 TTTCAGTTGA ACCCAACTGG TSTGGGTTGT GTTGACAACC GTGTGGGCAA CTGCTACCTG
AAGTTTGGAC CTGAGGGGACTGT GTTGCCACAC CCGAGATCGG GGTGGCGTA
AGTCCTCTT CATGCTGCTG CTCTCTGGGA AAGGCCTGG GAAACCCCGT TGAGACATGC 4740 4800 4860 CCCCCTGTCA ATAGCACTGA ATATTACACC CTGTGTCCCG GAGGTGAAGG CTTCAGACCT 4920 10 AACCCCATCA CAATCATTTT AGAAGACATT GACGAATGCC AGGAGTTACC AGGTCTCTGC 4980 CAGGGTGGAA ACTGCATCAA CACTTTTGGG AGCTTCCAGT GTGAGTGCCC ACAAGGCTAC 5040 TACCTCAGCG AGGATACCCG CATCTGTGAG GATATTGATG AGTGTTTTGC ACATCCTGG 5100 GTOTOTOGGC CTGGGACCTG CTATAACACC CTGGGAAATT ACACCIGCAT TTGCCCACCI 5160 GAGTACATGC AGGTCAATGG AGGCCACAAC TGCATGGACA TGAGAAAAAG CTTTTGCTAC 5220 CGAAGCTATA ATGGAACCAC TTGTGAGAAT GAGTTGCCTT TCAATGTGAC AAAAAGGATG 5280 TOCTGCTGCA CATATAATGT GGGCAAAGCT GGGAACAAAC CTTGTGAACC ATGCCCAACT 5340 CYAGGAACAG CTGACTITAA AACCATATGT GGAAATATTC CTGGATTCAC CTTTGACATT 5460 CACACAGGAA AAGCIGITGA CATTGATGAA TGTAAAGAGA TTCCAGGCAT TTGTGCAAAT GGTGTGTGCA TTAACCAGAT TGGCAGTTTC CGCTGTGAAT GCCCTACAGG ATTCAGTTAC 5520 20 AATGACCTGC TGTTGGTTTG TGAAGATATA GATGAGTGCA GCAATGGTGA TAATCTCTGC CAGCGGAATG CAGACTGCAT CAATAGTCCT GGTAGTTACC GCTGTGAATG TGCCGCGGGT 5500 5640 TTCAAACTT CACCCAATGG GGCCTGTGTA GATGGCAATG AATGTTAGA AATTCCTAAC GTTTGCAGTC ATGGCTTGTG TGTTGATCTG CAAGGAAGTT ACCAGTGCAT CTGCCACAAT GGCTTTAAGG CTTCTCAGGA CCAGACCATG TGCATGGATG TTGATGAGTG CGAGCGGCAC 5820 GESTITIANGS CTITISTAGGA COMMISCORIS TRANSMANT TRANSMANT GAMEGACIAN CONTINGAA ARGAMACTES TAAAAACACC STUGANCTA ARACTESTE STOETACOCA GESTITICAAC TAATCATAA TAATAATTIC CTGUACATAA ARGANGGAS TROCTITITIA GOTCAGGITT GOMGAATGG ROSTISTIT AATGAAATTG GTTCTITCAA GIGTCAROT AACGAAGGIT ACGAACTAC COCAGATGGC AMMANCTGTA TAGACACTAA TRANSTGTC 25 5880 5940 6000 6060 GCCCTTCCCG GCTCTTGCTC TCCTGGTACC TGTCAGAATT TGGAGGGATC CTTCAGATGC 6120 30 ATCTGTCCCC CAGGGTATGA AGTANAAGC GAGAACTGCA TTGATATAAA TGAATGTGAT 6180 GARGATCCCA ACATTGTCT TTTTGGTTCC TGTACTAATA CTCCAGGGGG CTTCCAGTGC 6240 CTCTGCCCCC CTGGCTTTGT ACTATCTGAT AATGGACGGA GATGCTTTGA TACTCGCCAG 6300 AGCTTCTGCT TCACAAATTT TGAAAATGGA AAGTGTTCTG TACCCAAAGC TTTCAACACC ACMANAGCAA AATGCTGCTG TAGTAAGATG CCAGGAGAGG GCTGGGGGGGA CCCCTGTGAG 35 CTGTGCCCCA AAGACGATGA AGTTGCATTT CAGGATTTGT GTCCATATGG CCATGGAACT 6400 STOCCTAGTO TTCATGATAC ACGTGAAGAT GTCAATGAGT GTCTTGAGAG COCAGGCATT 6540 TOTTCRAATG GTCRATGTAT CRACACOGAC GGATCTTTTC GCTGTGAATG TCCAATGGGC TACAACCTTG ACTACACTGG AGTACGCTGT GTGGATACTG ATGAGTGTTC AATCGGCAAT 6600 COGTGTGGAA ATGGTACATG CACCAATGIT ATTGGGAGTT TTGAATGCAA TTGCAATGAA 6720 COSTOTOGRA ATGGTACATO CACCALTET ATTOGRATT TRANSLAA ITUCANIUM GOCTITICAGE CAGGICCCUT ATGALTETI GAAGNITCH AGGANITGHA COMARACCA CTOCTOTOGI CTITACOCTO CATGALCAT TITUGATICCI ATGALTGAC GTOCCOATT GOCTATOCC TCAGGAAGA TCAAAAGAT TOCAAAGAT TOGAATGAAT TOCTGAAGG TITACACGACT GTGAATCHAG GGCCATGATG TOTAAGAATC TAATOGACC CTICAATGG 40 6780 6840 6900 ATCTGCCCTC CTGGAATGGC CCGAAGGCCC GATGGAGAAG GCTGTGTAGA TGAAAATGAA 7020 45 TOCAGGACCA AGCCAGGAAT CTGTGAAAAT GGACGTTGTG TTAACATTAT TOGAAGCTAT 7080 7140 AGATGTGAGT GTAATGAAGG ATTOCAGTCA AGTTCTTCAG GCACTGAATG CCTTGACAAT CGACAGGGTC TCTGCTTTGC AGAGGTACTG CAGACAATAT GTCAAATGGC ATCCAGTAGT 7200 COCAATCTCG TCACTAAGTC AGAATGCTGC TGTGATGGTG GGCGAGGCTG GGGCCACCAG 7260 TOCGROCTTT GCCCACTTCC TGGAACTGCC CAGTACAAAA AGATATGTCC TCATGGCCCA 7220 50 GGATATAGAA CTGATGGAAG AGATATTGAT GAATGTAAGG TAATGCCAAA CCTCTGCACC AATGGTCAGT GCATCAATAC CATGGGCTCA TTCCGATGCT TCTGCAAGGT TGGCTACACC 7200 7440 ACAGACATCA GTGGAACCTC TTGTATAGAC CTTGATGAAT GCTCCCAGTC CCCGAAACCA 7500 TGCAACTACA TCTGCAAGAA CACTGAGGGG AGTTATCAGT GTTCATGTCC GAGGGGGTAT GTCCTGCAAG AGGATGGAAA GACATGCAAA GACCTTGATG AATGTCAAAC AAAGCAGCAT 7620 55 AACTGCCAGT TCCTCTGTGT CAACACCCTG GOGGGGTTTA CCTGTAAATG TCCACCTGGT 7680 TTCACCAGC ATCACACTGC TTGTATCGAC AACAACGAAT GTGGGTCTCA ACCTTGCTT TCTGCAGGAA AGGGAATCTG TCAAAACACT CCAGGCAGTT TCAGCTGTGA ATGCCAAAGA 7740 7800 GOGTTCTCT TTGATGCCAC CGGACTGAAC TGTGAAGATG TTGATGAATG TGATGGGAAC CACAGGTGCC AACACGGCTG CCAGAACATC CTGGGTGGCT ACAGATGTGG CTGCCCCCAA 7920 60 GOCTACATCC AGCACTACCA GTGGAATCAG TGTGTGGATG AGAATGAATG CTCCAATCCC 7980 ARTGCCTGTG GCTCTGCTTC CTGCTACAAC ACCCTGGGGA GTTACAAGTG CGCCTGCCCC 8040 TOGGGGTTOT COTTOGACCA GTTCTCCAGT GCCTGCCACG ACGTGAATGA GTGCTCGTCC 8100 TOCAAGAACC CCTGCAATTA CGGCTGCTCT AACACGGAGG GGGGCTACCT CTGTGGCTGC CCCCCTOGGT ATTACAGAGT GGGACAAGGC CACTGTGTCT CAGGAATGGG ATTTAACAAG 9220 65 GOGCAGTACC TGTCACTGGA TACAGAGGTC GATGAGGAAA ATGCTCTGTC CCCAGAAGCA 9290 TOCTACGAGT GCAAAATCAA CGGCTATCCT AAGAAAGACA GCAGGCAGAA GAGAAGTATT 8340 CATGRACCTE ATCCCACTOC TOTTGRACHA ATCRCCATOR AGAINSTONA CATGRACCTOR AGAINSTONA CATGRACCTOR AGAINSTONA CATGRACCTOR AGAINSTONA CATGRACCATOR AGAINSTONA CATGRACCATOR AGAINSTONA CATGRACCATOR AGAINSTONA CATGRACCATOR AGAINSTONA AGAINSTONA AGAINSTONA AGAINSTONA CATGRACCATOR AGAINSTONA AGAINSTON 9400 8520 70 GACAGOGTOT TOCGCATOCA CCAAAGGAAT GGGCTCAGCT ACTTGCACAC GGCCAAGAAG 8580 AAGCTCATGC CCGGCACATA CACACTGGAA ATCACTAGCA TCCCTCTCTA CAAGAAGAAG 8640 GAGCTTAAGA AACTOGAAGA GAGCAATURG GATGACTACC TCCTRAGGGGA GCTTGGGGAG GCTCTCAGAA TGAGGCTGCA GATTCAGCTC TATTAACCGT TCRCRGACTT GGGCCCAGGC 8700 8760 TUBBATCUTA GUACAGCUAG TUTGUAGAAG CATTIGAAAA GTUAAGGAUT AATTITAAAG 75 AGGARAGATA ATRATACTC TTGTTTCTTT CCTCCCTGTC TTAGACTTTG AATGTTGACC 8886 CTCACAGGGA GGGATAATTT AGACTCTGGT ATGGCCAAAG ATTTGAGCTC AAAGGCAACC 8940 GUGGITACUG TATTUUTAT ATAACUTCAT TUTAAAATAT AUTAAAAGAA ACCUAAAUGT 9000 TCARGATATC AGCATATGGC ACTARATGCA CARARATAAT GTGAGCTTTT TTTTTTTTT CCTGTTAGCA GTCTGTAACA CTTTGGGTAT TTTGCTATAG TTGCTAATTA AAAAAATATA 9120 GATGITTATT TATTITTAAT GCAGTAATAT ATOGAGAAAT GAACAAACTA TGTAAACAAA 20 91.00 AAGGGAAACT CACTTGTTTT TCTTTAGATT TATAAATTTG AGCTATTTTT TTTAGAGGTG 9240 CTTTTTAAAA ATCCAATAGA TACAAGAGAT GTTTCCTTTG GTTTTCTGCC AGTCATCCAG 9301 CTGATACACA CCTGATCGAT TITAAAGAAA GCCACACAGA GCTGAATCGG GCAGTGCTAA 9360 TCAATAATTT AAAAGACATG AATGTCATTA GATCCTTTAT AACGTAGATC GAAGCCAAAG 9420 85 CAGCTCATTT GTGACAACAT TTCATATCAC CAGACACACC AGGCAACAGA AGTTGAAGCA 9480 CAACCACTGT AGCAAAATAC CTTGACTGCT TGTGACGACCA TTAGGATTGC AGGCCAAACCCGTACTGTATT TCCTTCTCTAT AACCTCAAGG AACCATATGT GCTACCCACA ACACCTCATT 9540 9600

WO 02/086443 CTTACCCAGG GTGCGCTGCG TCCTCATGGT ACTGTAGGCA GCTGAAGAAC CGCCGTTCCC 9660 TTGAAAGGGA ACACCTGGCA TTCTGTGGTG TTTCGTGCTG TCTTAAATAA TGGTGCATTT 9720 ATTATGTTCA AGTTATTTCA GGATTGCCAT ATGTGCAAAC AAATCATGCA ATGCAGCCAA 9780 GGAATATATG TIGITGTTGT TGTTTTAAAC CCATTTTTTT TTTAGAATTT TCATTAATAC 9840 TETROTTATA CACCATATGC CTCATTTAT CATAGCCTAT IGTGTATGAA AGATGTTGT 9900
ACAAGGAATT GATGTTTAGT TUCCTTTAGT CATITAAAAG AGATGTTGC GAGCAGTAGGC
9960
TATTAAGAGA CAGTATCCAT TATTCTTCT AACCCAAGA CCTGTTTCCT GAGCAAGGA CCARACCTCA TATGGAAAT GGCCAAAGCA CATGCAGGCT CCTGGTTGTT CCTCTCAAAC 10080 CTGTGCTGAC CAAAGATTAG TAACCAGTTA TACCCAGTAT TTTGAGGTTT TATTGTTTTT 10140 10 TTANTAACTA AAAAAAAACT CGTGCC Seq ID NO: 459 Protein sequence Protein Accession #: NP_001990.1 15 31 41 MGRRERLCLO LYPLWLGCVV LWAGGTAGOP OPPPPKPPRP OPPPQQVRSA TAGSEGGFLA PEYRHEGAAV ASRVRRRGOO DVLRGPHVCG SRFHSYCCPG WKTLPGGNQC IVPICRNSCG 120 DGFCSRPNMC TCSSGQISST CGSKSIQQCS VRCMNQGTCA DDHCQCQKGY IGTYCGQPVC 180 20 ENGCONGERC LAGPCACVYG FTGFQCERDY RTGFCFTQVN NOMCQGQLTG IVCTKTLCCA 240 ENGLANGED EMPAGEOR FIGHTENIN GACQDVDECQ AIRGICQGGN CINTYGSFEC TTGRAMGHPC EMCPAQPQPC RRGFIPHIRT GACQDVDECQ AIRGICQGGN CINTYGSFEC RCPAGHKOSE TTOKCEDIDE CSIIPGICET GECSNTYGSY FCVCPRGYVT STDGSRCIDQ 300 RTGMCFSGLV NGRCAGELPG RMTKMQCCCE PGRCWGIGTI PEACPVRGSE EYRRLCMDGL 420 PMGGIPGSAG SRPGGTGGNG FAPSGNGNGY GPGGTGFIFI PGGNGFSPGV GGAGVGAGGG GPITGLTIL NOTIDICKHH ANLCLMGRCI PTVSSYRCEC NMGYKQDANG DCIDVDECTS 480 25 540 NPCTNGDUN TPGSYYCKCH AGFORTPIKQ ACIDIDECIQ NGVLCKNGRC VNSDGSFQCI CNACFELTID GKNCYDEDEC TTINNCLNUM CINEDGSFKC ICKGGFVLAP NGRYCTDVDE 600 660 COTPGICKING HCINSEGSFR CDCPPGLAVG MDGRVCVDTH MRSTCYGGIK KGVCVRPFPG AVTKSECCCA NPDYGFGEPC OPCPAKNSAE FHGLCSSGVG ITVDGRDINE CALDPDICAN 780 30 GICENLEGSY RONCHSGYEP DASGREGIDI DECLYNELLC DWGLCRWTPG SYSCTCPPGY 840 UPPTPTPTCW DINECTENDO UNGACENNIA SENCECCEOS ELSCIGLICI DELEGICUM 900 IODSRCEVNI NGATLKSECC ATLGAAWGSP CERCELDTAC PRGLARIKGV TCEDVNECEV FPGVCPNGRC VNSKGSFHCE CPEGLTLEGT GRVCLDIRME QCYLKWDEDE CIHPVPGKFR 1020 MDACCCAVGA AWGTECEECP KPGTKEYETL CPRGAGFANR GDVLTGRPFY KDINECKAFP 1080 1140 GMCTYGKCRN TIGSFKCRCN SGFALDMEER NCTDIDECRI SPDLCGSGIC VNTPGSFECE CFEGYESGFM MAXXCMDIDG CERNPLICEG GTCWNTBGSF QCDCPLGHEL SPSRECVDI NECSLSDNIC RNGKCVNMIG TYQCSCNPGY QATPDRQGCT DIDECMIMMG GCDTOCTMSE 1200 1260 GSYECSCSEG YALMPDGRSC ADIDECENNP DICDGGQCTN IPGEYRCLCY DGPMASNEMK 1320 TCIDVMECDL NSNICMFGEC ENTKGSFICH COLGYSVKKG TTGCTDVDEC EIGAHNCDMH 1390 40 ASCLAIPOSF KOSCREGWIG NGIKCIDLDE CENGTHOCSI NAQCVETPOS YROASBEFT GOGFICSDVD SCRAINILCE NGCLHWFGA YROECEMGFT PASDRSSQU IDECSFORD VSGTCHRIPG MEHICIDDGY ELDRIGGNCT DIDECADPIN CYNSLCWIFF GRYECKCEPP 1440 1500 1560 FOLNPIGVEC VENEVENCYL KFEPRODESL SCHIELEVEV SESSCESLE KAWENPETTE PPVNSTEYYT LCPGGEGFRP NPITIILEDI DECQELPGLC QGGNCINTFG SFQCECPQGY 1680 YLSEDTRICE DIDECFAHPG VCGPGTCYNT LGNYTCICPP EYMQYNGGHN CMDMRKSFCY 1740 RSYNGTICEN ELPFHVIKRM CCCTYNVGKA GNKPCEPCPT PGTADPKTIC GNIPGFTFDI 1800 HTGKAVDIDE CKEIPGICAN GVCIMOIGSF RCECPTGFSY NDLLLVCEDI DECSNGDNLC 1860 ORNADCINSP GSYRCECAAG FKLSPNGACV DRNECLEIPN VCSHGLCVDL QGSYQCICRN 1920 GPKASODOTM CMDVDECERH PCGNGTCKNT VGSYNCLCYP GFELTHANDC LDIDECSSFF 1980 50 GOVERNGREF NEIGSFRELE NEGYELTFDG KNCIDTNECV ALPGSESPGT CONLEGSFRE 2040 ICPPGYEVES ENCIDINECD EDPHICLEGS CTHTPGGFQC LCPPGFVLSD NGRRCFDTRQ 2100 SFCFTNFENG KCSVPKAFNT TKAKCCCSKM PGEGWGDPCE LCPKDDEVAF QDLCPYGHGT STORTHERM VERCLESPOI CSNGCCINTO GSFRCECHMS VNLDYTORC VPTDECSIGN 2220
PCONDICTIVO IGSFRCNCHE GFEROMMON EDINECANNI LLCARCHUT FOSSECTIVE 2240
GYALREDOM (CDLDECASE LHCCSSROM (CMILITPMC LOPPGMARR) DGSGCVDENE 2340 55 CRYKPGICEN GRCVHIIGSY RECENESFOS SSSCIECLDN RGGLCFAEVL OTICOMASSS 2400
RNLVTKSECC CDGGRGWGHQ CELCPLPOTA QYKKICPHGP GYTTDGRDID ECKVMPNLCT 2460 NGOCTNYMGS FRCFCKVGYY TDISGTSCID LDBCSOSPKP CNYICKNYEG SYQCSCPRGY 2520 VLOEDSKYCK DLDECOTKOH NCOFLCVNTL GGFTCKCPPG FTCHHTACID NNECGSQPLL 2580 60 COGKGICONT PGSFSCECOR GFSLDATGLN CEDVDECDGN HRCQHGCQNI LGGYRCGCPQ 2640 2700 GYIGHYOWNG CVDENECSNP NACGSASCYN TLGSYKCACP SGFSFDQFSS ACHDVNECSS SKNPCNYGCS NTEGGYLCGC PPGYYRVOOG HCVSGMGFNK GOYLSLDTEV DEENALSPEA 2760

Seq ID NO: 460 DNA sequence Nucleic Acid Accession #: NM_013372.1 Coding sequence: 63.617

65

70 31 41 61 GCGGCCGCAC TCAGCGCCAC GCGTCGAAAG CGCAGGCCCC GAGGACCCGC CGCACTGACA GTATGAGCCG CACAGCCTAC ACGGTGGGAG CCCTGCTTCT CCTCTTGGGG ACCCTGCTGC 120 75 CGCTGCTGA AGGGAAAAAG AAAGGGTCCC AAGGTGCCAT CCCCCCGCCA GACAAGGCCC 180 AGCACAATSA CTCAGAGCAG ACTCAGTCGC CCCAGCAGCC TGGCTCCAGG AACCGGGGGC 240 GGGGCCAAGG GCGGGGCACT GCCATGCCCG GGGAGGAGGT GCTGGAGTCC AGCCAAGAGG CCCTGCATGT GACGGAGCGC AAATACCTGA AGCGAGACTG GTGCAAAACC CAGCCGCTTA 360 AGCAGACCAT CCACGAGGAA GGCTGCAACA GTCGCACCAT CATCAACCGC TTCTGTTACG 420 80 GCCAGTGCAA CTCTTTCTAC ATCCCCAGGC ACATCCGGAA GGAGGAAGGT TCCTTTCAGT 480 CCTSCTCCTT CTGCAAGCCC AAGAAATTCA CTACCATGAT GGTCACACTC AACTGCCCTG
AACTGCCCCG ACCTACCAAG AAGAAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT 540 600 CCATCGATTT GGATTAAGCC AAATCCAGGT GCACCCAGCA TGTCCTAGGA ATGCAGCCCC 660 AGGAAGTOCC AGACCTAAAA CAACCAGATT CTTACTTGGC TTAAACCTAG AGGCCAGAAG 720 AACCCCCACC TGCCTCCTGG CAGGAGCCTG CTTGTGCGTA GTTCGTGTGC ATGAGTGTGG 780 ATGGGTGCCT GTGGGTGTTT TAGACACCA GAGAMAACGA ASTCTCTGCT AGAGAGGGC CCCTATTTTT TAAACATATC TGCTTTAATG GGGATGTACC AGAAACCCAC CTCACCCGG 840

CYECKINGYP KKOSROKRSI HEPDPTAVEC ISLESVOMOS PYNNKFMLSH LGSKRHIEE 2820 RPAIQPLNNH IPYVISQGND DSVFRIHQRN GLSYLHTAKK KLMPGTYTLE ITSIPLYKKK 2880

	WO 02/	/086443					
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	GGGGACCAGA	ATCTCCTTTC	GGAATGAATG	TTCATGGAAG	AGGCTCCTCT	GAOOGCAAGA	1020
	GACCTGTTTT	AGTGCTGCAT	TCGACATGGA ATCCATCTCT	AAAGTCCTTT	TAACCTGTGC	TIGCATOCIC	1140
5	CITTCCTCCT	CCTCCTCACA	CCTAAATTAA	TCTTAAGTTG	CAMCAGGACIA	ANGRETOTICA	1200
,	ATCTCTTGTT	ACCOMMOGIT	CTCTGGGAGA	accusations.	GGCANGGACA	DATADDATAG	1260
	TOGAGTGAGA	ABGGGAGGGT	GGAGGGTGAG	CCCABATCAG	GTCCAGCAAA	AGTCAGTAGG	1320
	GACATTGCAG	AAGCTTGAAA	GGCCAATACC	AGAACACAGG	CTGATGCTTC	TGAGAAAGTC	1380
	TTTTCCTAGT	ATTTAACAGA	ACCCAAGTGA	ACAGAGGAGA	AATGAGATTG	CCAGAAAGTG	1440
10	ATTAACTTTG	GCCGTTGCAA	TCTGCTCAAA	CCTAACACCA	AACTGAAAAC	ATAAATACTG	1500
	ACCACTCCTA	TGTTCGGACC	CAAGCAAGTT	AGCTAAACCA	AACCAACTCC	TCTGCTTTGT	1560
	CCCTCAGGTG	GANANGAGAG	GTAGTTTAGA	ACTOTOTOCA	TAGGGGTGGG	AATTAATCAA	1620
	AAACCKCAGA	GGCTGAAATT	CCTAATACCT	TTCCTTTATC	GTGGTTATAG	TCAGCTCATT	1680
15	TCCATTCCAC	TATTTCCCAT	AATGCTTCTG	AGAGCCACTA	ACTTGATTGA	TAAAGATCCT	1740 1800
13	GCCTCTGCTG	AGTGTACCTG	ACAGTAAGTC GGGGTCTTTT	TAAAGATGAR	AGAGTTTAGG	GACTACTCTG	1860
	TTTTAGCAAG	ARATATTRIG	AGGARATARA	COCETAMORO	TOTOTOMOGR	GACTARCTTA	1920
	CONCORNACIONA	CACCACAGIA	ATGTAAGGGA	MATICA COTTOC	CPPECTPEAT	OTOCTOACTO	1980
	ACCATORGAG	agas Coctat	TAGGAGAGCA	TAGCATCATG	ATGTATTAGC	TGTTCATCTG	2040
20	CTACTICATE	GATGGACATA	ACTATTGTAA	CTATTCAGTA	TTTACTGGTA	GGCACTGTCC	2100
							2160
	AGGGTGGGTG	AACTTTATTG	TACTTTGGAT	TTGGTTAACC	TGTTTTCTTC	AAGCCTGAGG	2220
	TITTATATAC	AAACTCCCTG	TACTTTGGAT AATACTCTTT	TTGCCTTGTA	TCTTCTCAGC	CTCCTAGCCA	2280
	AGTCCTATGT	AATATGGAAA	ACAAACACTG	CAGACTIGAG	ATTCAGTTGC	CGATCAAGGC	2340
25	TCTGGCATTC	AGAGAACCCT	TGCAACTOGA	GAAGCIGTTT	TTATTTCGTT	TTTGTTTTGA	2400
	TCCAGTGCTC	TCCCATCTAA	CAACTAAACA	GGAGCCATTT	CAAGGCGGGA	GATATTTTAA	2460
	ACACCCAAAA	TGTTGGGTCT	GATTTTCAAA	CTTTTAAACT	CACTACTGAT	GATTCTCACG	2520 2580
	CTAGGCGAAT	TTGTCCAAAC	ACATAGTGTG CATTCTCCAA	TGTGTTTTGT	ATACACTOTA	TORCCCCACC	2640
30	COAAATCTTT	GTATTGTCCA	TTTTGAGGGT	COCROROLA	PARAGOGARA	CARCOCKARA	2700
50	DOLLARDON	a Caccacida	COTATATA	CATTCAGAAC	CAGCAAACAC	TGAATTTCTC	2760
	TRATEGRATE	AACTCTGCCA	CARCARTOCA	ATTTCGTTAA	TGGAGATGAC	TTAAGTTGGC	2820
	AGCAGTAATC	TTCTTTTAGG	CAAGAATGCA AGCTTGTACC	ACAGTCTTGC	ACATAAGTGC	AGATTTGGCT	2880
							2940
35	TAAAAGCATA	TCACTAGCCA	AAGAGGGAAA GTCTTCCAAC	TATCTGTTCT	TCTTACTGTG	CCTATATTAA	3000
	GACTAGTACA	AATGTGGTGT	GTCTTCCAAC	TTTCATTGAA	AATGCCATAT	CTATACCATA	3060
	AEOTTATTTT	GTCACTGATG	ATGTAATGAT	ATATTTTTTC	ATTATTATAG	TAGAATATTT	3120 3180
	TTATGGCAAG	ATATTTGTGG	TCTTGATCAT	ACCTATTAAA	ATAATGCCAA	ACACCAAATA	3240
40	TGAATTTTAT	GATGTACACT	TTGTGCTTGG TACTGTAGGT	CATTAGGAGA	ANGAGRETA	CATCCIGGAA	3300
40	TOCHOCAGA	CATANTTOC	ACTOTOTOGA	PECTGENTE	DESCRIPTION	ACTTATGCTT	3360
	ATTTAATTTA	ATTATTACTT	CAAATCCTTT	GGTCACTGTG	ATTTCAAGCA	TGTTTTCTTT	3420
	TTCTCCCTTTA	TATGACTTTC	TOTGROTTGG	GCAAAGAAGA	AGCTGACACA	COGTATGTTG	3480
	TTAGAGTCTT	TTATCTGGTC	AGGGGAAACA	AAATCTTGAC	CCAGCTGAAC	ATGTCTTCCT	3540
45	CAGTCAGTGC	CTGAATCTTT	ATTTTTTAAA	TTGAATGTTC	CTTAAAGGIT	AACATTTCTA	3600
	BAGCARTATT	AACAAAGACT	TTARATGTTA	TTTTGGAAGA	CTTACGATGC	ATGTATACAA	3660
	ACGAATAGCA	GATAATGATG	ACTAGTTCAC	ACATAAAGTC	CTTTTAAGGA	GAAAATCTAA	3720
							3780 3840
50	AGTTCTATTG	ACATTCCTCA	AGATATTAA	TATCAACTGC	ATTATGTATT	ATGTCTGCTT	3940
30	AAATCATTTA	AAAACGGCAA	AGAATTATAT CTCATAAAAC	AGACTATGAG	GTACCTTGCT	TOTAL TOTAL	3960
	ATGAAAGGGG	AGTIGATAGT	CCAATAATGT	TARTITOGCI	CTTTCCTATA	GROCARCTER	4020
	TABATTABAC	CTATTCTTTC	DARRESSE	ICINIMINOC	CITIOCIDO		
	IMMIIIMAC	CIAIICITIC	AAAAAAAA				
55	Sea ID NO:	461 Protein	seguence				
	Protein Acc	cession #: 1	SP 037504.1				
	1	11	21	31	41	51	
c0	1	1	1	1	1	1	
60	MSRTAYTVGA	LLLLLGTLLP	AABGKKKGSQ LHVTERKYLK	GAIPPPDKAQ	HNDSEQTQSP	QQPGSRNRGR	60 120
	GOGRGTAMPG	EEVLESSQEA	CSFCKPKKFT	RDWCKTQPLK	QTIREE3CNS	RETINRECES	180
	TOLD	IRKEEGSFQS	CSPCKPKKFT	THMATTMCAR	POPPTKKKKY	INVALUENCES	100
	IDDD						
65	Ser ID NO.	462 DNA se	mence				
•••	Nucleic Ac:	id Accession	. #: Bos se	quence			
		uence: 12		-			
=0	1	11	21	31	41	51	
70	1	1		1	1	<u> </u>	60
	ATGAAAGTTG	GASTGCTGTG	GCTCATTTCT	TTCTTCACCT	TCACTGACGG	CCACGGYGGC	120
	TTCCTGGGGA	AAAATGATGG	CATCAAAACA ATATCAGCTG	MAAAAAGAAC	TCATTGTGAA	TUVOUNUMA	180
	CATCTAGGCC	CAGTCGAAGA	TTTTCTCAAG	CIGCITO NOG	CHOCKERATE	AMOUNCACAT	240
75	CCCCTAATTA	CAATTATCAG	AGCAAAGGCT	ACCACAGACT	GCAACAGCCT	GAATGGAGTC	300
	CTGCAGTGTA	CCTCTCIAAGA	CAGCTACACC	TOGTTTTCCTC	CCTCATGCCT	TGATCCCCAG	360
		PEG 01 0000	TGGAGCACTC	CCAAGCTGTG	AATGTCATCT	CAACAACCTC	420
	AACTGCTACC				and ammoust		480
	AGCCAGAGTG	TCAATTTCTG	TGAGAGAACA	AAGATTTUUU		WILLWICH	
00	AGCCAGAGTG	TCAATTICTG	TGAGAGAACA	TCTGCTATAT	ACTCCAAATA	TGCAAATGGA	540
80	AGCCAGAGTG AGGTTTACAA ATTGAAATTC	TCAATTTCTG ATGACCTTTT AACTTAAAAA	TGAGAGAACA GAATTCATCT AGCATATGAA	TCTGCTATAT	ACTCCAAATA GTTTTGAGTC	TGCAAATGGA GGTTCAGGTC	540 600
80	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCBATTTC	ATGACCTTTT AACTTAAAAA GAAATGGAAG	TGAGAGAACA GAATTCATCT AGCATATGAA CATCGTTGCT	TCTGCTATAT AGAATTCAAG CGGTATGAAG	ACTCCAAATA GTTTTGAGTC TTGTTGGCTC	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA	540 600 660
80	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC	TCAATTICTG ATGACCTTTT AACTTAAAAA GAAATGGAAG TGTCAGCCAT	TGAGAGAACA GAATTCATCT AGCATATGAA CATCGTTGCT TGAACATGTT	TCTGCTATAT AGAATTCAAG GGGTATGAAG GCCGAGAAGG	ACTCCAAATA GTTTTGAGTC TTGTTGGCTC CTAAGACAGC	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG	540 600 660 720
80	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC CTGTTTCCAT	TCAATTICTG ATGACCTTTT AACTTAAAAA GAAATGGAAG TGTCAGCCAT TAGAAGACGG	TGAGAGAACA GAATTCATCT AGCATATGAA CATCGTTGCT TGAACATGTT CTCTTTCAGA	TCTGCTATAT AGAATTCAAG GGGTATGAAG GCCGAGAAGG GTGTTCGGAA	GTTTTGAGTC TTGTTGGCTC CTAAGACAGC AAGCCCAGTG	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG TAATGACATT	540 600 660 720 780
	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC CIGTTTCCAT	TCAATTICTG ATGACCTTTT AACTTAAAAA GAAATGGAAG TGTCAGCCAT TAGAAGACGG	TGAGAGAACA GAATTCATCT AGCATATGAA CATOGTTGCT TGAACATGTT CTCTTTCAGA	TCTGCTATAT AGAATTCAAG GGGTATGAAG GCCGAGAAGG GTGTTCGGAA TATACCCTGC	ACTCCARATA GTTTTGAGTC TTGTTGGCTC CTAAGACAGC AAGCCCAGTG CCTGCAGCAG	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG TAATGACATT TGGCTACAGG	540 600 660 720 780 840
80 85	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC CTGTTTCCAT GTCTTTGGAT GCGAACATCA	TCAATTICTG ATGACCTTTT AACITAAAA GAAATGGAAG TGTCAGCCAT TAGAAGACGG TTGGGTCCAA CAGCCAAGTG	TGAGAGACA GAATTCATCT AGCATATGAA CATOGTTGCT TGAACATGTT CTCTTTCAGA GGATGATGAA TGAGTCCTCT	TCTGCTATAT AGAATTCAAG GGGTATGAAG GCCGAGAAGG GTGTTCGGAA TATACCCTGC GGGTGGCAGG	ACTOCARATA GTTTTGAGTO TTGTTGGCTO CTARGACAGO ANGCOCNGTG CCTGCAGCAG TCATCAGGGA	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG TAATGACATT TGGCTACAGG GACTTGTGTG	540 600 660 720 780
	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC CTGTTTCGAT GTCTTTGGAT GGAAACATCA CTCTCTGGC	TCAATTICTG ATGACCTTTT AACTTAAAAA GAAATTGGAG TGTCAGCCAT TAGAAGACGG TTUGGTCCAA CAGCCAAGTG TTGAAGACCT	TGAGAGAACA GAATTCATCT AGCATATGAA CATOGTTGCT TGAACATGTT CTCTTTCAGA	TCTGCTATAT AGAATTCAAG GGGTATGAAG GCCGAGAAGG GTGTTCGGAA TATACCCTGC GGGTTGGCAGG TTCAGTATGA	ACTOCARATA GETTEGAGTO TEGETEGACEC CTARGACAGC ANGOCCAGTG CCEGCAGCAG TCATCAGGGA TEGETAGGGA	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG TAATGACATT TGGCTACAGG GACTTGTGTG TGCCACTGAG	540 600 660 720 780 840 900

85

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WO 02/086443 ACACTGGGGGA ATCTGGCTTC GGTGGTGTCS ATTCTGAGCA ATATTTCATC TCTGTCACTG 1080
GCCAGCCATT TCAGGGTGTC CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAAT 1140 ATCCTTAATT CAGCCTCAGT AACCAACTGG ACAGTCTTAC TGCGGGAAGA AAAGTATGCC 1200 AGCTCACCCT TACTAGAGAC ATTAGAAAAC ATCAGCACTC TGGTGCCTCC GACAGCTCTT 1260 CCTCTGAATT TTTCTCGGAA ATTCATTGAC TGGAAAGGGA TTCCAGTGAA CAAAAGCCAA 1320 CTCAAAAGGG GTTACAGCTA TCAGATTAAA ATGTGTCCCC AAAATACATC TATTCCCATC 1380 AGAGGCCGTG TGTTAATTGG GTCAGACCAA TTCCAGAGAT CCCTTCCAGA AACTATTATC 1440 AGCATGGCCT CGTTGACTCT GGGGAACATT CTACCCGTTT CCAAAAATGG AAATGCTCAG GTCAATGGAC CTGTGATATC CACGGTTATT CAAAACTATT CCATAAATGA AGTTTTCCTA 1560 10 TTTTTTCCA AGATAGAGTC ARACCEGAGC CAGCCTCATT GTGTGTTTTG GGATTICAGT CATTTGCAGT GGAACGATGC AGGCTGCCAC CTAGTGAATG ARACTCAAGA CATCGTGACG 1620 1680 TOPPATOTA CTCACTIGAC CTCCTTCTCC ATATTGATGT CACCTTTTGT CCCCTCTACA 1740 ATCTTCCCCC TTGTAAAATG GATCACCTAT GTOGGACTGG GTATCTCCAT TGGAAGTCTC 1800 ATTTTATGCC TGATCATCGA GGCTTTGTTT TGGAAGCAGA TTAAAAAAAG CCAAACCTCT 1860 15 CACACACGTC GTATTTGCAT GGTGAACATA GCCCTGTCCC TCTTGATTGC TGATGTCTGG 1920 TITATICTIC CICCACACT CCACACCACC CICAACCCTT CICCACTCTC CACACCTCT 1980 CTGTTCTTTA CACACTTCTT CTACCTCTCT TTGTTCTTCT GGATGCTCAT GCTTGGCATC 2040 CTGCTGGCTT ACCGGATCAT CCTCGTGTTC CATCACATGG CCCAGCATTT GATGATGGCT GTTGGATTTT GCCTGGGTTA TGGGTGCCCT CTCATTATAT CTGTCATTAC CATTGCTGTC 2160 20 ACGCAACCTA GCAATACCTA CAAAAGGAAA GATGTGTGTT GGCTTAACTG GTCCAATGGA 2220 AGENTACIONE RECUGGERRA ROPROSCOTO GENERAGERA TROPOGERATO GANCITECTO 2280 CTGGTGCTGC TAGTTCTCAC AAAGCTCTGG AGGCCGACTG TTGGGGAAAG ACTGAGTCGG GATGACAAGG CCACCATCAT CCGCGTGGGG AAGAGCCTCC TCATTCTGAC CCCTCTGCTA GGGCTCACCT GGGGCTTTGG AATAGGAACA ATAGTGGACA GCCAGAATCT GGCTTGGCAT 2460 25 GTTATTTTTG CTTTACTCAA TGCATTCCAG GGATTTTTTA TCTTATGCTT TGGAATACTC 2520 TTGGACAGTA ACCTGCGACA ACTTCTGTTC AACAAGTTGT CTGCCTTAAG TTCTTGGAAG CARACAGANA ASCARACTC ATCASATTA TOTOSCARAC CCARATTOTC RARGOCTITO
ARCCOCTIGO ARACAMACTG CONTINUOS TITTOTCHA CTGGAGATTC CTCCGACAAC ATCATGCTAA CICAGTTTGT CTCAAATGAA TAA 30 Seg ID NO: 463 Protein sequence Protein Accession #: Bos sequence 35 MKYGYLWLIS PFTFTDGHGG PLGKNDGIKT KKELIVNKKK HLGPVEEYOL LLQVTYRDSK EKRDLRNFLK LLKPPLLWSH GLIRIIRAKA TTDCNSLNGV LQCTCEDSYT WFPPSCLDPQ NCYLHTAGAL PSCECHLINL SOSVNFCERT KIWGTFKINE RFINDLINSS SAIYSKYANG IEIOLKKAYE RIOGPESVOV TOFRMGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 200 LSILEELNKN FSMIVONATE AAVSSFVONL SVIIRONPST TVONLASVVS ILSNISSLSL ASHPRVSNST MEDVISIADN ILNSASVINN TVILREEKYA SSRLLSTLEN ISTLVPPTAL 420 PLNFSRKFID WKGIPVNKSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQRSLPETII SMASLITUMI LEVSKNONAQ VNOPVISTVI QNYSINEVPL PFSKIESKIS QPHCVFNDFS HLQWNDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPST IPPVVKNITY VGLGISIGSL 540 ILCLIIRALF WKQIKKSQTS HTRRICMUNI ALSLLIADVW FIVGATVDTT VNPSGVCTAA VPFTHPPYLS LPFUMLNIGI LLAYRIILVF HHMACHIMMA VGFCLGYGCP LIISVITIAV TOPSNITYKEK DUCKLAWSNG SKPLLAFUVP ALAIVAVNEV VYLLVLIKLW RPIVGERLSR DDKATIIRVG KSLLILTPLL GLTWGFGIGT IVDSONLANH VIFALLNAFO GFFILCFGIL 50 LDSKLROLLF NKLSALSSWK OTEKONSSDL SAKPKFSKPF NPLONKGHYA FSHTGDSSDN INLTOFVSNE Sen ID MO: 464 DNA semience Nucleic Acid Accession #: AB035089.1 55 Coding sequence: 9845..10219 41 61 GGGCATGCAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60 CAGITCINGT ARANGGGAGA ACNICANTAT AGGAIGITTC TIAGCARTAG ARAARGAAGG CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTTGGT TROOPEROAL ACCORDANCE AND TOWNS TOTAL CONTROL OF THE STATE OF THE STAT AGGAGGAAGG GAGGCAAGAG ATAATATCAT TITCICTGTG CTCCAACTGT ACTTACATAT GAGACTATTT CCCTCTCTGC TTTTCAAACC TTACTGGAGT TGTTTTCCCT CATGAAAACC 360 AAGAAAGGAA AGCTAGTTAG TCTTGTTCTG AGGTTGTTCA ATGTATACAT ATCTATATCT 420 GTAGACAGAA TOCTTOGGAA TACAGTAATT GACATATATT CTGTTATTIG ATGCTTGAAA AATCTCCTCC ACTAACCAGT TTCCCTATAG ATTGCCACAA GCACATAATA AGAACAATA 540 AATAAAATGT TCTCTTGACT TTGTTACTTA ACAATGCTGA GAAAACTTTA CAGCCTTCAT 600 AAGGAAGTGA GOTCCAGGAA AATCTAGGAG ATATTTCTTA ACCAATCTAT AAAGGCATTA 660 70 GTAATGACAG GATATTTCCT GAAAGTGTAA TITCCCAFTG AGGATTTGTT TITAATTTCT 900 75 TTCAACCITC AGGGCAAACC TCCGTGCCTC AGACGTTTAG CCATAGTCTG AAATTCTCTT

2340 2580 2640 120 360 600 660 720 900 120 180 240 480 720 790 1020 1080 CCATAGATIC CICCCCIGTA ACCCCGGITT GICTCAGCTI GITATCCIGT TITTTCTTC 1140 CCTCCATTCC CAGGATGAGC TTGTTGCTTC TGTCCTATGA GACATTAGAT TCCTTTTCTT 1200 TGGTACCOGA GTAAATCCAT CCTACTCCAA TAGAGGAAGG TCCATTITTG TCTTATAGCG 1260 CTGGATGCAG ACTCAGCTGA GAAGACCATT ATTCATTTTT GGAATTCTTT ATCTCAGATA 1220 TITECTCTTC TITETTTTC TICTATETT GGATTTTAG TOCATCAAGG CCCCATTAGT
CTATTCCCCG ACTTCAATCA GGGAACTTAT ACCTCTTAAA CTCATTCAGA GACTCAAAAC 1380 1440 ATATATATTG ATACAGGAGA CCTAAGAAGA GCATGTCTTG GGGGTTGAGG AAACAGGCAG 1500 GTGAGAAATT TCCAGATTGG AAACACAGCT TCCTTTCTCC CATCCAGCCC CTACTTTCAG 1560 CCTATGTGTT TCTGGCACCT TGTTGTAGAT AAATCTCCCT TGACTTTGTG ATGTGCTGAG 1620 ANARCARCT CACGCTGGT GTTRARANGG GCCCATGACA ATACCAAGTG TTGGGGGAGAA
TGGGGGAGAA TCACAACTCT ATTCACGCTC GGTTGGAATG CACACTTGTG CAGAATTCTA 1680 1740

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	TTTCATTCAT	AGGTTTATAC ACAACATCAT	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
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5	ATCARCTTAT	MICHAGRA	CCATCCAMC	ATTOMINGAL	ACCATGABA	TAACACTAGA	2040
-	mmx x x co a c c	CACTOACAAA	ACCACTPACT	CTATCATTCC	ATTTACCTGA	APETTTEGA	2100
	ATAGGCAAAT	CCATAGAAAC	AGGAGGTAGA	TTCCTGGTTT	CCAGGGTCTC	CAGGAAGGGA AGATCATGAT	2160
	AGAATGAAGT	ACAAGATTTC	TTTTGGAGGT	AGTGAAATTG	TTGTGGAATG	AGATCATGAT	2220
10							2280 2340
10	TATATAAATT	ATATGTTAAT	AAAAAGGGGG	CCACACAAAC	CCCTCTCCCC	CCACTCTGGT GGCCACAGAC	2400
	ATTOTTCAGA	TTACABGATA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	
	ARACAGAAGG	ACCATTGAGA	AATGTTGTGA	TCCTGACAGG	TCAAGCAATT	GCCAGGTGCT TATTTTTCGG	2520
	CTICATTTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTTAAA	ATGGCCCGTC	TGTTTCAATT CTGCTGATAA CCACGTGATT	2580
15	GCTCTTCTCA	GTGTCAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAATTGG	GCTTAGAGTT	GCTGCAAGAG	2760
	AACATGAGGA	ACCACACA	GRAGARACCC	CTGATAAACC	CATCGGATCT	CCTGAGGCTT	2820
	AAGATGAGGA ATTAACTATC	ATGAGAATAG	CACAAGAAAG	ACCGGCCCCC	ATGATTCAAT	TACCTCTACC	2880
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	GGGAACACAG AACAGAAAAC	CCAAACCATA	TCACTCAGCA	AGGCAGATAA	CTTTCTCACT	GAGCCTATGC	3000
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	CAAAGCTGAG	CACTCAGGAG	AAGGCAATAG	AATCCTATTC	MACCACEACA	CONTROLL	3180
25	TACEGARAGA	TTACTAGGA	AATTCATAGG	ATGACAAAAA	CTTTCAGAAC	TTCCTTGTTA TGAAAAACAG	3240
							3300
	CAAGAAAAGA	ATGGTGGGGT	TTTTGTTTGT	TIGGITTIGI	TTTTGTTTTA	CAGCTGGAGT	3360
	AGAATACAAA	GGGATGGAGT	TGAAACAAAT	GAGAGGAAAT	TGGAAT TCTA	CAGCTGGAGT AACTTATTCT	3420
30	CATTGGCATT	AGANAGGCAC	CTACATGTAT	TTCACATGAG	CCGGTGACTG	CTGACTTGCA AATCCTGTCC AATCTGAAGT	3480
30	TTCTTATTTT	TTCCCTATAG	ATTAAAAAGG	AGGTACAATG	GIMONACIGI	AMPORTANCE	3600
							3660
							3720
	GGAACACAGG	TAAGAGCTTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTGAGAAT ATATTTTACT ATCTAAATTG	3780
35	AATAATGATA	CIGIGITA	TATCATGCAT	CTCCTGCATT	CTGTCTGATT	ATATTTTACT	3840
	TATTCTGCCA	GAGCAAAATT	AAAATACCTA	TTTCATCTGA	TTTGTCCTTT	ATCTAAATTG	3900
	CTTAGTICCA	AGTAAACCAA	GUCACITITA	DOMESTICACIÓN.	MOOTE CONTROL	CTTGCAGCCA	4020
	AGGRETETE	TTAGCATTCA	TTGTAAGGC	ATCCTACCTA	GCTCTAGTGT	AACCAGCAAT	4080
40	GAAAGAAAGA	TAAAGAGGGT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTTG	4140
	TAAGCCTTCT	AATTAGGACA	TTAATATATT	TAATATATGC	ACATTGTAGA	AAGATTGAAG ATATCATTTC	4200
	COTTANAAAT	AAGAGAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTC	4260
	TTTAAGAAAA	TTGTACTACA	AAATACCATT	CCATTTATTA	ANGTCATTCT	GACAGGAATC	4320
45	TGATGCTTTT	CCAGGAGTTC	CAGATCACAT	ACAGETCACC	ATGAATTCAC	GACAGGAATC TCAGTGAAGC AGAACAACAT GAGCCAAAGA CCTGTGCAG	4440
73	CTTCTATTCC	CCTATCAGCA	TCACATCAGC	ATTAGGGATG	GTCCTCTTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCAG	4560
							4620
50	AGCACAGGGG	GCTGTGCAGG	AATTCCCATA	ACTGTGAGAC	CACTGACTTA	AA CAGATCTT TTGATCAAGT	4740
30	TTGAGTAAAG	TTTTCTTGTC	CCGCTTCATG	TOTOTTOCAG	ACTICATION CACAGO	CACTCTGATT	4800
	CACAGAGAAC	TOCCTGAACA	GCTCATAGTT	TABACCTGGA	ACTTCACAAA	CACTCTGATT AACTAAGAAA GGGTTGGCAT	4860
	AGGCCAGTTT	TAGGGAAAAT	CTTGGACACA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
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55	CCTCAGAGCA	TAGGTCTGGA	TCAGGATAGG	CTGGGTTCAG	ACTCCAGCTT	TGCTCTTCAC	5040
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65	PROCENTAGE	CLOTCLATOT	GEOGRAPH	ATANTAGCAC	CAACAGGTAT	AACAGGGCTT	5640
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							5760
	AACOCTTTAA	ACCAACAAGG	AGAAAATCTA	CTGGTAGACA	GCGCTGCATC	TTTAGTTCAG TCAAATATAA AACATCAAAG	5820
70	AAGAGAAAAG	ATTGCAGTAC	GTTAGAGCAA	GAAGAATTTT	CTGGAAGAAG	TCAAATATAA	5880
70	GGTGGATTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAT	AACATCAAAG	6000
	GTCCTCAATG	AGACTACCAG	CATTTAGGGA	COTTO	TOTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TGGGTTTAGT TTGATAGGTC	6060
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75	AATTTCACCT	GGCCTACCCA	CATTTCATTT	GCATCCTGAT	GTCTGTGTCT	TTTTACAGGT CTGAGTGGCC	6240
	GTGCATTAGC	TCCATTTCCA	CAACTCTCCC	CUACTGGAGT	GICCCAGACC	CCAACGATAC TGTAATAGAG	6360
	ATCACTGAAG	TOTGGATTTA	GUGATAATCT	TGTGATAAAA	CCCACTGACT	CACTUACATA	6480
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	GTGAGTTCCT	GAGAATAGTT	GAGGAAGTAC	CAGGAAATAT	TGAATGCACA	GGATGAANGA	6600
							6720
85							6840
03	TTTTGCATTG	CCTACATGAC	ACCTGTATAA	TACABATAN	TANGTTOGGA	TACTGCATCT	6900
	TACATAAATT	ACTOCTAATT	CCTACTTCTT	CCTTCATATC	TCAAAGGAAT	ATTTAGATGC	

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	CATCAAGAAA	TTTTACCAGA AAGATTAACT	CCAGTGTGGA	ATCTACTGAT	TTTGCAAATG	CTCCAGAAGA	7020
	TEATACAAAC	ACCOUNTED A	BACCESTOCC	ACTGAGCCTT	GEGGETTGACA	CTGCATGGGG	7140
	GAACAGGTGT	GGGGATTGAG CARATGAATA	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
5	AGGATTTGTC	CARATGARTA TGGARACACA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260 7320
	GCCAATTAGA	CCCTGTCTCC	CCCCAGAGAAT	ATTTTCACATA	CATATOCTTT	ACTIVADANC	7380
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10	CTGCCTGGAT	CACATCTGTA	GCCAATGTGT	TCTGCAGGGA	TTATCACAGC	TCTCTTCCCC	7560 7620
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	GTTTATCAGT	ATTCCAAATC CAAGAAGTGA	AGATGATTGG	AGACATTCAT	ACACAGAGAA	COTGAACTCC	7920 7980
	AGNANGETGE	атстоотова	CCACTGGTCA	GTGAGTCTAA	CAATTCAAAG	ATCAAAGTCA	8040
	GEGRATETCA	AGCAGGGATT	TGGGGTCAATA	ATTAACGATC	AGTCACGAAC	ATTTGCAAAG	8100
20	CATCTTCCAG	ACAAGCCATT	TGTAGCTTGT	GTAAAAGACT	CTTTTATTCT	TTCCCTTGCA	8160
	GAAAAAATTA	AAAACCTATT	TCCTGATGGG	ACTATIGGCA	ATGATACGAC	ACTGGTTCTT	8220 8280
	GTGAACGCAA	TCTATTTCAA	AGGGCAGTGG	TOTATATAT	ATTTATATATA	TOTALTATOT	
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25	TTGTTCATGT	CTGTTATTTT	GTTGTTTTAC	TCTTATAACT	TTATTTAGTT	AGGAATACCT	8460
	GAAAAACTAT	TGTTTCTAAC	TCATGGAATT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520 8580
	TGTTGCTATC	TCAATAATAT	TATCTTTTT	CTCTTGIGIT	CAUGIGITA	TACEATTCCT	8640
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	CTTGCATCTA	CAACTCTTCC	TTCTACTGCC	GGACATTTTT	CCARAGATAC	CAAGTTTAAA	8820
	CAAGGTAAAA	GCTTATGACC	GAGTTGCCTC	AAAATGATGA	MANATTUTAR	MODA A COMMA	8880 8940
	ATGACTCACC	COTTOTOTO	TOTTATTON	ATTATTATAA	TACTTTAAGC	TTTAGGGTAC	9000
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	CCATTAACTC	ATCATTTAGC	GTTAGGTATA	TCTCCTAATG	CTATCCCTCC	CCCCTCCCCC	9120
	CACCCCACAA	CAGTCCTCAG	AGTGTGATGT	TACCTTCCTG	TGTCCAAGTG	TTCTCATTGT	9180 9240
	TORATTOCCA	TCTATGATTT TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
40	AGAAATATAT	ACCAATGTGA	GGAAAGTTTA	CAAATAGGCC	GAGTAGAAAA	GGGAATACAA	9360
	GAAAAATATG	ATGAGCCTAT ACAGTTCATT ACATACATAT	TAAAAATTGA	CACATGTAGT	AGGCTGTTGG	CACAAGAAAT	9480
	AGTGATACAT	ACAGITCATT	GTGTACAAAA	ACATATACET	ABBABCATCA	TTCTGTTTTT	9600
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	CCAAAATAAC	GAATCTCCAC	ATAGTCAATT	CATTGTTAAG	GTGTATTAGA	GATCGACAGT	9780 9840
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	CARTATOTTO	ANTIGOGGATO	CAGACCTCTC	AGGCATGACC	TGGAGCCACG	GTCTCTCAGT	10020
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	TTCTCTCTTT	CTCTTAATAA	GCCCACATAT	AAATGTACTT	TTOCTTCCAG	AAAAATTTCC	10440
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	GGGGCATAAA	ATTATCATAT GAAAGAACAG	CCACATCTAG	AAAATACATC	TCTGGCTACG	CTGATATCAA	10980
	TGGATGCGAG	GAAAGAACAG	TGTGGTTACC	ATATATAAAT	TAGGAAATCA	TTAGAGTATT	11040
70	GGGAGTGGAA	ATOGAGAGAA	AGAAAGAGCC	TGGGGGGAATT	ATTTAGGAAA	TAATAGTTAC	11100
/0	AGAAAGACAT	CTAAGTTGCT	CAUCTATCTG	ACTUSATEGA CTACTTCATC	AATTAAGGTA	CTTTTAATAT	11220
	TCAAATGGAT	TTGCCTGGCA	GGCACTTGAA	GATATTAGTC	TARATCTCAG	AAACAGAATA	11280
	TGATCTGAAG	TTGCCTGGCA CTCTAAATTT	GTGATATTCA	ATATAAATAC	TTTAGAGTCA	TIGGGATAAA	11340
76	TATGGTAGTT	GTAGCTAAAA	GCANAANTAA	GATACTAGGG	AGAAAGGATA	AAGTTAGAAG	11400
75	AAAGAAGAAT	CTAGAATTGA TTCCAGAAAG	CCTTGAAGTA	TATCAGCATG	TOTALAGATC	CATAGATTGAT	11520
	TCCC	TYCCAGAAAG	TAGCITTTCT	INGGGTTCLA	INTIIMCICC	CHARGATTCI	11320
0.0	Seq ID NO:	465 Protei	n sequence				
80	Protein Ac	cession #:	BAB21525.1				

1 21 31 41 51

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PRESIDENT ENTRY PROPURE SERVICE PROPURE ELIMANCIA CONSTRUCTOR
DAIREVOTS VESTURARS ESSERCISSI VESOTREKE MILHOROTOR UTTILVIOLAT
PROCORDET RESTRUCTURE PRESENTATIVES OPERCUTARS PALLEDURAS. VELLEPPERSO

85

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	TMGMVNIFNG	IDGLQKLEEK DADLSGMTWS	LTAEKLMEWT HGLSVSKVLH	SLQNMRETCV KAPVEVTEEG	DLHLPRFKME VEAAAATAVV	ESYDLKDTLR VVELSSPSTN	300 360
5	Seq ID NO: Nucleic Act	FFIRQNKTNS 466 DNA set id Accession sence: 50	uence	910.1			
		11	21	31	41	51	
10	GGAGAGAAGA CCTTCTTTTG GCCCCTCAGG	AAGGAGGGG CTGCTGGTGC	CAAGGGAGAA TCCTGGAGCT	GCTGCTGGTC	GGACTCACAA CAAGGATCCC	TGAAAACGCT	60 120 180
	GCCCCTCAGG		TOGACATGAT	CCAGTTCACC	GEACGGAGGC		240
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	CCCTCTGTG	CCACAGAACT	TCACTGTCAT		GGCTCCTCCA AGCAGGTTCC		360 420
	GTCCAGCACA	TACAGCCAGC	CAGGTCAATC	TTTCTCCATT	CAGTATGGAA	CCGGGAGCTT	480
20			ACCAAGTCTC AGCCAGGCCA				540 600
20	TCTGGGCCTG	GGATACCCCT	CCTTGGCTGT	GGGAGGAGTG	ACTCCAGTAT	TTGACAACAT	660
	GATGGCTCAG	AACCTGGTGG	ACTTGCCGAT TGATTTTTGG	GTTTTCTGTC	TACATGAGCA	GTAACCCAGA	720 780
	CCTGAATTGG	GTCCCCAGTCA	CCAAGCAAGC	TTACTGGCAG	ATTGCACTGG	ATAACATCCA	840
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	CCCCCCCCCAT	GGAGAATATG	CCGACAAGAT	TGCCAACCTT	AACGTCATGC	CGGATGTCAC	1020
	CTTCACCATT	AACGGAGTCC	CCTATACCCT	CAGCCCAACT	GCCTACACCC	TACTGGACTT	1080
30	CGTGGATGGA	TGGATCCTGG	GCAGCAGTGG	CRITICAAGGA	TTTTACTCAG	ACCCTCCAGC	1140
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	CCTGCCTGTC	TGACAGACCT	TGAATATGTT		ATTCTTTACA	ACCARACAGA	1320
	ACATGAGAAT	ACACACACAC	ACACACATAT	ACACACACAC	ACACTTCACA	CATACACACC	1440
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	GCAGAGATCA	TGGTATAATA	AATCCCTTTG	CAACTCCACT	CAGCCCTGAC	AACCCATCCA	1620
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40	TACCIGGAT	AAATATACAA	CAAATTCCGA TCGGAATTCA	AGCATCTCCC			1800
	CTGTTTTTGT	AGTTGGATTG	TTTGTATTAG	GATTCAAGCA	AGGCCCATAT	ATTGCATTTA	1860
	TTGAAATGT	CTGTAAGTCT	CTTTCCATCT	ACAGAGTTTA	GCACATTTGA	ATAAAATGGT	1920
4.5	AGTTAGATCT	GGAGGTCTGA	TTTTGTGGCA	AAAATACTTC	CTAGGTGGTG	CTGGGTACTT	2040
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	Seq ID NO:	467 Protein ession #: 1	n sequence				
50	Process Ac-						
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	MKTLLLLLLV	LLELGEAQGS	LHRVPLRRHP	SLKKKLRARS	QLSEFWKSHN	LDMIQFTESC	60
55	SMDQSAKEPL	INYLDMEYFG	TISIGSPPON TGSLSGIIGA	PTVIFDTGSS	NEWVESVYCT	SPACKTHSRF	120 180
55	PROTECTION	ST-AUGGUTPV	PRIMMAGNILY	DLPMFSVYMS	SMPEGGAGSE	LIFGGYDHSH	240
	FSGSLNWVPV	TKOAYWOIAL	DNIQVGGTVM PDVTFTINGV	FCSEGCQAIV	DIGISLITGP	SDKIKQLQNA	300 360
	HPPAGPLWIL	GDVFIROFYS	VFDRGNNRVC	LAPAVP	DDD1 4DG/4Q1	Copproduct	300
60							
	Mucleic Ac:	468 DNA sei id Accession ence: 319.	n#: NM_018	3058.1			
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	GACGGCCGGG	AGGAGATCTA	CTTCCTCAAC	ACCANTANTO	CCTTCTCGGG	GGTGGCCACG	120
70	GTCAACGTGG	CCCGTGGTGT	CCCCACCCTC	TTTGCCGGAC	GCTCTGTGGC	CTGTGTGGAC	240
	AGANAGGGCT	CTGGACGCTA	CICTATCTAC	ATTGCCAATT	ACGCCTACGG TCTCCCGGGG	TAATGTGGGC	300 360
	CTGATGCCC	TCATTGAAAT	GGACCCTGAG	GCCAGTGACC		AGGCOTCAGC	420
75	GTGGGCCCCA	TCCTCAGCAG	CAGTGCCTCG	GATATCTTCT	GCGACAATGA	GAATGGGCCT	480
75		TCCACAACCG CCCACCAGCA	GGGCGATGGC		ACGCTGCGGC	CCGTGATOR	540 600
	AAAGTGGACA	TOSTCTATGG	CAACTGGAAT	GGCCCCCACC	GCCTCTATCT	GCAAATGAGC	660
		AGGTCCGCTT TCATCACCGC	CCGGGGACATC	GCCTCACCCA AATGACCAGG	AGTTCTCCAT	GCCCTCCCCT	720 780
80	AACATTGCCT	ACCGCAGCTC	CTCAGCCAAC	CCCCTCTTCC	GCGTCATCCG	TAGAGAGCAC	840
	GGAGACCCCC	TCATCGAGGA	GCTCAATCCC	GGCGACGCCT	TGGAGCCTGA	GGGCCGGGGC	900 960
	GGAGAGTCCA	TOGCTCAGCC	CTTCGACGGA	TTCCGGGGGCA	ATCAGGGCTT	CAACAACAAC	1020
0.5	TOGCTGCGAG	TOGTGCCACG	CACCCGGGTT	GGGGCCTTTG	CCAGGGGAGC	TANGGTCGTG	1080
85	TOTALGATION	NOCCCOTTOGC	ACACTTTTCCC	CTGGGGAAGG	ATGRAGCCAG	AGGCTACCTG CAGTGTGGAG	1140
	aman acmada	CRGATGGCAA	GATGOTGAGC	COGRACCING	CCAGOGGGGA	GATGAACTCA	1260

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			TTCCCATTCG			TACGAGCCCA	1380
			GTGGGGACTC				1500
5	CCCCCACCGC	TOCTGCTGCC	ACTGCCGCTG	CTGCTGCCGC	TGCTGGAGCT	GCCACTGCTG	1560
	CACCGGTCCT	CGTAGATOGA	GATCTCAATC GGACATGAAC	TOGGGTCGGT	GGTTAAGGAG	AGCTGCGAGC	1620
	AAGTGGGCTT	GTGCTGCTGC	CTAGACAGTA	GGGATGTAAA	GGCCTGGGAG	CTAGACCCTC	1740
10	CCCAAGCCCA	TCCATGCACA	TTACTTAGCT	AACAATTAGG	GAGACTCGTA	AGGCCAGGCC	1800
10		CACATAGCTG	TGATCA CAGC CATATCTTAG	AGACAGGGTC	GCTGCCCTGA	TGGCGCTTAC	1860
	CTGCACAGGA	AGTATGAGGA	CTTTAGTGTC	CTGAGTTCAA	ATCCTGATTC	AGGAACTCAC	1980
	AAAGCTATGT	GACCTTACAC	CAGTCACTTA	ACTTGTTAGC	CATCCATTAT	CGCATCTGCA	2040
15	AAATGGGGAT	TANGANTAGA	ATCTTGGGGT	TAGTGTGGAG	ATTAGATTAA	ATGTATGTAA	2100 2160
13	GGGCTTTGTC		GCACATAGIA	Modercon	reception of	occiciono.	2200
		469 Protein					
	Protein Acc	ession #:)	I sequence				
20			_				
	1	11	21	31	41	51	
	MDPEASDLSR	GILALEDVAA	EAGVSKYTGG	RGVSVGPILS	SSASDIFCON	ENGPHFLEHN	60
25	RGDGTFVDAA	ASAGVDDPHQ	HURGVALADF	NRDGKVDIVY	GNWNGPHRLY	LOMSTHCKVR	120
25		MPSPVRTVIT EGRGTGGVVT	ADFONDQELE DFDCDGMLDL	IFFNNIAYRS	SSANRLFRVI	RREHGDPLIE	180 240
	RTRVGAFARG	AKVVLYTKKS	GAHLRI IDGG	SGYLCEMERY	AHFGLGKDEA	SSVEVTWPDG	300
	KMVSRNVASG	EMNSVLEILY	PRDEDTLQDP	APLETPMNAS	SSHSCALETS	PYVSTPMEAT	360
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	Coarua sedu	dence: 1	702				
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40	AGTAATCCCA	CCCAGCTCAA	CTATGGTGTG	GCAGTTACTG	ATGTGGACCA	TGATGGGGAC	180 240
40	CAGAAGCGGC	TOGTGGACAT	CGCGGTCGAT	GAGCGCAGCT	CACCCTACTA	CGCGCTGCGG	300
	GACCGGCAGG	GGAACGCCAT	CGGGGT CACA	GCCTGCGACA	TCGACGGGGA	CGGCCGGGAG	360
	GAGATCTACT	TCCTCAACAC	CAATAATGCC	CACA TOTTO	TGGCCACGTA	CACCGACAAG	420 480
45	CCTGGTGTGG	CCAGCCTCTT	TGCCGGACGC	TCTGTGGCCT	GTGTGGACAG	AAAGGGCTCT	540
			TGCCAATTAC				660
	COTGOTGLGG	CTGGGGTCAG	CARATATACA	GGGGGCCGAG	GOSTCAGOST	GGGCCCCATC	720
	CTCAGCAGCA	GTGCCTCGGA	TATCTTCTGC	GACAATGAGA	ATGGGCCTAA	CTTCCTTTTC	780
50	CACAACCOOG	GCGATGGCAC	CTTTGTGGAC	GCTGCGGCCA	GTGCTGGTGT	AGRACIACCCC	840 900
	GTCTATGGCA	ACTGGAATGG	CCCCCACCGC	CTCTATCTGC	AAATGAGCAC	CCATGGGAAG	960
	GTCCGCTTCC	GGGACATCGC	CTCACCCAAG	TICTCCATGC	CCTCCCCTGT	CCGCACGGTC	1020
55	ATCACOGCOG	CAGCCAACCG	TGACCAGGAG	GTCATCCGTA	GAGAGCACGA	AGACCCCCTC	1140
	ATCGAGGAGC	TCAATCCCGG	CGACGCCTTG	GAGCCTGAGG	GCCGGGGGCAC	AGGGGGTGTG	1200
	GTGACCGACT	TCGACGGAGA	COGGGGGCAAT	GACCTCATCT	TGTCCCATGG	AGAGTCCATG	1260 1320
	GTGCCACGCA	CCCGGTTTGG	GGCCTTTGCC	AGGGGAGCTA	AGGTCGTGCT	CTACACCAAG	1380
60	AAGAGTGGGG	CCCACCTGAG	GATCATCGAC	GGGGGCTCAG	GCTACCTGTG	TGAGATGGAG	1440
	CCCGTGGCAC	TOTTTGGCCT	GGGGAAGGAT GAACGTGGCC	AGCGGGGAGA	TGRACTCAGT	GCTGGGGGATC	1500 1560
	CTCTACCCCC	GGGATGAGGA	CACACTTCAG	GACCCAGCCC	CACTGGAGTG	TGGCCAAGGA	1620
65	TTCTCCCAGC	AGGAAAATGG	CCATTGCATG	GACACCAATG	AATGCATCCA	GTTCCCATTC	1680 1740
05	AACAAGAAGT	GCAGTCGGGG	CTACGAGCCC	AACGAGGATG	GCACAGCCTG	CCTCGGGGACT	1800
	CTCGGCCAGT	CACCGGGCCC	CCGCCCCACC	ACCCCCACCG	CTGCTGCTGC	CACTGCCGCT	1860 1920
	GCTGCTGCCG	CTGCTGGAGC	TGCCACTGCT	COCACOGGTCC	GAGCAGGGGT	GGGGCATGAA	1920
70	CCAGCGGATG	GAGTCCAGCA	GGGGAGTGGG	AAAGTGGGCT	TCTCCTCCTC	CCTAGACAGT	2040
	AGGGATGTAA	AGGCCTGGGA	GCTAGACCCT AAGGCCAGGC	CCCCAAGCCC	ATCCATGCAC	ATTACTTAGC	2100
	CAGACAGGGT	CGCTGCCCTG	ATGGCGCTTA	CATTCEMETG	GGTCTAATGA	CCATATCTTA	2220
70	GGACACAGAT	GTGCCCAGGG	AGGTGGTGTC	ACTGCACAGG	AAGTATGAGG	ACTITAGIGT	2280
75	CCTGAGTTCA	AATCCTGATT	CAGGAACTCA TCGCATCTGC	CARAGCTATG	TGACCITACA	ANTOTTOGO	2340
	TTAGTGTGGA	GATTAGATTA	AATGTATGTA	AGACACTTGG	CACAAAACCT	GGCACATAGT	2460
	AAAGGCTCAA	TAAAAACAAG	TGCCTCTCAC	TGGGCTTTGT	CAACACG		
80	Sert ID MO-	471 Protei	n secuence				
00	Protein Acc	cession #:	CAC08451				
			21	21	41	51	
	1	11	1	31 	î*	Ĩ.	
85	MSRMLPFLLL	LWFLPITEGS	QRAEPMFTAV	TNSVLPPDYD	SNPTQLMYGV	AVTDVDHDGD	60
	FEIVVAGYNG	PNIWLKYDRA	QKRLVNIAVD LFKFRMNRWE	DILEDRINUA	DROGNALGVT	SUACUDREGS	120
	D-11 DE INDA	- SOVALLIDA	D. A. MINNE		ALC:	5	_ 30

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WO 02/086443
GRETYLYIN YAMVORDAL IBGPEAREL SRGILALRDY AREGVERET ORROVEVET LESSEADITÉ DEROCHTÉLE BRECOTTO MALBIANDO BURICHOVALA DEBEGORIO LESSEADITÉ DEROCHTÉLE BRECOTTO MALBIANDO BURICHOVALA DEBEGORIO LESSEADITÉ DE BURICHOVALA DEBEGORIO LESSEADITÉ DE LESS 360 420 480 540

Seq ID NO: 472 DNA sequence

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15	1	11	21	31	41	51	
13) TOO COTTON	CGGGAGGACT	CCCAGCCCCC	TOCTOTOTT	GGATGGGACT	GGGTGGGCCC	60
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20	TCACCCTACT	ACGCGCTGCG	GGACCGGCAG	GGGAACGCCA	TCGGGGTCAC	AGCCTGCGAC	240
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	TOCTOCCTOC	GTCAGGCTTC	TOTGGACAGO	MGGCAGGGAG	AGAGGGTGCC	GGTTCCCTGC	480
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25	GGGGTGGCCA	CGTACACCGA	CAACTTGTTC	AAGTTCCGCA	ATAACCGGTG	ACCCAAATCA GGAAGACATC	600
	CTGAGCGATG	AGGTCAACGT	GGCCCGTGGT	GTGGCCAGCC	TCTTTGCCGG	ACGCTCTGTG TTACGCCTAC	660 720
× •	GCCTGTGTGG	ACAGAAAGGG	CTCTGGACGC	ATGGACCOCTG	AGATIGGGAA	CCTCTCCCGG	780
	GGCATTCTGG	CGCTCAGAGA	TOTOGCTGCT	GAGGCTGGGG	TCAGCAAATA	TACAGAAGGC	840
30	TTCTCCCACA	CTGCCTCTCC	AAGCATIGGT	GAGATATCTG	GCAGAACCGA	GGAGCGGGAA	900
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	TGCCGGCTGG	CTGGGGCAGC	COGGCAGTTC	AAGGAAGAAG	CAGCAGCTTT	GGTGGAGGAA	1020
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35	GCGCCTTCTC	CAGCCCACCC	TTTCCCTGCC	CGCCAAGCCC	CCCAACACTA	CCCTGTAGCC	1200
	CCCCTTGTCA	CTCAGCTAAT	GACACATGGA	CCTCTGGCTG	GAAAACTAGC	CCGGAGTGTC	1260
	CCCCACCCCC	GAGCCCCAGG AGGCTTTGGG	AATGGACCCC	AAATGTAAGG	GCCGCCATGC	TGAGCCCGGC	1320 1380
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40	GAGCTGGGAG	GTCCCTGGAG	CCAAGCCACA	CAGCACCTGC	CTGCTAGAGA	GCTGTATGAC	1500
	CTGGGAGAAC	CTCCCATTTT	ACANAGAACA	GACGGAGATC	CAGGGAGGAG	AAGGGACTCG	1560
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	TTCCACAACC	GGGGCGATGG	CACCTTTGTG	GACGCTGCGG	CCAGTGCTGA	ACCTCCTTTA	2160
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	CAGGGGGGCCC	CACCCTGCCT	TCTGGCAAGA	GCTCCCTGTG	TCCTGGGGTC	TCTGATCCCC	2460
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	TTGTCCTCTG	AAAGAGTCAA ACTTCAACCG	CGTGGGTGTG	GACGACCCCC	ACCAGCATGG	CTCCAATCCC	2580 2640
60	CCCCACCGCTG	TOTATOTOCA	AATGAGGAGG	CATGGGBAGG	TOGGOTTOGG	GGACATOGCC	2700
••	TCACCCAAGT	TCTCCATGCC	CTCCCCTGTC	CGCACGGTCA	TCACCGCCGA	CTTTGACAAT	2760
	GACCAGGAGC	TOGAGATETT	CTTCAACAAC	ATTGCCTACC	GCAGCTCCTC	AGCCAACCGC	2820
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65	BAGGTCBACA	CAGGECCCCT	CATCAGAAGG	CAGASAGGAA	GGAAGGACGA	GGACTGGGCA	3000
0.5	AGAGGCTGTG	GGRATGCAGG	GCAAAGCCTG	GCCAAGGAGC	CGGCCTCTGC	TATTGCAGGG	3060
	AAAGGGAAGG	GARATGTGGC	CCAAAGTGTG	CCCAGAACCC	AAGCGCCACA	AGATACAAAG	3120
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75	CCAGGAAAAG	GGGCTACAGG	GTCCAATCAC	TACCAGGAAA	AGGGGCTACG	GGGTCCAATC	3540 3600
15	ACTACCAGGA	ACCESSORS	GCTACAGGGT	CCARTCACTA	CCAGGAAAAG	GGGCTACAGG	3660
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	CGGGGTCCAA	TCACTACCAG	GARAGGGGC	TACGGGCTCC	AATCACTACC	AGGAAAAGAG	3780
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	GGCCGGGGGCA	CAGGGGGTGT	GGTGACCGAC	TTCGACGGAG	ACGGGATGCT	GGACCTCATC	4020
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85	AACAACAACT	GGCTGOGAGT	GGTGCCACGC	ACCOMMITTE	GGGCCTTTGC	CAGGGGAGCT	4140
03	AAGGTCGTGC	TCTACACCAA	GAAGAGTGGG	CACTETOGOCO	TOGGG A AGGA	CGGGGGCTCA TGAAGCCAGC	4200 4260
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5	GGAAGCTACA GGCACAGCCT CCCAAAAAGG CCGGGTTGCC	GGTGCCSGAC GCGTGGGTAC AGCTGCAACT GGCTGCTCCT CAGGTATTCC	CAACAAGAAG TGAGCTAGGC TTCCCAAGGC CAAAAGAGCT	TGCAGTCGGG TCTAGGCATA ATCTGCACCC CAGCTCCAGG	GCTACGAGCC CAATGACGTG CCGTCTGGTC CTGCTCCCAG	CAACGAGGAT GAAACCAAGG CTTTTTCCTG CACCCTTCTC	4560 4620 4680 4740
10	Seg ID NO:	473 Protein	sequence				
	1	11	21	31	41 .	51	
15	SPYYALRDRQ PPTTPAGLLG GVATYTDKLF	CSGWMGLGGP GNAIGVTACD LPPLSGRDFS KFRNNRWEDI	IDGDGREELY SSLGQASPDS LSDEVNVARG	FLNTNNAFSG ROGERVPVPC VASLFAGRSV	HSSSAQVPSG CRGGLRPTHE ACVDRKGSGR	LHRNRPVLKP PEPFLLRPKS YSIYIANYAY	60 120 180 240
20	GGDPREADRE SKSHLADKNL PHPRAPGMOP	MDPEASDLSR HSGDGSTSQL FGPPCYYSVC KCKGRHAEPG QHLPARELYD	CRLGWKDGQF APSPAHPFPA LMAEALGAWP	KERAAALVEE RQAPQHYPVA ALSTTVVPGG	QREAGAAGVP PLVTQLMTHG LRSWEBSROK	RGRVRTALQT RLAGKLARSV GOAMSRCALR	300 360 420 480 540
25	GPGRVAKREI LAWNOMEKEE SATHCGSMSF AFIVHLKYHL	GRETGAVGRP GKIHGDHEPR LGGRGVSVGP CRDFPHSLCH	LSHPLVPNFP FRLRKAREAE ILSSSASDIF LAETGPSSSC	SCLRPLEAGT FPPGSSEEPL CDNENGPNFL CPWHARLLOA	VPGAALPGNP LQFPSGLRGS PHNRGDGTFV PHCHHGLSMS	GNNVLDMAKA PVLQVGLGLA DAAASAERRL PTRTGSRPYS	600 660 720 780 840
30	SPKFSNPSPV GQGEGLRIRR KGKGNVAQSV	HRRTLSLOGS DDPHOHGRGV RTVITADPDN GGFPGPGGQA PRTQAPQDTK	DQELEIFFNN KVNTGPLMKK PHYHKKGLQG	IAYRSSANR QKGRKDEDWA PITTRKRGYG	LFRCSILARG RGCGNAGQSL VQSLPGKGAT	SSSLTAGGRN AKEPASAIAG GSNHYQEKGL	900 960 1020 1080
35	RGPITTRKRG RKGLRAPITT NHYQEKGLQG AMGSNHYOEK	YGVQSLPGKG RKRGYGVQSL PITTRKRGYR GLRAPITTRK	ATGSNHYQEK PGKGATGSNH VQSLPQKGAT RGYGVOSLPO	GLQGPITTRK YQEKGLRGPI GSNHYQEKGI KGATGSNVIR	RGYGLQSLPG TTRKRGYGLQ RGPITTRKRG REHGDPLIEE	KGATGSNHYH SLPGKGATGS YGLQSLPGKE LNPGDALEPE	1140 1200 1260 1320 1380
40	MNSVLEILYP GSYRCRINKK	FDGDGMLDLI AHLRIIDGGS RDEDTLQDPA CSRGYEPNED QLQAAPSTLL	PLECGQGFSQ GTACVGTELG	QENGHCMDTN SRHTMTWKPR	SVEVTWPDGK BCIQFPFVCP PKKELQLSQG	MVSRNVASGE RDKPVCVNTY ICTPVWSFFL	1440 1500 1560
	Seq ID No:	424 2012					
45	Nucleic Ac	id Accession	#: NM 003	661.1			
45	Nucleic Ac	id Accession	#: NM 003	661.1 31	41	51 I	
45 50	Nucleic Ac Coding segn 1 ATGAGTGCAC CAAAACGTTC GCTGCTGGCA	id Accession sence: 11: 11 	#: NM_003 L52 21 TGTGGGAGTG AGATACTGGA AGAGAGCAGT	31 AGGGCAGAGG GATCCTCAAA ATCTTTATTG	AAGCTGGAGC GTAAGCCCCT AGGATGCCAT	GAGGGTGCAA CGGTGACTGG TAAGTATTTC	60 120 180 240 300
	Nucleic According sequence of the control of the co	id Accession lence: 11: 11 TITTCCTTGG CAAGTGGGAC CCATGGACCC TGAGCACAC CTGGCTGCTGC CAGGACCAC GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	1 #: NM_003 152 21 TOTGGGGGGTG AGATACTGGA AGAGGAGCAGT GAATCTGCTA ACTGCCAG GATCATGAAA AGAGTTTCCT AGACATTCCT CAGCATTTCC	31 AGGGCAGAGG GATCCTCAAA ATCTTTATTG CTCCTGCTGA AAATGAGGCAG GACAAAAACT CGGTTGAAAA CAGAAGGTCC TCTGGCATCC	AMBCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GGCACGATAA GTGAGCTTGA ACAAAGGCAC TGACCCTCGT	GAGGGTGCAA CGGTGACTOG TAAGTATTTC GGCCTGGAAC TAAAGCTCTG AGGCCAGCAG GGATAACAT CACCATCGCC CGGCATGGGT	120 180 240 300 360 420 480 540
50	Nucleic Ac Coding seq 1 ATGAGTGCAC CAAAACGTTC GCTGCTGGCA AACGAAACTTG GACAACCTTG GACAACCTTG AACGAAACTTG AATGAGCTCC ATCACAACCG ATCACAACCG ACCACAGCCC ATCACAACCG ACCACAGCCC ACCACAGCCC ACCACAGCCC ACCACAGCCC ACCACAGCCC ACCACAG	id Accession pence: 11 ITTTCCTTGG CAAGTGGGAC CCATGGACCACACACACACACACACACACACACACACACA	1 #: NM_003 152 21 1 TSTGGGAGTG AGATACTGGA AGAGAGCAGT GAATCTGCTA ACTGCCCAGG GATCATGAAA AGAGTTTCC AGGCAGCCTT GATTACCAGG CCTGGTCATC ATCCAACTTT ATCCAGCTTCATC ATCCAACTTT	31 AGGGCAGAGG GATCOTCAAA ATCITTATTG CITCCTGCTGA AATGAGGCAG GACAAAAACT COGTTGAAAA CMGAAGGTCC GTACTCTTGG AGTACCATGG AGTACCATGG AAAGGCCTT CTTTCCTTAG CTCAGACGAG CTCAGACGAG	AAGCTGGAGC GTAAGCCCT AGGATGCCAT CTGATAATGA ATGAGCTCGG GGCAGGATAA GTAGAGCTGGA ACAAAGGCA TGACCCTGGT AACCTGGGAT ACTTGGAAT ACTAGGAATAC CTGGAATAC CTGGAATAC CTGGAATAC CTGGAATAC CTGGAATAC CTGGAATAC CTGCAATAC CTGGAATAC CTGCAATAC	GAGGOTGCAA GGGTGACTOG TAAGTATTTC GGCCTGGAAC TAAAGTCTG AGGCCACAG GGATAACATA CACATCGCC CGGCATGGGT GGAGTTGGGA GAAGTGGTG GGAGTGAGG TTACCAACTC TCTTCAGTCA	120 180 240 300 360 420 480 540 600 720 780 840
50 55	NUCLBIC ACCOMING SEPTIME ATTRACTOR SEPTIME ATTRACTOR SEPTIME ATTRACTOR SEPTIME ATTRACTOR SEPTIME ATTRACTOR	14 Accession enge 112 11 TITTICCTIGG CAAGGGGAC COATGGCC COATGGCCC COATGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COCCCTCAAGGC TCAAGGGAAGCA COCCCTGAAGCC AGGGGGTTAA COCCCCTGAAGCC TCAAGGCAAGC TCAAGGGAAGCA TCAGGAAGCA TCAAGGGAAGCA COCCCTGAAGCC AGGGAAGCA TCAGGGAAGCA COCCCTGAAGCC AGGGAAGCA COCCCTGAAGCC AGGGAAGCA COCCCTGAAGCC AGGGAAGCA COCCCTGAAGCC AGGGAAGCA COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAACC COCCCTCTCAACC COCCCTGAACC COCCCTGAACC COCCCTCAACC COCCCTCAACC COCCCCTCAAC	1 #: NM_003 152 21 TGTGGGAGTG AGATACTGGA AGAGAGGAGG GAATCTGCA ACTACCCCAGG GATCATGAA ACAGTTACCA AGAGGAGGCTT CAGCATTTCC AGCAGCCTGGATACA ACAGCCTGGACTAC ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ATCCAACTTC ACGCCCCGG CTCLTTCTT AGACCCAGC GGCAAAATCA	31 AGGGCAGAGG GATCCTCALA ATCETTRATTG CTCCTGCTGA AATGAGGCAG GGCAAAAAATA COGTTGANACA COGTGANACA COGTCGANCO GTACACCTTGG AGTACCATGG AGTACCATGG CTCAGAGGAG GTCACTGAGA ATCCTGAGA ATCCTGAGA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA GTGCTGGAA	AMECTOGAGE GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GGCACGATAA GTGAGCTTGA ACCAAGGCACC ACCATGAGCTCGA ACCAAGGCACC ACCACGGATAA CCAAAGTCAC CCAGGCCAA CCAAATTGAA CCAAATTGAA CCAAGCCAA CAATCTCAGG TAGGCAGGTAACCTACGT TAGGCAGGGTAACCTACGT TAGGCAGGGTAACCTACGT TAGGCAGGTGAAA	GAGOOTICAA CGGTQACTOG TAAGTATTTC GGCCTGGAAC TAAAGCCTG AGGCCAGCAG GGATAACATA CACCATCOCC GGGATTGGG GGAGTTGGG GAAGTGGT GGAGTGAGG TTACCAACTC TCTTCAGTCA TGAAAACTC CGTTTACGAA	120 180 240 300 360 420 480 540 600 660 720 780
50 55 60	Nucleic According sequence of the control of the co	14 Accession enge 112 11 TITTICCTIGG CAAGGGGAC COATGGCC COATGGCCC COATGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COGGCCC COCCCTCAAGGC TCAAGGGAAGCA COCCCTGAAGCC AGGGGGTTAA COCCCCTGAAGCC TCAAGGCAAGC TCAAGGGAAGCA TCAGGAAGCA TCAAGGGAAGCA COCCCTGAAGCC AGGGAAGCA TCAGGGAAGCA COCCCTGAAGCC AGGGAAGCA COCCCTGAAGCC AGGGAAGCA COCCCTGAAGCC AGGGAAGCA COCCCTGAAGCC AGGGAAGCA COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAAGCC COCCCTGAACC COCCCTCTCAACC COCCCTGAACC COCCCTGAACC COCCCTCAACC COCCCTCAACC COCCCCTCAAC	1 #: NM_003 15: NM_003 21 1 TTTGGGAGTG AGATACTGGA AGATACTGGA AGAGAGGAGGA GATCATGGA AGAGGAGGAGGA GATCATGGA AGAGGAGGAG GATCATGGA AGAGTTCCC AGACTGCA AGAGGAGCCC CCCGGTAGTA AGACTGCA AGACTA AGACTGCA AGACTA AGACTGCA AGACTGCA AGACTGCA AGACTGCA AGACTA AGACTA AGACTA AGACTA AGACTA AGACTA AGACTA AGACTA AGACTTA AGACTA AGACTA AGACTA AGACTA AGACTTA A	31 AGGGCAGAGG GATCCTCALA ATCETTRATTG CTCCTGCTGA AATGAGGCAG GGCAAAAAATA COGTTGANACA COGTGANACA COGTCGANCO GTACACCTTGG AGTACCATGG AGTACCATGG CTCAGACGAG GTCACTGAGA ATCCTGAGAA GTGCTGGAAA GTGCTGGAAA GTGCTGGAAA GTGCTGGAAA GTGCTGGAAA GTGCTGGAAA GTGCTGGAAA GTGCTGGAAA GTGCTGGAAA GTGCTGGAAAA GTGCTGGAAAAACTGCTGGAAAA GTGCTGGAAAAACTGCTGGAAAAACTGCTGGAAAAACTGCTGGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAACTGCTGAAAAAACTGCTGAAAAACTGCTGAAAAAACTGCTGAAAAAAACTGCTGAAAAAAACTGCTGAAAAAAAA	AMECTOGAGE GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GGCACGATAA GTGAGCTTGA ACCAAGGCACC ACCATGAGCTCGA ACCAAGGCACC ACCACGGATAA CCAAAGTCAC CCAGGCCAA CCAAATTGAA CCAAATTGAA CCAAGCCAA CAATCTCAGG TAGGCAGGTAACCTACGT TAGGCAGGGTAACCTACGT TAGGCAGGGTAACCTACGT TAGGCAGGTGAAA	GAGOOTICAA CGGTQACTOG TAAGTATTTC GGCCTGGAAC TAAAGCCTG AGGCCAGCAG GGATAACATA CACCATCOCC GGGATTGGG GGAGTTGGG GAAGTGGT GGAGTGAGG TTACCAACTC TCTTCAGTCA TGAAAACTC CGTTTACGAA	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1080
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50 55 60 65 70	Nucleic Ac Coding seq 1 1 1 ATGATICAC CARAGETTA ATGATICAC CARAGETTA AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGTO AGAGGAGTO AGAGGTO	Id Accession Length 1.12 ITTTCCTTGG CAADTGGGAC CATGGGCCAC CTGCTGGACC CTGGTGCTGA CAGGCCAC CTGCTGCTGA CAGGCCAC CTGCTGCTGAC CAGGCCAC CTGCTGCTGAC CAGGCCAC CTGCTGCTGAC CAGGCCAC CTGCTGCTGAC CTGCTGCTGAC CTGCTGCTGAC CTGCTGCTGAC CTGCTGCTGCAC CTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCTGCAC CTGCTGCAC CTGCTGCTGCAC CTGCTGCAC CTGCTGCAC CTGCTGCAC CTGCTGCAC CTGCTGCTGCAC CTGCTGCAC CTGCTGCTGCAC CTGCTGCAC M_00152 21 21 21 21 21 21 21 21 21 21 21 21 21	31 AGGICNARAGE GAPCOTCANA ANTONITORING CYCCISCTAN ANTONICORIC GARANACT COGPITORIAN CAGRAGATOC TOTROCORIC GARACT COTTORIO ANAMACTITO CTTOCORIC CTTOCORIC CTTOCORIC CTTOCORIC CTTOCORIC CTTOCORIC CTTOCORIC CTTOCORIC CTTOCORIC CTTOCORIC CTTOCORIC CTTOCORIC CAGRACORIC ANCORI	AMOCTOGOACO GTAAGCOCCE AMOCTOGOATA ANGACTOCCA GTAAGCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTACCA A	GAGGTGCAA GAGGTGCAA GAGGTGCAA GAGGTGCAA GAGCACCAC GAGGTGCAA GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC CACCAC CACCAC CACCAC CACCAC CACCAC	120 180 240 300 360 480 540 780 840 960 1020 1080 1140	
50 55 60 65 70	Nucleic AcCoding sep 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	dd Accession ence: 1 11 11 17 TTTTCCTTGG TTTTCCTTGG TTTTCCTTGG TTTTCCTTGG TTTTCCTTGG TTTTCCTTGG TTTTCCTTGG TTTTCCTTGG TTTTCCTGG TTTTCG TTCG	1 St. NM_001 21 1 TOTOGOAGTG ANTACTOGA ANTACTOGA ANTACTOGA ANTACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GAATACTOGA GATTACCAGCTT CABCATTTCC GATTACCAGCT GATTACCAGCT TOLACCCAGCT TOLACCCAGCT TOLACCCAGCT TOLACCCAGCT TOLACCCAGCT GATTACCAGCT GATTACCAGCT GATTACCAGCT GATTACCAGCT GATTACCAGCT GATTACCAGCT TOLACCCAGCT GATTACCAGCT TOLACCCAGCT GATTACCAGCT TOLACCCAGCT GATTACCAGCT TOLACCCAGCT GATTACCAGCT TOLACCCAG	31 AGGGCARAGG GATCCTCANA ANCETTATIO GTCCTGCAGA GACCANAGC GGTACCTCAGA GACAANAGC GGTTGANA AGAGAGT CTCTGCACC GGTTGANA CTCTGCACC GGTTGANA CTCTGCACC GGTTGCCTCAG GACAANAGC GTCCCTCCC GTTCCTCAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAACTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AAAAGCTTG CTTCGCTAGA AACAATAATT 31	AMOCTOGOACO GTAAGCOCCE AMOCTOGOATA ANGACTOCCA GTAAGCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTOCCA ANGACTACCA A	GAGGTGCAA GAGGTGCAA GAGGTGCAA GAGGTGCAA GAGCACCAC GAGGTGCAA GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC CACCAC CACCAC CACCAC CACCAC CACCAC	120 180 300 360 420 480 660 780 840 960 960 1020 1080 1140

WO 02/086443 AUGGGGACCT CTCCGAGCAG CAGCACCRCC CTCGCCTCCT GCAGCCGCAT CGCCCGCGGA GCCACAGCCA CGATGATCGC GGGCTCCCTT CTCCTGCTTG GATTCCTTAG CACCACACA GCTCAGCCAG AACAGAAGGC CTCGAATCTC ATTGGCACAT ACCGCCATGT TGACCGTGCC 180 ACCOGCCAGG TOCTAACCTG TGACAAGTGT OCAGCAGGAA CCTATGTCTC TGAGCATTGT 240 ACCARCACAA GCCTGCGCGT CTGCAGCAGT TGCCCTGTGG GGACCTTTAC CAGGCATGAG 300 PRODUCTURE PROFITAGE AND ARCHORAGE CONCRETE CONTROL CO W 360 TTACCTTGTG CTGCCTTGAC TGACCGAGRA TGCACTTGGC CACCTGGCAT GTTCCAGTCT AACGCTACCT GTGCCCCCCA TACGGTGTGT CCTGTGGGTT GGGGTGTGGG GAAGAAAGGG 420 10 ACAGAGACTG ACGATGTGCG GTGTAAGCAG TGTGCTCGGG GTACCTTCTC AGATGTGCCT 540 TCTAGTGTGA TGAAATGCAA AGCATACACA GACTGTCTGA GTCAGAACCT GGTGGTGATC 600 AAGCCGGGGA CCAAGGAGAC AGACAACGTC TGTGGCACAC TCCCGTCCTT CTCCAGCTCC 660 ACCTCACCTT COCCTGGCAC AGCCATCTTT CCACGCCCTG AGCACATGGA AACCCATGAA 720 STOCCTTCCT CCACTTATGT TCCCAAAGGC ATGAACTCAA CAGAATCCAA CTCTTCTGCC 780 15 TOTOTTAGAC CHARGOTACT GAGTAGCATC CAGGAAGOGA CAGTCCCTGA CAACACAAGC 840 TCAGCAAGGG GGAAGGAAGA CGTGAACAAG ACCCTCCCAA ACCTTCAGGT AGTCAACCAC 900 CAGCAAGGCC COCACCACAG ACACATCCTG AAGCTGCTGC CGTCCATGGA GGCCACTGGG 960 OGCGAGAGT CCAGCACGC CATCAAGGGC CCCAAGAGGG GACATCCTAG ACAGAACCTA 1020 CACAAGCATT TIGACATCAA TGAGCATTIG CCCTGGATGA TTGTGCTTTT CCTGCTGCTG 1080 20 GTGCTTGTGG TGATTGTGGT GTGCAGTATC CGGAAAAGCT CGAGGACTCT GAAAAAGGGG 1140 CCCCGGCAGG ATCCCAGTGC CATTGTGGAA AAGGCAGGGC TGAAGAAATC CATGACTCCA 1200 ACCORDANCE OCCUPANTE GARCENCERC RECENTERED ATCOTATORS TATOCHESIS 1260 CTTGTAGCAG COCAAGTGGG AAGCCAGTGG AAAGATATCT ATCAGTTTCT TIGCAATGCC 1320 ACTGAGAGGG AGCTTGCTGC TTTCTCCAAT GGGTACACAG CCGACCACGA GCGGGCCTAC 1380 25 GENGETETGE AGENETICAC CATCOGGGG CCCGAGGCCA GCCTCGCCCA GCTAATTAGC 1440 GCCCTGCGCC AGCACCGGAG AAACGATGTT GTGGAGAAGA TTCGTGGGCT GATGGAAGAC 1500 ACCACCCAGC TOGANACTON CANACTAGCT CTCCCGATGA GCCCCAGCCC GCTTAGCCCG 1560 1620 AGREGATION CHARGOSCALA COCCALACTE GAGRATICOS CICTOCOGAC GOTGGAGOCO TCCCCACAGG ACAAGAACAA GGGCTTCTTC GTGGATGAGT CGGAGCCCCT TCTCCGCTGT 1680 30 GACTOTACAT CCAGOGGOTO CTCOGOGGTG AGCAGGAACG GTTCCTTTAT TACCAAAGAA 1740 AAGAAGGACA CAGTGTTGCG GCAGGTACGC CTGGACCCCT GTGACTTGCA GCCTATCTTT 1900 GATGACATGC TCCACTITCT ANATOCTGAG GAGCTGCGGG TGATTGAAGA GATTCCCCAG 1860 GCTGAGGACA AACIAGACCG GCTATTOGRA ATTATTGGAG TCAAGGCCA GGAAGCCAGC CAGACCCTCC TGGACTCTGT TTATAGCCAT CTTCCTGACC TGCTGTAG 1020 35 Seq ID NO: 477 Protein seq Protein Accession #: NP_055267.1 31 40 MGTSPSSSTA LASCSRIARR ATATMIAGSL LLLGFLSTTT AQPEQKASNL IGTYRHVDRA TGOVLTCDKC PAGTYVSEHC THTSLRVCSS CPVGTFTRHE NGIEKCHDCS QPCPNPMIEK 120 LPCAALTDRE CTCPPGMFQS NATCAPHTVC PVGMGVRKKG TETEDVRCKO CARGTFSDVP 180 SSYMKCKAYT DCLSONLVVI KPGTKETDNV CGTLPSFSSS TSPSPGTAIF PRPEHMETHE 240 VPSSTYVPKG MMSTESNSSA SVRPKVLSSI QEGTVPDNTS SARGKEDVNK TLPNLQVVNH QOGPHERHIL KLLPSMEATG GEKSSTPIKG PKRGHPRONL HKHFDINEHL PWMIVLFLLL 360 VLVVIVVCSI RKSSRTLKKG PRQDPSAIVE KAGLKKSMTP TQNREKWIYY CNGHGIDILK 420 LVAAQVUSGW KDIYQFLCNA SEREVAAPSN GYTADHERAY AALQHWTIRG PEASLAQLIS ALRHRRNDU VEKIRGIMED TOLETDKIA LPMSPSDLSP SPISSPNAKL ENSALLIVEP 480 540 50 SPODKNKGFF VDESEPLLRC DSTSSGSSAL SRNGSFITKE KKDTVLRQVR LDPCDLQPIF DDMLHFLMPE ELRVIEEIPQ AEDKLDRLFE IIGVKSQEAS QTLLDSVYSH LPDLL Sen ID NO. 478 DNA semience Nucleic Acid Accession #: XM_044533 55 Coding sequence: 238..2751 31 41 GCTCTGCCCA AGCCGAGGCT GCGGGGCCGG CGCCGGCGGG AGGACTGCGG TGCCCCGCGG 60 AGGGCCTGAG TTTGCCAGGG CCCACTTGAC CCTGTTTCCC ACCTCCCGCC CCCCAGGTCC GGAGGCGGGG GCCCCCGGGG CGACTCGGGG GCGGACCGGG GGGCGGAGCT GCCGCCCGTG AGTCCGGCCG AGCCACCTGA GCCCGAGCCG CGGGACACCG TCGCTCCTGC TCTCCGAATG 240 CTGCGGCCC GGATGGGCCT GAGGAGCTGG CTCGCCGCCC CATGGGGGCGC GCTGCCGCCT CTGCCACCG TGCTTCCTCCTCCTGCTG CTGCTCCTGC TGCACCCCC GCTCCCGCACC 300 360 65 TEGGESCICA GCCCCOGGAT CAGCCTGCCT CIGGGCTCTG AAGAGCGGCC ATTCCTCAGA TICGAAGCIG AACACATCIC CAACTACACA GCCCTICIGC TGAGCAGGGA TGGCAGGACC 480 CTOTACOTOR GUICTOGADA GOCCOTOTTE GCACTUAGRA GCALCUTCAG CUTCUTGUCA 540 600 TTCANGGGCA AGGACCCACA GCGCGACTGT CAAAACTACA TCAAGATCCT CCTGCCGCTC 660 70 AGCGGCAGTC ACCTGTTCAC CTGTGGCACA GCAGCCTTCA GCCCCATGTG TACCTACATC 720 AACATGGAGA ACTTCACCCT GGCANGGGAC GAGAAGGGGA ATGTCCTCCT GGAAGATGGC 780 AAGGGCCGTT GTCCCTTCGA CCCGAATTTC AAGTCCACTG CCCTGGTGGT TGATGGCCAG 840 CTCTACACTG GAACAGTCAG CAGCTTCCAA GGGAATGACC CGGCCATCTC GCGGAGCCAA
AGCCTTCGCC CCACCAAGAC CGAGAGGTCC CTCAACTGGC TGCAAGACCC AGCTTTTTTG 900 75 SCCTCAGCCT ACATTCCTGA GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC 1020 TITTTCITCA GCCAGACTGG CCAGGAATIT GAGTTCITTG AGAACACCAT TGTGTCCCGC 1080 ATTGCCCGCA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC 1140 TCCTTCCTCA AGGCCCAGCT GCTGTGCTCA CGGCCCGACG ATGGCTTCCC CTTCAACGTG 1200 CTGCAGGATG TCTTCACGCT GAGCCCCAGC CCCCAGGACT GGCGTGACAC CCTTTTCTAT 1260 80 GGGGTCTTCA CTTCCCAGTG GCACAGGGGA ACTACAGAAG GCTCTGCCGT CTGTGTCTTC ACARTGAGG ATGTCCAGAG AGTCTTCAGC GGCCTCTACA AGGAGGTGAA CCGTGAGACA 1380 CAGGAGTGGT ACACGGTGAC CCACCCGGTG CCCACACCCC GGCCTGGAGC GTGCATCACC 1440 AACAGTGCCC GGGAAAGGAA GATCAACTCA TCCCTGCAGC TCCCAGACCG CGTGCTGAAC 1500 1560 TTCCTCAAGG ACCACTTCCT GATGGACGGG CAGGTCCGAA GCCGCATGCT GCTGCTGCAG 85 CCCMGGCTC GCTACCAGCG COTGGCTGTA CACCGCCTCC CTGGCCTGCA CCACACCTAC 1620

GATGTCCTCT TCCTCGGCAC TGGTGACGGC CGGCTCCACA AGGCAGTGAG CGTGGGCCCC

COCCUCACA TONTICAGGA GOTGOAGATO TROTONTOGG GACAGOCCOT GCAGAATCEG

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	CTCCTGGACA	CCCACAGGGG ACTGCAGCCT	GCTGCTGTAT	GCGGCCTCAC	ACTOGGGGGT	AGTCCAGGTG	1800 1860
	CCCATGGCCA	ACTGCAGCCT	GTACAGGAGC	TGTGGGGACT	GCCTCCTCGC	CCGGGACCCC	1920
	TACTGTGCTT	GGAGCGGCTC GGATCCAGGA	CAGCTGCAAG	CACGTCAGCC	AGGICCTTTG	CAGCIGGCC	1980
5	ACCAGGCUGT	CCCCGTCTTT	CATCGAGGGA	CCCAGCOCCA	CATOTOLOGCA	AGTOCAGTEC	2040
,	CLOGGIGGG	CAGTGAACAC	TOTALCANCA	COCCECTOTO	CCNACCTGGC	GACCCGACTC	2100
	TOCOTACO	ACGGGGGCCCC	COTCAATGCC	TOGGCCTCCT	CCACTIGCT	ACCCACTGGG	2160
	GACCTACGCA	TGGTGGGCAC	CCLACAGCTG	GGGGAGTTCC	AGTGCTGGTC	ACTAGAGGAG	2220
	GACCIGCIGC	AGCTGGTAGC	CARCTACTEC	CCAGAGGTGG	TOGAGGACGG	GGTGGCAGAC	2280
10	CARACAGATG	AGGGTGGGAG	TOTACCCCTC	ATTATCAGCA	CATCGCGTGT	GAGTGCACCA	2340
	GCTGGTGGCA	AGGCCAGCTG	GGGTGCAGAC	AGGTCCTACT	GGANGGAGTT	CCTGGTGATG	2400
	TOPACOCTOT	TTGTGCTGGC	CGTGCTGCTC	CCAGTTTTAT	TCTTGCTCTA	CCGGCACCGG	2460
	ABCAGCATGA	ADGRETTECT	GAAGCAGGGG	GAATGTGCCA	GCGTGCACCC	CAAGACCTGC	2520
	CCTGTGGTGC	TGCCCCCTGA	GACCCGCCCA	CTCAACGGCC	TAGGGCCCCC	TAGCACCCCG	2580
15							2640
	GAGTCAGAGA	AGAGGCCACT	CAGCATCCAA	GACAGCTTCG	TGGAGGTATC	CCCAGTGTGC	2700
	CCCCGGCCCC	GGGTCCGCCT	TOGCTCGGAG	ATCCCTGACT	CTCTCCTCTC	AGAGCTGACT	2760
	TOCAGAGGAC	GCTGCCCTGG	CTTCAGGGGC	TOTGAATGOT	CGGAGAGGGT	CAACTGGACC	2820
	TO COCCUTO COCC	TOTACTOTTO	GTGGAACACG	ACCGTGGTGC	CCGGCCCTTG	GGAGCCTTGG	2880
20	GGCCAGCTGG	CCTGCTGCTC	TCCAGTCAAG	TAGCGAAGCT	CCTACCACCC	AGACACCCAA	2940
	a caconstruc	COCCAGAGGT	CCTGGCCAAA	TATGGGGGCC	TGCCTAGGTT	GGTGGAACAG	3000
	TOCTOTTAT	GTABLCTGAG	CCCTTTGTTT	AAAAAACAAT	TCCAAATGTG	AAACTAGAAT	3060
	GAGAGGGAAG	AGATAGCATG	GCATGCAGCA	CACACGGCTG	CTCCAGTTCA	TOGCCTCCCA	3120
	GOGGTGCTGG	GGATGCATCC	ARRGTGGTTG	TCTGAGACAG	AGTTGGAAAC	CCTCACCAAC	31,80
25	TOGGCCTCTTC	ACCTTCCACA	TTATCCCGCT	GCCACCGGCT	GCCCTGTCTC	ACTGCAGATT	3240
-	CAGGACCAGC	TTGGGCTGCG	TGCGTTCTGC	CITGCCAGTC	AGCCGAGGAT	GTAGTTGTTG	3300
	CTGCCCTCGT	COCACCACCE	CAGGGACCAG	AGGGCTAGGT	TGGCACTGCG	GCCCTCACCA	3360
	agreemagge.	TOTAL COCAN	CTCCTGGACC	TTTCCAGCCT	CTATCAGGCT	GTOGCCACAC	3420
	GAGAGGACAG	CGCGAGCTCA	GGAGAGATTT	CCTGACAATG	TACGCCTTTC	CCTCAGAATT	3480
30							3540
	CCACCATATC	CACCCTCGCT	CCATCTTTGA	ACTCAAACAC	GAGGAACTAA	CTGCACCCTG	3600
							3660
	TCAACACTGC	CCAGCACAGG	GGCCCTGAAT	TTATGTGGTT	TTTATACATT	TTTTAATAAG	3720
	ATGCACTTTA	TGTCATTTTT	TAATAAAGTC	TGAAGAATTA	CTGTTT		
35							
	Seg ID NO:	479 Protein	n sequence				
	Protein Acc	ression #: 2	(P_044533.3				
	1	11	21	31	41	51	
40		1	1	1	1	1	
	MLRTANGLES	WLAAPWGALP	PRPPLLLLLL	LLLLLQPPPP	TWALSPRISL	PLGSEERPFL	60
	RFEAEHI SNY	TALLLSRDGR	TLYVGAREAL	FALSSNLSFL	PGGEYQELLW	GADAEKKQQC	120
	SFKGKDPQRD	CONVIKITED	LSGSHLFTCG	TAAFSPMCTY	IMMENFTLAR	DEKGNALTED	180
	GKGRCPFDPN	FKSTALVVDG	ELYTGTVSSF	QGNDPAISRS	QSLRPTKTES	SLNWLQDPAF	240
45		GST-OGDDDKT	YFFFSETGOE	PEPPENTIVS	RIARICKGDE	GGBRVLQQRW	300
			VLQDVFTLSP	SPQDWRDTLF	YGVFTSQWHR	GTTEGSAVCV	360
	TSFLKAQLLC	SCHUKEVNER	TOOMYTVTHP	VPTPRPGACI	TNSARERKIN	SSLQLPDRVL	420
	TSFLKAQLLC FTMKDVQRVF	SRPDDGFPFN SGLYKEVNRE	TOOMYTVTHP	VPTPRPGACI	TNSARERKIN	SSLQLPDRVL GRLHKAVSVG	420 480
	TSFLKAQLLC FTMKDVQRVF NFLKDHFLMD PRVHITERLO	SRPDDGFPFN SGLYKEVNRE GQVRSRMLLL IPSSGOPVON	TQQWYTVTHP QPQARYQRVA LLLDTHRGLL	VPTPRPGACI VHRVPGLHHT YAASHSGVVO	TNSARERKIN YDVLFLGTGD VPMANCSLYR	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD	420 480 540
50	TSFLKAQLLC FTMKDVQRVF NFLKDHFLMD PRVHIIEELQ PYCAWSGSSC	SREDDGFPFN SGLYKEVNRE GQVRSRMLLL IPSSGQPVQN KHVSLYOPQL	TQQWYTVTHP QPQARYQRVA LLLDTHRGLL ATRPWIQDIE	VPTPRPGACI VHRVPGLHHT YAASHSGVVQ GASAKDLCSA	TNSARERKIN YDVLFLGTGD VPMANCSLYR SSVVSPSFVP	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCEQVQ	420 480 540 600
50	TSFLKAQLLC FTMKDVQRVF NFLKDHFLMD PRVHIIBELQ PYCAWSGSSC	SREDDGFFFN SGLYKEVNRE GQVRSRMLLL IFSSGQFVQN KHVSLYQFQL CDLLSVLFF	TQQWYTVTHP QPQARYQRVA LLLDTHRGLL ATRPWIQDIE	VPTPRPGACI VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT	TNSARERKIN YDVLFLGTGD VPMANCSLYR SSVVSPSFVP GDLLLVGTOO	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCBQVQ LGEFOCWSLE	420 480 540 600
50	TSFLKAQLLC FTMKDVQRVF NFLKDHFLMD PRVHIIBELQ PYCAWSGSC FQPNTVNTLA BGFQQLUASY	SREDDGEPFN SGLYKEVNRE GQVRSRMLLL IFSSGQPVQN KHVSLYQPQL CPLLSNLATR CPRUVEDGVA	TQQWYTVTHP QPQARYQRVA LLLDTHRGLL ATRPWIQDIE LWLRNGAPVN DOTDEGGSVP	VPTPRPGACI VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA	TNSARERKIN YDVLFLGTGD V PMANCSLYR SSVVSPSPVP GDLLLVGTQQ PAGGKASWGA	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCBQVQ LGEFQCWSLE DRSYWKEFLV	420 480 540 600 660 720
50	TSFLKAQLLC FTMKDVQRVF NFLKDHFLMD PRVHIIBELQ PYCAWSGSSC FQPNTVINTLA EGFQQLVASY MCTLPVLAVL	SREDDGFPFN SGLYKEVNRE GQVRSRMLLL IFSSGQPVQN KHVSLYQPQL CPLLSNLATR CPEVVEDGVA LPVLFLLYRH	TQQWYTVTHP QPQARYQRVA LLLDTHRGLL ATRPWIQDIE LWLRNGAPVN DQTDEGGSVP RNSMKVFLKO	VPTPRPGACI VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT	TNSARERKIN YDVLFLGTGD V PMANCSLYR SSVVSPSPVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCEQVQ LGEFQCMSLE DRSYWKEFLV PLNGLGPPST	420 480 540 600
-	TSFLKAQLLC FTMKDVQRVF NFLKDHFLMD PRVHIIBELQ PYCAWSGSSC FQPNTVINTLA EGFQQLVASY MCTLPVLAVL	SREDDGEPFN SGLYKEVNRE GQVRSRMLLL IFSSGQPVQN KHVSLYQPQL CPLLSNLATR CPRUVEDGVA	TQQWYTVTHP QPQARYQRVA LLLDTHRGLL ATRPWIQDIE LWLRNGAPVN DQTDEGGSVP RNSMKVFLKO	VPTPRPGACI VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT	TNSARERKIN YDVLFLGTGD V PMANCSLYR SSVVSPSPVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCEQVQ LGEFQCMSLE DRSYWKEFLV PLNGLGPPST	420 480 540 600 660 720
	TSFLKAQLLC FTMKDVQRVF NFLKDHFLM PRVHIIEBLQ PYCAWSGSC FQPNTVHTLA EGFQQLVASY MCTLFVLAVL PLDHRGYQSL	SRPDDGPPFN SGLYKEVNRE GQVRSRMLLL IPSSGQPVQN KHVSLYQPQL CPLLSNLATR CPBVVEDGVA LPVLFLLYRH SDSPPGSRVF	TQQWYTVTHP QPQARYQRVA LLLDTHRGLL ATRFWIQDIE LMLRNGAPVN DQTDEGGSVP RNSNKVFLKQ TESEKRPLSI	VPTPRPGACI VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT	TNSARERKIN YDVLFLGTGD V PMANCSLYR SSVVSPSPVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCEQVQ LGEFQCMSLE DRSYWKEFLV PLNGLGPPST	420 480 540 600 660 720
	TSPLKAQLLC FTMKDVQRVF NFLKDHFLMD PRVHIIBELQ PYCAWSGSGC PQPNTVHTLA BGFQQLVASY MCTLFVLAVL PLDHRGYQSL Seg ID NO:	SRPDDGPPFN SGLYKEVNRE GQVRSRMLLL IPSSGQPVQN KNVSLYQPQL CPLLSNLATR CPEVVEDGVA LPVLFLLYRH SDSPPGSRVF 480 DNA 50	TQQNYTVTHP QPQARYQRVA LLLDTHRGLL ATRPWIQDIE LWLRNGAPVN DQTDEGGSVP RNSMKVFLKQ TESEKRPLSI Quence	VPTPRFGACH VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT QDSFVEVSPV	TNSARERKIN YDVLFLGTGD V PMANCSLYR SSVVSPSPVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCEQVQ LGEFQCMSLE DRSYWKEFLV PLNGLGPPST	420 480 540 600 660 720
	TSPLKAQLLC FTMKDVQRVF NFUKDHFLMD PRVHIIBBLQ PYCAWSGSSC PQPNTVHTLA BGFQQLVASY MCTLFVLAVL PLDHRGYQSL Seq ID NO: Nucleic Ac	SRPDDGPPN SGLYKEVNRE GQVRSRMLLL IPSSGQPVQN KHVSLYQPQL CPLLSNLATR CPEVVEDGVA LPVLPLLYRH SDSPPGSRVF 480 DNA se id Accessio	TQQNYTVTHP QPQARYQRVA LULDTHRGLL ATRPWIQDIE LWLRNGAPVN DQTDEGGSVP RNSNKVFLKQ TESEKRPLSI Quence n #: NM_0042	VPTPRFGACH VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT QDSFVEVSPV	TNSARERKIN YDVLFLGTGD V PMANCSLYR SSVVSPSPVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCEQVQ LGEFQCMSLE DRSYWKEFLV PLNGLGPPST	420 480 540 600 660 720
	TSPLKAQLLC FTMKDVQRVF NFLKDHFLMD PRVHIIBELQ PYCAWSGSGC PQPNTVHTLA BGFQQLVASY MCTLFVLAVL PLDHRGYQSL Seg ID NO:	SRPDDGPPN SGLYKEVNRE GQVRSRMLLL IPSSGQPVQN KHVSLYQPQL CPLLSNLATR CPEVVEDGVA LPVLPLLYRH SDSPPGSRVF 480 DNA se id Accessio	TQQNYTVTHP QPQARYQRVA LLLDTHRGLL ATRPWIQDIE LWLRNGAPVN DQTDEGGSVP RNSMKVFLKQ TESEKRPLSI Quence	VPTPRFGACH VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT QDSFVEVSPV	TNSARERKIN YDVLFLGTGD V PMANCSLYR SSVVSPSPVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCEQVQ LGEFQCMSLE DRSYWKEFLV PLNGLGPPST	420 480 540 600 660 720
55	TSPLKAGILC FTMKDVQRVF NFLKDHFLMD PRVHIIBELQ PYCHNSGSSC PQPNTVHTLA BGFQQLVASY MCTLPYLAVL PLDHRGYQSL Seq ID NO: Nucleic Ac Coding seq	SRPDOFFFN SGLYKEVNRE GQVRSRMLLL IFSSGQPVQN KHVSLYQFQL CPLLSNLATR CPEVVEDGVA LPVLFLLYRH SDSPPGSRVF 480 DNA se id Accessic uence: 58.	TQQHYTVTHP QPQARYQRVA LLLDTHRGILL ATRPWIQDIE LMLRNGAPVI DQTDEGGSVP RNSMKVFLKQ TESEKRPLSI Quence n #: NM_0042 .1092	VPTPRPGACI VHRVPGLHHT VAASHSGUVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT QDSPVEVSPV	TNSARERKIN YDVLFLGTGD V PMANCSLYR SYVVSPSFVP GDLLLVGTQQ PAGGKASMGA CPVVLPPETR CPRPRVRLGS	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCEQVQ LGEFQCMSLE DRSYWKEFLV PLNGLGPPST EIRDSVV	420 480 540 600 660 720
55	TSPLKAQLLC FTMKDVQRVF NFUKDHFLMD PRVHIIBBLQ PYCAWSGSSC PQPNTVHTLA BGFQQLVASY MCTLFVLAVL PLDHRGYQSL Seq ID NO: Nucleic Ac	SRPDDGPPN SGLYKEVNRE GQVRSRMLLL IPSSGQPVQN KHVSLYQPQL CPLLSNLATR CPEVVEDGVA LPVLPLLYRH SDSPPGSRVF 480 DNA se id Accessio	TQQNYTVTHP QPQARYQRVA LULDTHRGLL ATRPWIQDIE LWLRNGAPVN DQTDEGGSVP RNSNKVFLKQ TESEKRPLSI Quence n #: NM_0042	VPTPRFGACH VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT QDSFVEVSPV	TNSARERKIN YDVLFLGTGD V PMANCSLYR SSVVSPSPVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR	SSLQLPDRVL GRLHKAVSVG SCGDCLLARD TGEKPCEQVQ LGEFQCMSLE DRSYWKEFLV PLNGLGPPST	420 480 540 600 660 720
55	TSPLMAQLLC FTMKDVQRVF NFMKDVGRVF NFMKDMFLMD PRVHITBBLQ PYCAWSGSSC FQNNTVNTLA BGFQQUVASY MCTLFVLAVL PLDHRGYQSL Seq ID NO: Nucleic Ac Coding seq 1	SRPDDGPPN SGLYKEVNRE GQVRSRMLLL IFSSGDYUGN KHVSLYGPCL CPLLSNLATR CPETVEDGVA LPVLPLLYMATR SDSPPGSRVF 480 DNA se id Accession uence: 58.	TQQMYTTHP QPQARYQRVA LLLDTHRGLL ATRPWIQDIE LWLRNGAPVH QQTDEGGSVP RNSMKVFLKQ TESEKRPLSI Quence n #: NM_0042 .1092	VPTPRPGACT VHRVPGLHHT YANSHSUVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT QDSPVEVSPV	TNSARERKIN YDVLFLOTGD V PMANCSLYR SSVVSPSPVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR CPRPRVRLGS	SSLQLPDRVL GREHKAVSVG SCGDCLLARD TGEKPCBQVQ LGEFQCMSLE DRSYWKEFLV PLNGLGPPST EIRDSVV	420 480 540 600 660 720 780
55	TSPIKAGLIC FTMKDVQRVP NFHKDMFHMD PRVHITBELQ PYCHMSGSSC PQPNTVHTLA BGGQQLVASY MCTLFPLAVL PLDHRGYQSL Seq ID No: Nucleic Ac Coding seq 1	SRPDDGPPN SGLYKEVNRE GQVRSRMLLL IFSSGOPVON KHVSLYQPQL CPLLSNLATR CPEVVEDGVA LPVLFLLYRH SDSPPGSRVF 480 DNA se- id Accession uence: 58.	TQQNYTYTHP QPQRRYQPA LLLDTHRGLL ATRPHIQDLE LMLRNGAPYM DQTDEGGSVP RNSHCVFLKQ TESEKRPLSI Quence n #: NM_004: .1092 21	VPTFRFGACI VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLFT VIISTSRVSA GECASVHPKT QDSFVEVSFV 217.1 31 AGCTCTCCTC	TNSARERLIN YDVLFLOTGD YPMANCSLYR SSVWSPSFVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR CPRPRVRLGS 41	SSLOLPDRVL GRLHKAVSVG SCGDCLLARD TGERFCEOVG LGEFOCNSLE DRSYWKEFLV PLNGLGFPST EIRDSVV	420 480 540 600 720 780
55	TSPLKAGLIC FTMKUVGRVF NFLKDHFLMD PRVHITEBLQ PYCHMSGSSC POPNTVHTLA BGFQQLVASY MCTLFVLAVL PLDHRGYGSL Seq ID NO: Nucleic Ac Coding seq	SREDDGPFN SGLYKEVNRE GQVRSRMLLL IFSSGDVQN KNVSLYOPCL CPLLSNLAFR CPEVVEGOVA LPVLFLLYRH SDSPPGSRVF 480 DNA se id Accessic uence: 58. 11 jagdagagagagagagagagagagagagagagagagagag	TQQMYTTHPA QPQARYQPA QPQARYQPA LLLDTHRGLL ATRPWIQDIE LMLRMSAPVM DQTDEGGSVP RNSWKVFLKQ TESEKRPLSI QUENCE n #: NM_004: .1092 21 CTTGGACCCC	VPTRPGACT VHRVPGLHHT YANSHSGVVQ GASANDLCSA ASASCHVLPT VIISTSRVSA GECASVHPKT QDSFVEVSPV 217.1 31 AGCTCTCCTC TACGGCCGAC	TNSARERKIN YDVLFLOTGD YPMANCSLYR SSVVSPSFVP GDLLLVGTQQ PAGGKASWGA CPVVLPPETR CPRPRVRLGS 41 CCCCTTTCTC AGACGGCTCC	SSLQLPORVL GRLHKAVSVG SCGDCLLARD TGEKPCROVQ LGEFQCMSLE DRSYWKEFLW PLNGLGPPST EIRDSVV	420 480 540 600 660 720 780
55	TSPIKAGLIC FTMKUVGRVP NFIKUMFILMD PYCAMSGSSC POPNTYNITLA BGPOGLVASY MCTLFVLAVI Seq ID NO: Nucleic Ac Coding seq 1 GGCCGGGAGG GGCCCCCALAGG	SREDDOFPFN SGLYKEVWRE GQVRSRMLLL IFSSGQVVGN KHVSLYGPGL CPLLSNLATR CPEVVEDGVA LPVLFLLYRH SDSPFGSRVF 480 DNA se tid Accession uence: 58. 11 GTAGGAGTGC AGAACTCCTA	TQQMYTTHPA QPQARYQPA LLLDTHRGLL ATRPHIQDLE LMLRNGAPYN DQTDEGGSVP RNSMKVFLKQ TESEKRPLSI Quence n #: NM_0042 .1092 21 CTTGGACCCC CCCTGGCCCC	VPTPRFGACT VHRVPGLHHT YANSHSGVVQ GASANDLCSA ASASCHVLFT VIISTSRVSA GECASVHPKT QDSFVEVSPV 31 31 AGCTCTCCTC TACGGCCGAC	TNSARERLIN YDVLFLGTGD YPMANCSLYR SSVYSPSTVP GDLLLVGTQQ PAGGKASNGA CPVVLPPETR CPRPRVRLGS 41	SSLOLPORVL GRIHKAVSVG GRIHKAVSVG GRIGHCHARD TGERFCEQVG LGEFQCMSLE DRSYWKEFLV PLNGLGFPST EIRDSVV 51 TCTAAGGATG ATCTGGCCTG	420 480 540 600 720 780
55	TSPLKAGLIC FTMKUVGRVP NFLKDMFLMD PRVHIIBELQ PYCHMSGSSC FQPNTVHTLA BGFQGLVASY MCTLFVLAVL PLDHRGYGSL Seq ID NO: Nucleic Ac Coding seq 1 GGCCGGGAGA GCCCAGAGG AGCACCCTGC ATGAGCGCT	SREDDOFPFN SGLYKEVWRE GQVRSRMLLL IFSSGQPVGN KHVSLYGPGL CPLUSNLATA LPVLFLLYRH SDSPPGSRVF 480 DNA se id Accessic uence: 58. 11 j GTAGGAGTGC AGAACTCCTA CCCAGGGGT CCAATTCCAA	TQQMYTYTHPA QPQARYQMA LLLDTHRGLL ATRPWIQDIE LMLENGAPVN DQTDEGGSVP RNSHKVPLKG TESEKRPLSI Quence n #: NM_0042 .1092 21 CTTGGACCCC CCCCGGGACC CCCCGGGACCC CCCCGGACAGC	VPTFFFGACT VHRVPGLHHT YAASHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVIPKT QDSFVEVSPV 31. 31. AGCTCTCCTC TACGGCCGAC GAGCCTGTCA GCCCTGGCC	TNSARERIIN TOVLFLOTOD VPMANCSLYR SSVVSPSEVP GDLLLVGTQQ PAGGKASMGA CPVVLPPET CPRPRVRLGS 41 COCCTTTCTC AGAGGGCTGC AGAAGGGTGT	SSLOLIPORVL GRLHKAYSVG SCGDCLLARD TGERPCSOVG LGEPGCNSLE DRSYMKEFLV PLNGLGPPST EIRDSVV 51 TCTAAGGATG ACTOTOCCTC ACTOTOCCTC GGAGAATAGC	420 480 540 600 660 720 780
55	TSPLKAGLIC FTMKUVGRVP NFLKUMFLND PYCHITEBLO PYCAMSGSS POPMTVHITEBLO PYCAMSGSS POPMTVHITEBLO PYCAMSGSS POPMTVHITEBLO PYCAMSGSS SEQ ID NO: Nucleic Ac Coding seq I GCCOGGAGGA GCCCCGCAGAGG AGCACCCTGC ATGAGCCGGT ATGAGCCGTC	SREDDOFPFN SGLYKEVWRE GQVRSRMLLL IFSSGQVVGN KHVSLYGPGL CPLLSNLATE CPEVVEDGVA LPVLPLLYRH SDSPPGSRVF d480 DNA se- id Accessic uence: 58. 11 TAGGCAGTGC AGAACTCCTA CCCAGGGAGT CCCAAGGGAGT CCCAGGGAGT CCCAAGGGAGT CCCAAGGGAGT CCCAAGGGAGT CCCAAGGGAGT CCCAAGGAGT CCCAAGGCGAGT CCCAAGGGAGT	TQQMYTYTHPO PQQARYQRVA LLLDTHRGLL ATTEMIQDIE LMLRNGAPVN DOTDEGGSVP RNSHCVFLKQ TESSKRFLSI QUENCE n #: NM_004: .1092 21 CTTGGACCCC CCCCTGGGCCC CCTCCGGGAAA GCCCACAGCT	VPTPRPGACT VHRUPGLEHT YANSHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVSA GECASVHENT ODSFVEVSPV 217.1 31 AGCTCTCCTC TACGGCCGAC GAGCCTGTCA GCCCTGGCC TTCACAGATTC	TNSARERKIN YDVLFLGTGD YPMANCSLYR SSVVSPSTVP GDLLLVGTQ0 PAGGKASMGA CPVVLPPETR CPRPRVRLGS 41	SSLOLIPORVL GRIHKAVSVG SCBCCLLARD TGEKPCEQVG LGEPQCMSLE DRSYMKEFLV FLNGLGFPST EIRDSVV 51 TCTAAGGATA ACTTGCCTC GGAGATAGC GATTGGGCGT GATTGGGCGT GATTGGGCGT	420 480 540 600 660 780 780
55	TSTEMROLLE TSTEMROUPE TSTEMENTEN NFINITEN THE TOTAL THE	SREDDOFPFN SGLYKEVWRE GOVRSRMLLL IPSSGOPUON KHUSLYOPQL CPLLISNLATR CPEVVEDGVA LPVLFLLYRH SDSPPGSWA 480 DNA se id Accessic uence: 58. 11 GTAGGAGTGC AGGAGTGC CGAGGGGTC CGAGGGGTC CGAGGGGTC CGAGGGAGTGC AGGGGAGTGC CGAGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGAGTGC AGGGAGTGC AGGGGAGTGC AGGGGAGTGC AGGGAGGGAGTGC AGGGGAGTGC AGGGAGGAGTGC AGGGAGGGAGTGC AGGGAGGAGTGC AGGGAGGAGTGC AGGGAGGAGTGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGC AGGGAGGAGC AGGGAGGAGC AGGGAGC AGGGAGC AGGGAGGAGC AGGGAG	TQQHYTYTHPA QPQARYQMA LLLDTHRGLL ATRPWIQDIE LMLENGAPVH DQTDEGGSVP RNSHKYPLSI Quence n #: NM_0042 1.1092 21 CTTQQACCCC CCTCGGAAA GCCCACAGCT AACGGGCCAC	VPTRPGACT VHRVPGLHHT YANSHSGUVQ GASARDLCS ASASCHVLPT VIISTSRVSA GECASVHEXT QDSFVEVSPV 31. 31. AGCTCTCCTC TACGGCCGAC GAGCCTGTCA GCCCTGGCC TTCACAATTG TACTGGCTC	TNSARERINI TOVALIGATION VPMANCSLYR SSVYSPSTVP GDLLLVGTQQ PAGGKASMGA CPVULPPTC CPRPRVRLGS 41	SSLOLIPORVL GRLHKAVSVG SCGDCLLARD TGERFCSOVG LGEFGCASLE DRSYWKEFLV FINGLGFPST EIRDSVV 51 TCTAAGGATG ACTTGCCTG GGGGAATAGC GATTTCAGGCTTT AGCCATTTC	420 480 540 600 720 780 120 180 240 3300
55	TSPLKAGLLE FYMKUVGRVF NFLKUMFLND PYVHITABLE PYCHMSGSSC POPMYTWITA BGFQQLVASY MCTLFYLAVU PLDHRGTQSL Seq ID NO: Nucleic Ac GGCCGGGAGA GCCCGGGAGA GCCCAGAAGG GCCCAGAAGG AGCACCTGG ATGAGCGGC CCTTGGGGC ATGAGCGGC CCTTGGGCA ATGAGCGGC CCTTGGGCA ATGAGCGGC CCTTGGGCA ATGAGCGGC CCTTGGGCA ATGAGCGGC	SREDDOFFFN SGLYKEVWRE GQVKSRMLLI LFSSGQVM KHVSLYQPGL CPLLSNLAR CPEVVEDGVA LPVLPLLYAR SDSPPGSRVF 480 DNA se id Accessio uence: 58. 11 GTAGGAGTGC AGAACTCTT AAGGCAGTT CCAAGGCAGTT CCAAGGCAGTT CTAAGGTCCT TCAAGGTCT TCAAGGTCCT TCAAGGTCCT TCAAGGTCCT TCAAGGTCCT TCAAGGTCCT TCAAGGTCCT TCAAGGTCCT TCAAGGTCCT TCAAGGTCCT TCAAGGTCCT TCAAGGTCCT TCAAGTCCT TCAAGTCCT TCAAGGTCCT	TQQMYTYTHPA QPQARYQPA LLLDTHRGLL ATREMIQDIE LMLRNGAPVN DQTDEGGSVP RNSHKVFLKQ TESSKRFLSI Quence n #: NM_004: .1092 21 CTTQQACCC CCCCTGGCCC CCCCTGGCCC CCTCCGGAAA GCCCACAGCT TGGAAACTGC TTCAAGTCC TTCAAGTCC	VPTPRFGACT VHRVPGLHHT YANSHSGVVQ GASAKDLCSA ASASCHVLPT VIISTSRVY 217.1 31 AGCTCTCCTC TACGGCCGAC GCCCTGGCC TTCACAATTG TACTTGGCTC TACGTTGGATT TACTTGGTGT TACTTGGTGT TACTTGGTGT TACTTGGTGT TACTTGGTGT TACTTGGTGT TACTTGGTGT	TNSARERINI TNYSARERINI TOVILIGATED VPMANCSLYR SSVVSPSPVP PAGGKASNGA CPVULPETR CPPRPRVRLGS 41 COCCTTTCTC AGAGGGTCAT AGAGGTCAT ATGACTTTGA AGGAGAGAAGA AGGAAGGAAGAAGAAGAAGAGGAAGGAGAGGAG	SSLOLIPORVL GRIHKAVSVG SCGDCLLARD TGEKPCBOVG LGEPQCMSLE DRSYWKEFLV S1	420 480 540 660 720 780 120 120 240 300 3420
55 60	TSFLKAGLLC TSFLKAGLLC TSFLKAGLC NFTMUNFLM NFTWINFLM NFTW	SREDDGFFFN SGLYKEVWRE GQVKSRMLLL IFSSGGVHL IFSSGGVHL KHVSLYOPGL CPLLSNLH CPEVVEDGVA LPVLFLLINH SDSPPGSRVF 480 DNA se unce, 58. 11 GTAGCAGTGC AGRACTCCTA CCCAGCGAGT CCAATGTCCA CCAAGGACT TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTCC TCAAGGTC TCAAGGTC TCAAGGTC TCAAGGTC TCAAGGTC TCAAGGTC TCAAGGTC TCAAGGTC TCAAGGTC TCAAGGTC TCAA	TOOMYTYTHYA OPOARYONA LLLDTHRGLL ATREMIQDIE LMLRNSAPVM DOTDEGGSVP RNSWKVFLKO TESEKRPLSI QUENCE n #: NM_0042 21 CTTGGACCCC CCCCTGGGCC CCTCCGGAAA GCCCACAGCT AACGCGCCAG CCAGGCCCCC CCTCGAGCCCC CCTCGAGCCCC CCTCGAGCCCC CCTCGAGCCCCC CCTCGAGCCCCC CCCCAGGCCCCCCCCCC	VPTPRPGACT VHRVPGLHHT YANSHSGVVQ GASANDLCSA ASASCHVLPT VIISTSRVLPT ROSPVEVSPV 217.1 31 AGCTCTCCTC TACGGCCGAC GAGCCTGTCA GCCCTGGCC TICACAATTG TACTGGCCC CAGATAGASA CTGCACCATC	TNSARERKIN TOVLHEAGO V PMANCSLYR SEVVSPSEV GDLLLVGTOQ PAGGRASH CPVVLPPETR CPRPRVRLGS 41 COCCTTTCTC AGAGGGCTCC CCCATCTGC AGAAGGTGAT ATGACTTGAA AGGAGGAGTAA	SSLOLIPORVL GRIHKAVSVG SCGICLLARD TGBEPCESUC LGEPCCKSLE BRSYWKEPLV PLNGLGPPST EIRDSVV 51 TCTAAGGATG ACTTOGCCTG ACTTOTCCTC GGAGAATAGC GATTOGCGTT GGAGCATCAG GOGTCTCTAC	420 480 540 600 720 780 60 120 120 240 340 340 480
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555 60 65 70	TEPLEAGLE PRINCIPAGE PER PER PRINCIPAGE PER PRINCIPAGE PER PRINCIPAGE PER PER PER PER PER PER PER PER PER PE	SREDDOFPTM SREJYENMELL GOVERNMELL	TOOHYTYTHE OPPRIVATE OPPRIVATE LITERIO DI LITERIO DI LITERIO	VPTPROMCT VPTPROMCT VPTPROMCT VPTPROMCT VPTPROMCT VPTPROMCT 31 AGCTCTCTC TAGGGCGGAC AGCCCTGGC TTCACATCTCACAT TTCACATTCACAT TTC	TISARERINI TISARERINI TIVUTELOTO TPU	SSLQLEPSYL GRILHRAYSY SCHICLLARD TERPHCROV LEBYOCHSLE PLINELEPSYL STEPHINGLEPSYL I TETANGGATG ANTHOGOCTO ANTHOGOCTO ANTHOGOCTO ANGOCHTOLA ANGOCHTOLA CONCESSION	420 480 600 660 720 780 120 180 240 420 480 900 900 1080 1080 1080 1080 1080 1080

1 11 21 31 41 51

WO 02/086443 PCT/US02/12476 MACKENSYPW PYGROTAPSG LSTLPORVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN SSGTPDILTR HPTIDDFEIG RPLGKGKFGN VYLAREKKSH FIVALKVLFK SQIEKEGVEH 120 OLRREIEIOA HLHHPNILRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDBQRTATI 190 MEELADALMY CHOKKVIHRD IKPENLLIGE KGELKIADFG WSVEAPSLER KTMCGTLDYL PPRMIEGEMH NEKUDLNCIG VLCYELLVGN PPFESASHNE TYRRIVKUDL KFPASVPTGA 240 ODLISKLIRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSVA Seg ID NO: 482 DNA sequence 10 Nucleic Acid Accession #: AK055663 Coding sequence: 38..1423 31 15 AGAACSGCTT CCGGCGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTCG ANALOGACHA AGATOCTITT TTOGCAGGII GITACGGGAA TITAGACTIG TAGCAGCTGA CCGAAGGTCC TGGAAGATAC TGCTCTTTOG TGTAATAAAC TTGATATGTA CTGGCTTCCT 120 GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT TTTTGATCTT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC
TAGCCCTGTC TATTCATTTG GGTTTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCTCCAC 200 360 AGTCTTGGCA CAGTGGGAG CTCTCTTAT ATTAAAAGAA AGTGCAGAAC GCTTTTTGGA ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA 420 CCTGTTCACG ATGCTTTCTA TTCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG TACGAGCTGG CTTCAAGAGC ATGTTGCAGA TCTTAGTCGA AGCTTGGTGG GAATTATTCC
GGGACTTAGC AGTATCTTCC TTCCCCGAAT GAATCCATTT GTTTTGATTG ATCTTGCTGG 600 2.5 660 AGCATTTGCT CTTTGTATTA CATATAGCT CATTGAAATT AATAATTATT TTGCCGTAGA 720 CACTGOCTOT GCTATAGTA TEGCETIGAT GACATTEGG ACTACTAGT COATGATGT
GTACAGTGG ARACTETTA TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA ACTICATIONG GAGGIATICTA CUTTAGATGG AGITTITAGAA GTCCGAAATG AACAITTITG 900 30 GACCCTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTGGAC GAGATGCCAA 960 TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC 1020 TOTTCAAATT TTCAAGGATG ACTGGATTAG GCCTGCCTTA TTGTCTGGGC CTGTTGCAGC TOTTCARATT TECHNICATE ACTIGNATION CATCOCARTS CONTITUTAR AGGITACTOR
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TGCCTRAGC TCCGAGTAG CTGGAGTTAC AGGCACTGC CACCAGGC AGCTATTT 2046
TGTATTTTTA GTANARAGGG GOGATTTCC CACCAGGC AGGCAGTC TGAACTCCTC 2100 50 TOTATITTA OTAMBAGOS GOGATITAC CANTILUZC REGIMENT MARAGALIA ACCIANGAI CACCACACT TRACETOCA REGIGIORGE ATTAGOTICO REGIOCAGOA CETOGOCGAI ATTICITTA ATGALATITA TANATATICI TETUGATAR TEXCATITI AGUALDOGO ANATOTICO TECANAMOT ARAG 2160 2220 2280 TTTTTAGCAG AAATTTTGGA ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA 2400 55 GATTITIGTT AAAGTITCTC TCCFTTAAAA ATTITAGTAC ATTIGTAAAT Seq ID NO: 483 Protein sequence Protein Accession #: BAB70980.1 60 31 MOTIHLERKE ORSEFGKLLE EFELVAADER SWKILLEGVI NLICTGELLM WOSSTNSIAL MOTTHERRY (REFFORLER BERUVANDER SWATHERVI MURCHERE VLAUFASTVI AGGALFILK TAYTYLTIFD LFSLMTCLIS YWVILRKPSP VYSFGFERLE VLAUFASTVI AGGALFILK ESARRFUEOP EINTGRLUG TYVALCFALF TMLSIRNKFF AYVSKAASTS WLQENVADLS 180 EGARRYLEGP EHYGGLIVO TPVALCHNE TOLSINKEY AVSKAASIS WLJENVALUS RELGGIIPG SSTIEPSNOT PVILDLAGFA ELGTTYNLE INDYFAVOTA SATALAMTF GTWYRMSY'S GKVLLGTTPP RVIGGLIKLI REVSTLODYL EWNEHFATL GFGSLAGSVI WEIRROAMEQ MVLAHVINEL YTLWSTLIVQ IFKODNIRPA LLSGYVANNV INFSDREVLT MPLIKATODL MPVISTPAKE SSPPERSEN TIGINVIPVI LIANTYRRYG FELMIGHTPY 65 240 300 SSMLNQGLGV PGIGATQGLR TGPTNIPSRY GTMNRIGQPR P 70 Seq ID NO: 484 DNA sequence Nucleic Acid Accession #: FGENESH predicted Coding sequence: 1..900 75 ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CGCCCCGC TCCGGGCCCC GACCCCTCCC GCCGTGGGCA AGRGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180 20 COGCCCACTG COCTOGACAC CTTCTCTGGT ACGTACUTTC AATCGCCCGT GCGGCCGCGT 240 GGCTGCGGG GGGCTGTGCA CCGGGGAGCT GGGGCGGGGG TCTCGGCGGG AGGGCGCAGA GGACCCCGGG GAGGAGACTG GAGCAGGCCC CGAGGTGGCG CTGGTGCGGC CCAGGACGCT 300 360 CTTCCTAACT CAGGCTCTCC CCGCCCCGCC CCTGCAGTGC AAGTCCTGGT GGATGGAGCT CCGGTGCGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTTCC 480 85 540 600

5	GACCAGGGGG ATCCGAGCCT TTTGACTCGG	086443 GCOGGRAGG GCTGCTACCT CTATTCTCAG TGCGCACCCT	TGAGTGCTCA TGCCATTGAG	GCCTTGACGC CACAAAGCCC	AGAAGAACTT GGCTGGAGAA	GAAGGAAGTA	720 780 840
,	Seq ID NO: Protein Acc	485 Protei: ession #: 1	sequence GENESH pred	licted			
10	RPTALDTPSG LPNSGSPRPA PONITEKWLP	11 PPPLRAPTPP TYVQSPVRPR PAVQVLVDGA EIRTENPQAP	PVRIELWDTA VLLVGTQADL	GAGVSAGGER GQEDFDELES EDDVNVLIQL	GPRGGDWSRP LCYPDYDVFL DQGGRBGPVP	RGGAGAAQDA ACFSVVQPSS QPQAGGLAEK	60 120 180 240
15	Seq ID NO: Nucleic Aci	486 DNA sed d Accession dence: 17	FDSAILSAIE quence 1 #: XM_063	HKARLEKKLN	AKGVRTLSRC	RWKKFFCFV	
20	1	11	21	31	41	51	
25 30	CCGCGGGGGC GCCGTGGGCA CGGCCCACTG ATTGAGCTCT CCGGATACCG ATCACAGAGA	GGGAGCTGAG GTAGCGCGCC AGAGCAGCCT CGCTGGACAC GGGACACAGC ATGTCTTCCT AATGGCTGCC AGGCCGACCT	CATCGTCAGC CTTCTCTGTG GGGACAGGAG GGCGTGCTTC	GGCATCAAGT TACACCTGCA CAAGTCCTGG GATTTTGACC AGCGTGGTGC ACCCACAAGC	GCGTGCTGGT ATGGGTACCC TGGATGGAGC GACTTCGTTC AGCCCAGCTC CCCAGGCGCC	GGGCGACGGC CGCGCGCTAC TCCGGTGCGC CCTTTGCTAC CTTTCAAAAC TGTGCTGCTG	60 120 180 240 300 360 420 480
	GGCCGGGAGG TGCTGCTACC GCTATTCTCA	GCCCCGTGCC TTGAGTGCTC GTGCCATTGA TCTCCCGCTG	CCAACCCCAG AGCCTTGACG GCACAAAGCC	GCTCAGGGTC CAGAAGAACT CGGCTGGAGA	TGGCCGAGAA TGAAGGAAGT AGAAACTGAA	GATCOGAGCC ATTTGACTCG TGCCAAAGGT	540 600 660
35	Seq ID NO:	487 Protein	sequence				
		ession #: 1	CP_063832.1		41	51	
40	RPTALDTFSV ITEKNLPEIR	11 PPPLRAPTPP QVLVDGAPVR THNPQAPVLL	PRRRSAPPEL IELWDTAGQE VGTQADLRDD	DFDRLRSLCY VNVLIQLDQG	AVGKSSLIVS PDTDVFLACF GREGPVPQPQ	YTCNGYPARY SVVQPSSFQN AQGLAEKIRA	60 120 180
45	Seq ID NO: Nucleic Act	QKNLKEVFDS 488 DNA se id Accession sence: 64	nuence		VKTLSRCKNK	KFFCFV	
50	1	11	21	31	41	51	
	ACCATOCCCC	CGGGGCCTGC GGCAGCTCAG	CGCGGCGGCC	GCGCTCTTCG	CGTCCCTGGC	CGTAATTTTG	60 120
55	ACTGCAGCAG CCTCACCAAA ACAGTAAAAA ATTACCTACA	GTCAAATGAG CAACAGTACA CTTTAGCAGC TTCCAACAAC CCCTGGTCAC	GGACATAAAA AAGATTCATG TACCCCAGCA AACCCAGGCC	AAACCTGTCC GATGGTCATA ACTACAAAAA ACACCCAACA	AGCAACCAGC TCACCTTTCA ACACTGCAAC ACTCACACAC	TAAGCAAGCA AACAGCGGCC CACCAGCCCA AGCTCCTCCA	180 240 300 360 420
60	CCACCAGCTC ACTCAACCCA ACAACCGGTC AATACCACCC	TTACAGTOGG ATACAGCTGG GTAACCAGAC AGAAGCCTGA GCACAGCTGC	AACCAGTTCA CACCCTTCCA TCAACCCACC ACCTGCCTCC	TCAACCGTCA GCAACTTTAT CATGCCCCAG ACGGTTCCTG	GCCACACAC CGATAGCACT GAACAACGGC GGCCCACCCT	TGGGAACACC GCACAAAAGC AGCTGCCCAC TGCACCTCAG	480 540 600 660 720 780
65	GCAGAGATGG TACTTCAACA AACCTTCTGT TCATATTATA	GGATACAGCT TCGACCCCAA TGAATTTTCA TCAGTGAAGT	GATTGTTCAA CGCAACGCAA GGGCGGATTT GGGAGCCTAT	GACAAGGAGT GCCTCTGGGA GTGAATCTCA TTGACCGTCT	CGGTTTTTTC ACTGTGGCAC CATTTACCAA CAGATCCAGA	GACAGTTAC	940 900 960 1020
70	CAAGGAATCA GTGAGTGAAC CTTCAAGCCT TACACAATTG GGTGTCTATA	AACATGCGGT AGAGCCTCCA TTGATTTTGA TGCTTCCTGT AAATGCGCCT	GGTGATGTTC GTTGTCAGCC AGATGACCAC GATTGGGGCC AAGGTGTCAA	CAGACAGCAG CACCTGCAGG TTTGGAAATG ATCGTGGTTG TCATCTGGAT	TCGGGCATTC TGAAACAAC TGGATGAGTG GTCTCTGCCT ACCAGAGAAT	CTTCAAGTGC CGATGTCCAA CTCGTCTGAC TATGGGTATG CTAATTGTTG	1080 1140 1200 1260 1320
75	TTGGGAAATT AATGAAGTGA GTTTATTTA GCCACTCAAA	GTCAACATTT	ATTTAAGTTC AGTGAGCTGT GAGATATGTT	CAAACAATGT AGGCAGCACA TTATTTTCTA GAATTAACAT	AAACCACCAT TCAATTTCTA GTTTCCTTTA AATATATGTA	AATACITTTT GAATATITTA AAGTAGAATA	1380 1440 1500 1560 1620
80	ATTITATITE GCTTTTACTA ACTCCTTTTC	CACTTTAAAT	TTAACAAAGC ATGGTTTCAT TTGTTTTTGT	CTTTGCTTTG GTAACATACA TTTTTGAGAC	TATCAAATG TATTCCTGGT GGAGTTTCAC	GACTTTCAGT	1680 1740 1800 1860 1920
85	TGATTCTCCT GCTAATTTTT CTCTTGACCT	GCTTCAGCTT	CCCGAGTAGC TATAGACGGG ACCCACCTCA	TOGGATTACA TTTCACCATG GCCTCCCAAA	GGCACACACT TTGGCCAGAC GTGCTGGGAT	ACCACGCCTG TGGTCTTGAA TACAGGCATG	1980 2040 2100 2160

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	GTTGTCTAAG	TGTTTTTATG	TAAAACCAAC AATTGCTAGA	AAAAAGAACA	AATCAGCTTA	CATCCTACAA	2220
	CTRAACAATA	AGCAAGAGAC	DTAATAATA	CCCCTTAATT	ATTAACAAAG	TGCCAGAGTC	2340
5	TAGGCTAAGC	ACTUTATOTA	TATCTCATTT	CATTCTCACA	ACTTATAAGT	GAATGAGTAA	2400
5	ACTGAGACTT	AAGGGAACTG	AATCACTTAA	ATGTCACCTG	GCTAACTGAT	GGCAGAGCCA	2460
	CAGCTTGAAT	CATGTTGGT	CTGACATCAA ACACTCTGCC	TOBAGGCTCA	CACCTCATAC	CACCARGITA	2520
	TCACCTTACA	COCCAAATOGG	TTTATCCAGG	ATCATGAGAC	ATTAGGGTAG	ATGAAAGGAG	2640
10	ACCTTTGCAG	ATARCARAT	AGCCTATCCT	TAATAAATCC	TOCACTOTOT	GGAAGGAGAC	2700
10	TGAGGGGCTT	TGTAAAACAT	TAGTCAGTTG TAAACTCAAA	CTCATTTTTA	TGGGATTGCT	TAGCTGGGCT	2760 2820
	ACTTOCCTAR	COMMOTORA	TARACTCAM	GTATAGCCCC	ATTTTTTTGA	AACTTGCTGC	2880
	TTCTGCACTT	CATATCCATA	TTTCTTGAGT	TTCACTTTAT	TCTGTAGAGC	AGCCTGCCAA	2940
1.5	GAATTTTATT	TCTGCTGTTT	TTTTTGCTGC	TAAAGAAAGG	AACTAAGTCA	GGATGTTAAC	3000
15	AGAAAAGTCC	ACATAACCCT	AGAATTCTTA TGTTTCCTTA	GTCAAGGAAT	AATTCAAGTC	AGCCTAGAGA	3060 3120
	TROTCTTART	AAAACATTGA	ATTGTAGTAA	AGGTTTTTGC	AATAAAAACT	TACTTTGG	3120
20		489 Protein	sequence NP_0552				
20	Protein Acc	cession #:	NF_0552	13.1			
	1	11	21	31	41	51	
	1	1	1	1	1	1	60
25	MPRQLSAAAA	CHIMPOWAR	DGSQMRAKAF VKIPTTPAT	PETROYSUPT	WWINDINK	PAUCLANDAN	120
20	TRUTIMIDEL A	DVST.DDTTTD	DAHTACTERS	TVEHTTONTT	OPSNOTTLPA	TLSIALHKST	180
	TGOKPDOPTH	APCTTAAAHN	TTRTAAPAST	VPGPTLAPQP	SSVKTGIYQV	LNGSRLCIKA	240
	EMGIQLIVQD	KESVFSPRRY	FN IDPNATQA	SGNCGTRKSN	LLLNFQGGFV	NLTFTKDRES	300 360
30	ON PREFERENCE	TVSDPETVYQ	GIKHAVVMFQ TIVLPVIGAI	TAVGHSFRCV	ARGREGISTOR	SGVORT	360
50	ONLDI SDDIII	GAVDECOOD I		***************************************	· · · · · · · · · · · · · · · · · · ·		
	Seq ID NO:	490 DNA se	puence				
	Nucleic Ac:	id Accession	1 #: NM_005	409.3			
35	course sed						
	1	11	21	31	41	51	
	nnoownnoo.n	onnor corm	TCTACTCCTT	CONTRACTOR	CACCABACCE	GARCTAGCAG	60
	CARCACICACC	ACCACCAACA	CCARARACA	AACATGAGTG	TGAAGGGCAT	GGCTATAGCC	120
40	TIGGCTGTGA	TATTGTGTGC	TACAGTTGTT	CAAGGCTTCC	CCATGTTCAA	AAGAGGACGC	180
	TGTCTTTGCA	TAGGCCCTGG	GGTAAAAGCA CTGTGACAAA	GTGAAAGTGG	CAGATATTGA	GAAAGCCTCC	240 300
	ATAATGTACC	GARGTARCAA	TOTOTALATOR	ATMUARGUA	GGCTTATAAT	CAAAAAAGTT	360
	GAAAGAAAGA	ATTTTTAAAA	TCCCAAATCG ATATCAAAAC	ATATGAAGTC	CTGGAAAAGG	GCATCTGAAA	420
45							480
	AGACTTTTCT	ATGGTTTTGT	GACTTTCAAC GAAATACAGT	TTTTGTACAG	TTATGTGAAG	GATGAAAGGT	540 600
	COCCOCCAAAC	CACCCCACCA	ACCURAGOS	TTTCTAGGAA	ARGUTACUTT	AAGRAAGGCT	660
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50	GCATTTCTAG	GCTAGAGAAC	CTTCTAGATT	TGATGCTTAC	AACTATTCTG	TTGTGACTAT	780 840
	GAGAACATTT	CTGTCTCTAG	AAGTTATCTG TTGACATTAT TTCCTCAAAC	TUTGTATTCA	PROCESSAL	ATATTACIAT	900
	CATCTATGTG	TOGTAAAGCA	TTCCTCAAAC	ATTTTTTCAT	GCAAATACAC	ACTTCTTTCC	960
	CCAAATATCA	TGTAGCACAT	CAATATGTAG TGTAATTCAT	GGAAACATTC	TTATGCATCA	TTTGGTTTGT	1020
55	TTTATAACCA	ATTCATTAAA	TGTAATTCAT ACATATTTCA	AAAATGTACT	AAAAAAAA	TTATAOGCTA	1080
	TGGGATACIG	GCAACAGTGC	CATTGAGATG	TAACCAAATT	ATTAGGATAT	GTGTGTTTAC	1200
	TGTACTTTTT	GTTTTGATCC	GTTTGTATAA	ATGATAGCAA	TATCTTGGAC	ACATTTGAAA	1260
	TACAAAATGT	TTTTGTCTAC	CAAAGAAAAA	TGTTGAAAAA	TAAGCAAATG	TATACCTAGC	1320
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	GTCATTTTTT	TOTOTATAG	ACTACCACAA	CCTTTCTTTT	TTAAAAAAAA	AAA	1440
65	Seg ID NO:	491 Protei	n sequence				
65	Protein Acc	491 Protein cession #: 1	₹P_005400.1				
65	Protein Acc	491 Protes: cession #: 1	n sequence FP_005400.1	31	41	51	
65	Protein Acc	cession #: 1	(P_005400.1 21 	i -	Ĭ.	1	
65 70	Protein Acc	cession #: 1	IP_005400.1	LCIGPGVKAV	Ĭ.	1	60
	Protein Acc 1 MSVKGMAIAL EVIITLKENK	11 	P_005400.1 21 GFPMFKRGRC QARLIIKKVE	LCIGPGVKAV	Ĭ.	1	60
	Protein Acc 1 MSVKGMAIAL EVIITLKENK Seq ID NO:	11 	P_005400.1 21 GFPMFKRGRC QARLIIKKVE	LCIGPGVKAV RKNF	Ĭ.	1	60
70	Protein Acc 1 MSVKGMAIAL EVIITLKENK Seq ID NO: Nucleic Ac:	11	NP_005400.1 21 GFPMFKRGRC QARLIIKKVE guence	LCIGPGVKAV RKNF	Ĭ.	1	60
	Protein Acc 1 MSVKGMAIAL EVIITLKENK Seq ID NO: Nucleic Ac:	11 	P_005400.1 21 GFPMFKRGRC QARLIIKKVE guence 1 #: NM_000	LCIGPGVKAV RKNF	KVADIEKASI	 MYPSHWCDKI	60
70	Protein Acc 1 MSVKGMAIAL EVIITLKENK Seq ID NO: Nucleic Ac:	11	NP_005400.1 21 GFPMFKRGRC QARLIIKKVE guence	LCIGPGVKAV RKNF	Ĭ.	1	60
70	Protein Acc 1 MSVKGMAIAL EVIITLKENK Seq ID NO: Nucleic Acc Coding sequent	11 AVILCATVVQ GQRCLNPKSK 492 DNA seid Accession dence: 41	P_005400.1 21 GPPMFKRGRC QARLIIKKVE guence 1 #: NM_000 21	LCIGPGVKAV RKNF	KVADIEKASI	MYPSNNCDKI	60
70 75	Protein Acc	11 AVILCATVVO QQRCLNPRSK 492 DNA sei id Accession wence: 41	P_005400.1 21 GFPMFKRGRC QARLIIKKVE Numence 1 #: NM_000 520 21 TGTCCTATCA CCAGGAGAT	LCIGPGVKAV RKNF 0577.1	KVADIEKASI 41 ATGGCTTTAG AGAATCTGGG	 MYPSHNCDKI 51 AGACGATCTG ATGTTAACCA	60 120
70	Protein Acc 1 MSVKGMAIAL EVITILKENK Seq ID NO: Nucleic Ac: Coding sequ 1 GCCACGACGC COGACCTC COGACCTC COGACC	11 1 1 1 1 1 1 1 1 1	P_005400.1 21 GPPMFKRGRC QARLIIKKVE Quence 1 #; NM_000 220 21 TGTCCTATCA CCAGGAGGAT	LCIGPGVKAV RKNF 0577.1 31 31 GCCCCTCCCC GCAAGCCTTC	KVADIEKASI 41	MYPSHNCDKI 51 AGACGATCTG ATGITTARCGA CACCAAATGT	60 120 180
70 75	Protein Acc	11	P_005400.1 21 GFPMFKRGRC QARLIIKVE BUENCE 1 #; NM_000 520 21 TGTCCTATCA CCAGCAGAT ACAACCAACTA	LCIGFGVKAV RKNF 0577.1 31	KVADIEKASI 41 ATGGCTTTAG AGARTCTGGG TACTTGGAAG	MYPSHNCDKI 51 AGACGATCTG ATGTTAACCA CACCAAATGT TCTTGGGGAAT	60 120
70 75	Protein Acc 1 MSVKGMAIAL EVIITLKENK Seq ID NO: Nucleic Ac: Coding sequ 1 COCACCAGGG COCACCACCAGGG COCACCACCAGGG COCACCACCAGGG COCACCACCAGGG COCACCACCACCAGGG COCACCACCACCACCAC COCACCACCACCAC COCACCACCACCAC COCACCACCAC COCACCACCAC COCACCACCAC COCACCACCAC COCACCACCAC COCACCACCAC COCACCAC COCACCAC COCACCAC COCACCAC COCACCAC COCACCAC COCACCAC COCACCAC COCACCAC COCACCAC COCACCAC COCACCAC COCAC	11	P_005400.1 21 GPPMFKRGRC QARLIIKVE BUCHCC 1 #: NM_000 21 TUTCCTATCA CCAGCARGAT ACARCCARCT TOTCCTGTGT TOTCCTGTGT TOTCCTGTGT TOTCCTGTGT TOTCCTGTGT TOTCCTGTGT TOTCCTGTGT TOTCCTGTGT	LCIGPGVKAV RKNF 0577.1 31 GOCCCTCCCC GCAAGCCTTC AGTTGCCCGA CATTGAGCCT CAACTCTGGT GGACCAGGTCT	41 ATGCTTTAG AGARTCTOGG TACTTGCAGG CATCCTCTGT CATCAGCACAGCA	51 J AGACGATCTG ATGTTRACCA CACCAAATGT TCTTGGGGAT CACTCCAGCT	60 120 180
70 75 80	Protein Acc 1 MSVKGMAIAL EVITLKENK Seq ID NO: Nucleic Ac: Coding sequ 1 COCACGAGGG GOGAGCOTTC CAATTAGAGG GGAGGGCAGTT GATCAGGGGGGGGGG	11 1 AVILCATVVO GORCLNPKSK 492 DNA seid Accession mence: 41 11 1 GAACACCTCC GOGAGARAAT TATCTGAGGA GAANGATAC AACATCTCCC AACATCACTG	P_005400.1 21 GPPMFKRGRC QARLIIKKVE SUCCE THE NM_000 21 TGTCCTATCA CCAGCAAGAT ACAACCAACT ACAGCAACT ACTGGTACCA TGTCCTGTGT ACCTGTGTACCA CCACCACCAGCACCACCACCACCACCACCACCACCACCAC	LCIGPGVKAV RKNF 31 GOCCETCCC GCAAGCETTC AGTTGCCGGA CATTGAGCET CAAGTCTGGT GAACAGAAAG TITTGAGTCT	41 ATGGCTTTAG AGARTCTOGG TACTTGCAAG CATCGTCTGT CATCAGACCA CAGGACAAG GCGCGCTGCC	51 AGACGATCTC ATTTTAACCA CACCAAATCT TCTTGGGAAT CACTCCAGCT GCTTCGCCTT COGGTTGGTT	60 120 180 -240 300 360 420
70 75	Protein Acc 1 NSVKGMAIAL EVITILKENK Seq ID NO: Nucleic Ac: Coding sequ 1 GCCACGAGGG CGGAGGAGGTC CAATTAGAA CCATGGAGGG GGAGGCAGTT CATCGGCTCA CATCGGCTCA	11	IP_005400.1 21 GPPMFKRGRC QARLIIKKVE guence 1 #; NM_000 22 CCAGCAGCAT ACCAGCAGCAT ACTOGTACC ACCAGCAGCACAT ACCTGAGGGA CCACCAGC CTGACCACCAGCG CTGACCACCAGCC CTGACCACCAGCC CTGACCACCAGCC	LCIGPGVKAV RRNF 2577.1 31. 00000000000000000000000000000000000	41 ATGGCTTTAG AGASTCTIGGAG CATCAGACCA CATCAGACCA CAGGACAAGC GCGGCTGCC	51 AGRACGATCTG AGRACGATCTG ATGTTAACCA CACCAAATGT TCTTGGGGAT TCTTGGGGTC GCTTCGCCTT CCGGTTGGCTT CCGGTTGGCTT CCGGTTGGCTT	60 120 180 -240 300 420 480
70 75 80	Protein Acc 1 MSVKGMAIAL EVITLKENK Seq ID NO: Nucleic Acc Coding sequ 1 COCACCACGA COCACCACGA COCACCACGA COCACCACGA COCACCACGA COCACCACGA CATGAGA CATGAGAG COTCATGACA COTCATGACA COTCATGACA COTCATGACA COTCATGACA COTCATGACA	11 AVILCATVVQ OGRCINPKSK 492 DNA sei id Accession uence: 41 11 GAACACCTCC CCGAGAAAAT TATCTGAGGA AACATCACTG AACATCACTG CAAGATCACTG CACATCGCC CCGATGGACC CCGATGACC CCGATGACC CCGATGGACC CCGATGACC CCGATGGACC CCGATGGACC CCGATGGACC CCGATGGACC CCGATGGACC CCGATGACC CCGATGGACC CCGATGGACC CCGATGGACC CCGATGACC CCGATGACC CCGATGACC CCGATGACC CCGATGACC CCGATGACC CCGATGACC CCGATGACC CCGATGACC CCCATGACC	P_005400.1 21 GPPMFKRGRC QARLIIKKVE SUCCE THE NM_000 21 TGTCCTATCA CCAGCAAGAT ACAACCAACT ACAGCAACT ACTGGTACCA TGTCCTGTGT ACCTGTGTACCA CCACCACCAGCACCACCACCACCACCACCACCACCACCAC	JECIGPGVKAV RNNF DS77.1 31 J GOCCCTCCCC GCAAGCCTTC AGTTGCCGAA CATTGAGCCT CAAGTCTGGT GAAGACCTTC GTCAAGCCTC GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTCTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCCT GTAGCT GTA	41 ATGGCTTTAG AGASTCTGGAG CATCCTCGTG CATCAGACCA CAGGACAAGG GCCGCCTGCC ACCAATATGC	51 AGACGATCIG AGACGATCIG ATOTTRACCA CACCAAATGT TCTTGGGGAAT CACTCGCGT CCGGTTGGTT CTGACGAAGG GCTGCCTGT	60 120 180 -240 300 360 420

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	GCTATGGGGG	CACTGAGGAC	CAGCCATTGA	GGGGTGGACC	CTCAGAAGGC	GTCACAACAA	660
	CCTGGTCACA	GGACTCTGCC	TCCTCTTCAA	CTGACCAGCC	TCCATGCTGC	CTCCAGAATG	720
	GTCTTTCTAA	TGTGTGAATC	AGAGCA CAGC CCGACCACCT	AGCCCCTGCA	CAAAGCCCTT		780 840
5		CATTCCACCT	POCCANOCACCT	SCCCHACCIG	AGGCCACTTG	ATCACCCCCA	900
,	ACCAAGTGGC	TOTCACACCC			ACCAGTCCAT		960
	TTTAAGGGTT	TGTGGAAAAT	GAAAATTAGG	ATTTCATGAT	TITTTTTTT	CAGTCCCCGT	1020
	CAACGAGAGC	CCITCATITG	GAGATTATGT	TCTTTCGGGG	AGAGGCTGAG	GACTTAAAAT	1080
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10			TTGTAAAAAT				1200
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	TOCTATORGA	AGTTTCTCAG	CTCCCAAGGC	TCTGACCAAA	TGTGGCTCCT	GGGGGTTCTT	1380
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		CATGACTCGT	ATATGTCTCA	GGTCCCTGCA	GGGCCAAGCA	CCTAGCCTCG	1560
	CTCTTGGCAG	GTACTCAGCG	AATGAATOCT	GTATATGTTG	GGTGCAAAGT	TOCCTACTTC	1620 1680
	CTGTGACTTC	ACCTCTGTTT	TACAATAAAA	TCTTGAAAAT	GCCTAAAAAA	AMMUMMAAA	1680
20	AAAAAAA	AAAAAAAAA	AMOUNAMON	ANNANA			
20	Seq ID NO:	493 Protein	sequence				
	Protein Acc	cession #: 1	P_000568.1				
25	1	11	21	31	41	51	
43	I TOTAL	I CONTROL II	RINDVNQKTF	NA MINISTERIA	VI OCIMIUM P	PRITOWNETED	60
	HALFIGHES	AWG SCAKOU	DETRLQLEAV	NITDLSENDE	ODKREAFIRE	DSCPTTSFRC	120
	AACPONFLCT	AMEADQPVSL	TIMPDEGVMV	TKFYFQEDE			
30	Cam TD NO.	404 TWD 004	w.anga				
50	Nucleic Ac	494 DNA sec Ld Accession	guence 1 #: NM_002	081.1			
		ence: 222.					
	1	11	21	31	41	51	
35	ī	ī	ī	Ĭ	i	i	
	GGCTGCCCGA	GCGAGCGTTC	GGACCTCGCA	cocceoecec	COCGCGCCCCC	coccocccc	60
	CCCTTTTCTT	GTCTCCGCCT	CCTCGGCCGC	OGCCCCCTCT	GGACCGCGAG	COGCGCGCGC	120
		GCTCTGCCCT		GAACTGCGCA		AGGATCCGAG	180
40				COGGCCCCGC		GACCCGGCCA	240
40	GCTGGTGGCT GCAAGAGCCG	GCTATGTGCG	GCCGCAGCGC		AGOCAAGGGC	TTCAGCCTGA	360
	GCGACGTGCC	CCAGGCGGAG	ATCTCGGGTG	ACCACCTGCG	GATCTGTCCC	CAGGGCTACA	420
	CCTGCTGCAC	CAGCGAGATG		TGGCCAACCG	CAGCCATGCC	GAGCTGGAGA	480
	CCGCGCTCCG	GGACAGCAGC		AGGCCATGCT	TGCCACCCAG	CTGCGCAGCT	540
45	TCGATGACCA	CTTCCACCAC	CTGCTGAACG	ACTCGGAGCG	GACGCTGCAG	GCCACCTTCC	600
	CCGGCGCCTT	COGAGAGCTG	TACACGCAGA	ACGCGAGGGC	CTTCCGGGAC	CTGTACTCAG	660
		GTACTACCGC	GGTGCCAACC	TOCACCTOGA	GGAGACCCTG	CTGCCTGATG	720 780
	GGGCCCGCCT ACTACCTCGA	GCTCGAGCGC	CTCTTCAAGC	AGCTGCACCC AGGCGCTGCG	CCAGCTGCTG		840
50	GAGAGCTGGG	CTGCCGGGCC	ACCCGTGCCT	TOSTGGCTGC	TCGCTCCTTT	GTGCAGGGCC	900
50	TGGGGGTGGC	CAGCGAGGTG	GTCCGGAAAG	TGGCTCAGGT	CCCCCTGGGC	CCGGAGTGCT	960
	CGAGAGCTGT	CATGAAGCTG		CTCACTGCCT	GGGAGTCCCC	GGCGCCAGGC	1020
	CCTGCCCTGA	CTATTGCCGA		AGGGCTGCCT	TGCCAACCAG	GCCGACCTGG	1080
55	ACCCCCGACTC	GAGGAACCTC	CTGGACTCCA	TGGTGCTCAT	CACCGACAAG	TTCTGGGGTA	1140
22		GCACAGTGTC	ATCGGCAGGG ACGCTCACGG	CCAAGGTCAT		GCCATCAACC	1200
	CCCTCCAGGA AGGTCAACCC	CAACAGGGAC		AGAAGGGGGG		CTOGCCCCCC	1320
	GGGAGAGGCC	ACCTTCAGGC	ACGCTGGAGA	AGCTGGTCTC	TGAAGCCAAG	GCCCAGCTCC	1380
	GCGACGTCCA		ATCAGCCTCC	CAGGGACACT	GTOCAGTGAG	AAGATGGCCC	1440
60		CAGTGATGAC	COCTGCTGGA	ACGGGATGGC	CAGAGGCCCG	TACCTCCCCG	1500
-	AGGTCATGGG	TGACGGCCTG	GCCAACCAGA	TCAACAACCC	CGAGGTGGAG	GTGGACATCA	1560
	CCAAGCCGGA			TCATGCAGCT	GAAGATCATG	ACCAACCGGC	1620
	TGCGCAGCGC		AACGACGTGG		CGCCAGTGAC	GACGGCAGCG	1680
65	GCTCGGGCAG		TGTCTGGATG		CCGGAAGGTC	AGCAGGAAGA CAGGAAGGAC	1800
0.5	GCTCCAGCTC AGAAGACCTC	GGCTGCCAGC	TTGACCCATG	CCCCGACCTT	CCTCCTGCCC		1860
	TCCTGCCCCT	TACAGTAGCC	AGGCCCCGGT	GGCGGTAACT	GCCCCAAGGC	CCCAGGGACA	1920
	GAGGCCAAGG	ACTGACTTTG	CCAAAAATAC	AACACAGACG	ATATTTAATT	CACCTCAGCC	1980
	TGGAGAGGCC	TGGGGTCGGA	CAGOGAGGGC	CGGCGGCTCT		AGGCGCAGAG	2040
70	GTCCCAGCCC	CAGGCCTGGC	CTCGCCTGCC	TTTCTGCCTT	TTAATTTTGT	ATGAGGTCCT	2100
	CAGGTCAGCT	GOGAGCCAGT	GTGCCCAAAA		TCAGGGACCT	CAGGGGCACC	2160
	TCCGGCTGCC	TAGCCCTCCC	CCCAGCTCCC	TGCACCGCCG	CAGAAGCAGC	CCCTCGAGGC	2220
	CTACAGACCA	GGCCTCAAAG		CCCACCAGCC	CGAGCCTGTG AGCCCTGGCC	CACCCCCCAG	2340
75			GGGCTGTCTG		ATCCAGGGTC	TGGCAGAGCC	2400
, ,	TCTGAGAGA	TOCATGATGC	CCTCCCCTCA	COGCAGGCTG	CAGAGCCCCG		2460
	CTGCGCCCTT	GAGGGGCCCC	AGCGTCTGCA	GGGTGACGCC	TGAGACAGCA	CCACTGCTGA	2520
	GGAGTCTGAG	GACTGTCCTC	CCACAGACCC	TGCAGTGAGG	GGCCCTCCAT	GCGCAGATGA	2580
00	GGGGCCACTG	ACCCACCTGC	GCTTCTGCTG	GAGGAGGGGA	AGCTGGGCCC	AAAGGCCCAG	2640
80	GGAGGCAGCG	TGGGCTCTGC		TGCCCCTCGC		CACAGGGCAG	2700
	GCCTTGCTGG		TGTTGGAGGA		TGAGGAGCAG	TGACACAGGT	2760
	CAGGGCTCAG	TCCTCACCCA ACTGACCCTC	GATCAGGAAC	CAGGGCCTCC	CIGITCACGG		2820
	CCCCGCACTG		TGCCTAGGTC	CCTTCCCCCAC	CCAGCCAGCT	GCACTGCAGG	2940
85	GCACGGGGAC	CTCGATAGTT	AAGGGCTTTT	CCAAACATGC	ATCCATTTAC	TGACACTTCC	3000
55	TGTCCTTGTT	CATCGAGAGC	TGTTCGCTCC	TCCCAGATGG	CTTCGGAGGC	CCGCAGGGCC	3060
	CACCTTGGAC	CCTGGTGACC	TCCTGTCACT	CACTGAGGCC	ATCAGGGCCC	TCCCCCAGGC	3120

5	TOTOGRATOR TOCTGAACCG COCACAGTGG CTGACTTTAG CCCTGCCAGT CAGCACTCCC TCTCTGGAAG	086443 corcettece graagggee actgaceetg acgacgtece atgttttggg georggeog georgeacee aggeageeet caaggteee	CTGCAGOGOG AGGAGGCCGC CCGGTTGCTG ATCAGGAGCC GCTGGGGACT GACGGCCTAG GAGTGGTCAC	AGGAGGACTT TTAGTGCTGC GTCAGGTCCC CCCAACACAG CTGGCACAGT GGGTGGCCCT TGGTCAGGCC	GGAGGGTCTG TTTGCTTTTC CATGGCTTGT GCAGGTCCAC GATGCCGGGC CAGACCCCAC AGTGGCCAAG	OGGGCAGCTG ATCACCOTCC TCTCTGGAAC CCCATAATAA GCCAGGACAG CCTACGCTCA CCTGCTGTGT	3180 3240 3300 3360 3420 3480 3540 3600
10	TCCTTGTATG	AATAAAAGGC 495 Protein	TGGAAACCTA	AA	0104001010		
	Protein Acc	cession #: 1	P_002072.1				
15	1	11	21	31	41	51	
20	ICPOGYTCCT TLQATFPGAF QLLLPDDYLD PLGPECSRAV TDKPWGTSGV RGKLAPRERP RGRYLPEVMG	LCAAAALVAC SEMEENLANR GELYTQNARA CLGKQABALR MKLVYCAHCL EEVIGSVHTW PSGTLEKLVS DGLANQINNP	SHABLETALR FRDLYSELRL PFGEAPRBLR GVPGARPCPD LAEAINALQD EAKAOLRDVO	DSSRVLQAML YYRGANLHLE LRATRAFVAA YCRNVLKGCL NRDTLTAKVI DFWISLPGTL	ATQLESFEDH ETLAEFWARL RSFVQGLGVA ANQADLDAEW QGCGNPKVNP CSEKMALSTA	LERLFKQLHP SDVVRKVAQV RNLLDSMVLI QGPGPEEKRR SDDRCWNGMA	60 120 180 240 300 360 420 480
25	ASDDGSGSGS						
30	Nucleic Ac	496 DNA sec id Accession Lence: 40.10	#: NM_001	650.2			
	1	11	21	31	41	51 Ì	
35	AGGCCCTGGG GGGGTCTGGA TTTGTTCTCC GTCGACATGG	ATGAGAGETG GTAAGTGTGG CTCAAGETTT TCAGCCTGGG TTCTCATCTC TCAGCGGTGG	ACCTTTGTGT CTGGAAAGCA ATCCACCATC CCTTTGCTTT	ACCAGAGAGA GTCACAGCGG AACTGGGGTG GGACTCAGCA	ACATCATGGT AATTTCTGGC GAACAGAAAA TTGCAACCAT	GGCTTTCAAA CATGCTTATT GCCTTTACOG GGTGCAGTGC	60 120 180 240 300 360
40	AGGAAGATCA ATTGGAGCAG ACCATGGTTC TTTCAATTGG TCAATAGCIT	GCATCGCCAA GAATCCTCTA ATGGAAATCT TGTTTACTAT TAGCAATTGG	GTCTGTCTTC TCTGGTCACA TACCGCTGGT CTTTGCCAGC ATTTTCTGTT	TACATOGOAG COTOCCAGTG CATOGTOTOCA TGTGATTOCA GCAATTGGAC	COCAGTOCCT TOGTOGGAGG TOGTTGAGTT AACGGACTGA ATTTATTTGC	GOGGGCCATC CCTGGGAGTC GATAATCACA TGTCACTGGC AATCAATTAT	420 480 540 600 660
45	GAAAACCATT TATGAGTATG AAAGCTGCCC GAGACGGATG	GCATGAATCC GGATATATTG TCTTCTGTCC AGCAAACAAA ACCTGATTCT	GGTTGGGCCC AGATGTTGAA AGGAAGCTAC AAAACCTGGA	ATCATAGGAG TTCAAACGTC ATGGAGGTCG GTGGTGCATG	CTGTCCTCGC GTTTTAAAGA AGGACAACAG TGATTGACGT	TGGTGGCCTT AGCCTTCAGC GAGTCAGGTA TGACCGGGGA	720 780 840 900 960
50	GGCACTGAAA GAAACAGATT GTCTAAACAA TCCAAATCTA	AGGGGAAAGA GCAGACAAGA TGTTATAAAT TAAATATTTC AAAAAAGAAA	CTCCTTAGAA TAGAAATGTG ATAATTTACA TATTTTTAAG	CTGTCCTCAG CAGGTTTGTT AAGGAGGAAC ATGTTCTTAA	ATTTCCTTCC GTTTCATGTC GGAAGAAACC GCAAATATAT	ACCCATTANG ATATTACTCA TATTGTGAAT ACCTATTTTA	1020 1080 1140 1200 1260 1320
55	CCTGACAGAA	TTTCATTAAC CTCAAAGACA TATTTGAATA	CGTCTATCAG	CTTATTCCTT	CTCTACTGGA	ATATTGGTAT	1380
60		497 Protein					
	1	11	21	31	41	51	
65	GTEKPLPVDM AQCLGAIIGA KRTDVTGSIA AVLAGGLYEY	GKCGPLCTRE VLISLCFGLS GILYLVTPPS LAIGFSVAIG VPCPDVEPKR KGKDQSGEVL	IATMVQCPGH VVGGLGVTMV HLFAINYTGA RFKBAFSKAA	ISGGHINPAV HGNLTAGHGL SMNPARSFGP	TVAMVCTRKI LVBLIITFQL AVIMGNWENH	SIAKSVPYIA VFTIFASCDS WIYNVGPIIG	60 120 180 240 300
70	Nucleic Ac	498 DNA sec ld Accession Lence: 11	#: AB0206	584.1			
75	1	11	21	31	41	51	
	TTOGTACCOGG GACGGTTACC	ATTATACAT ATTATACCA AGAGGAGAAG TATGTTGCTG	AAATAATGGA GACTCAGTCC	CTTGATTGGT	TGTGAAGGAT	AGATATGTTG	60 120 180 240
80	CATATATGGC CTTTTTCAAT	ACATATTTAA CATGGAGAGT TTTCTTGTTC GGAAGCTTGA	GTGGCAGCCG GTACCCGTGT TTYAGATGTT	ATTAGGAGGC AATGTGGACA GCTAGTGACT	CTGGTTACAG CCACCTCTCC CATATTCTCA	TGTTGTGCTT GTGAAAGCTT GGGCTACAAA	300 360 420 480
85	GCAGTTTGCT CGGGTACATT ACTTGTTTT	CAGTTTGTAC GATATATGTA GTTTGATGT ATTTGGGGTA	TTCTTACTCA AATTACGGAA TTGGGAACTC	GATTGCATCA GATCATTTAT AATGTTATTA	TTATTTGCAG ATACACATGA ACTTCTTATT	TATATGTTGT TTTCTCTTGC ATGCTTCTTC	540 600 660 720

	1110.00	mnc 4 4 2					
	WO 02/	/086443 TTATGGGTTA		-	mamaan nama	mores owns	780
		TTATGGGTIA					840
	ATCAAAATTC	TTTAGTTATA	AGGATTTTGA	TACTTTATTG	TATACCTGTG	CAGCGGAGTT	900
5	TGACTTTATG	GANAANAGAGA	CTCCACTGAG	ATACACAAAG	ACATTATTGC	TTCCAGTTGT	960
3	TCTTGTAGTG	TTTGTTGCTA ACACATGTAA	CANACACCA	GATTATTAGT	GATATGTGGG	TTTACCATGC	1020
		TTAGCATATA					1140
	GACACCACAC	ATGTGTGTTA	TGGCATCACT	GATCTGCTCA	ACACAGCTAT	TTGGATGGCT	1200
10	CTTTTGCAAA	GTACATCCTG AATCTGCAAA	GTGCTATTGT	GTTTGCTATA	TTAGCAGCAA	TGTCAATACA	1260 1320
10		ATAGAATGGA					1380
	CATGOCCAGG	ATGGCAAGTG	TTAAGCTCTC	TGCACTTCGG	CCCATTGTGA	ATCATCCACA	1440
		GCAGGCTTGA					1500 1560
15	AGCAGCCGAA	GAAGTGAAGC TGTGTAAGAA	CAGAACTGAT	MAAGTTAAAA	GIGAACTATT	ACATTCTAGA	1620
13	AGAAGATCCT	GCCAATGCTG	GGAAAACTCC	CTTATGTAAC	CTCTTGGTGA	AGGATTCCAA	1680
	ACCTCACTTC	ACCACTGTAT	TCCAGAACAG	TGTTTACAAA	GTCCTAGAAG	TTGTAAAAGA	1740
	ATGACTGCTA	CATGACCTGC	TGCCTACGGA	GAACTACATC	TGTAATGGTT	TTAATGTTTT	1800 1860
20	GCTARGTCAT	GTGTTGTTCA TTGGTCAATT	TGAATGTCAT	TCTAATTATAG	AAAATGACTT	ACACCTTTAT	1920
20	CAATTGGTTA	CTATTTCAAT	GCACCCTTTA	AAATTTGCTA	TGCAAATCAG	TATATGCTTG	1980
	TACTTGACTT	TAATATTTGT	GCTAAAGTGA	GCAAAGCTAC	CTGTATAAAG	AAAACACAGT	2040
		AAGGATGACA GAACTATTAA					2100
25	TOGACATTTC	AGTGATTGTA	AGTTOTTOGG	TCATGTCAGC	COCTGTCATC	AACTTGAGTT	2220
	ACAGTAGATG	GGGCAGACAT	GGAGTGTTTG	CTATATAAAA	CTATCTGTTT	GTTTTACTTC	2280
	CTTGTGCGCT	TTTTGTTCTC	TGTTCTCTTG	TTAATGAAGC	TTTTCCTGCC	CATTATTAAT	2340
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30		GTTTACTCAT		ATCAAGTACT	TATTCTTGGT	TTTAAAAAAA	2520
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	CTTTAAACCA	CTTTAAAGTT ATATAGTGCA	TTTTCATGTT	TAATTATAGT	TTTAAGAAAA	ACTATTTGA	2640
	TOGARCAGTA	GACTGTAGTA	CATGGTAATT	TTTCTTTTAC	TATTAAGATA	CAATAAAACA	2760
35	TGACTAATTT	TGCTGTCAAA	AATGTAAAGA	ATAATGATAA	ATGGAGTTTT	TTATATTTTA	2620
	CTTTTAAGAT	TGCCTGTCTT	TAATAAGACA	AAGCCTTAAG	CCTTATGTTA	TAATTTTGGT	2880
	TCTAAAAACC	ATCATTTCAG TTATTTTTAT	TATAAGGAAT	TTCTACACCT	CGTCCTCCTC	TTTAGTTTTT	3000
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40	ATAGCTCTGA	GAAAAGGTTT	TAGGGTTTTA	AATTCTAAGC	AAAGOGTGAC	TATGGCTGAC	3120
	AGACTACACA	TTTAATTATA	CAGCTTCTCT	TTCTTAACCA	CAGGCAGATT	AACCTCATTG	3180 3240
	GCTGTTCCCT	TTCAGACCTT	TTACCAGAGC	CAIGGITICE	GOTTGGCCACT	GGGGAAGCAG	3300
	CAGCTTGCTG	ACATAAGTCA	GCTGCAAAGG	CTGAGGAGTG	TGCCCTCAGA	GAAGCACCGC	3360
45	CCCCCAGTCT	TGTGCCAGCG	CCTAGAGCCG	CAGCTCCCAG	GGATGCTCCT	TCCCTGGAGG	3420
		GAGGGACTCT GTTTTTATTT	GGCAGCGTTC	TTCAGATTTG	TGGCCACTGT	GAAGCAGCCC	3480 3540
	TTGATTTGTG	GATTAAAAGC	AACATTTGAG	CGATGATGCA	CAACAGTCCA	GGAAAATGGG	3600
	CGGTGGACAC	TTGAGGCTGA	GGATGGGAGT	TGACATGAGC	AGGGAGAGGG	AGGTGCGCGC	3660
50	TGCTTATCTG	TGATTGTTGC ATTATACTTT	TCACCTGAGT	GTGGCTGATT	GTGTACATCC	AGCAGTTACA	3720
	TCCAAAGAAG	TTCACATGTA	ATABGTAGAA	ATTCTGTATA	GGAAAAAAGC	ATTAAAAATA	3840
	CTATTATAAC	TGCTTCATTT	GCTGGGAACC	ATTAAAAGTA	ATATAAATTA	GCTTTTTCCA	3900
55	GAAGGATCCT	TTTGTAGCAG	TGTTTATGAA	TGTAACCCCC	AGCAAAATAT	GGCTATATAT	3960
33	TAGGGGAGCC	AGTTTGGAGC AGCACTGTGG	AGAGGCCTGA	AGGTCCCTGC	CAATGCAGCCG	TOGCCACAGC	4020 4080
	TTCCATAGGC	GTACAAAACA	GTATTAAAGC	TCAGTGTTTT	GCATATTGTT	AGCATTTACA	4140
	AATATTTTTG	CTTTAGTATG	AGGAAAGTAA	GGATGGGCAA	AGAAGCGATC	AAAATAGCTA	4200
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00	GRANGETT	ATCAGGAATA	ATATAGIGIT	GCATAGGAGT	ACTGATATTA	TATGAATTTT	4380
	ATGCCAGTTG	TTTACATGTA	CTATATATGT	TAAATTAAAA	AAAATCATGA	GAAATG	
65	Seq ID NO:	499 Protein cession #: 1	sequence				
05	FIOCEIN AC	cession #	MA /4300.1				
	1	11	21	31	41	51	
	DE LITTURE UND	NLYPEVILAS	Man Therestee	LIGIOMYTON	memorat en	TROCKET COD	60
70	ACTYVAVITI	LNGLMMALFF	TYGTYLEGER	LGGIATVICE	PENHGECTRY	MUTPPLRESE	120
	SYPFLVLQUL	LVTHILRATK	LYRGSLIALC	ISNVFFMLPW	QFAQFVLLTQ	IASLFAVYVV	180
	GYIDICKLRK	IIYIHMISLA	LCFVLMFGNS	MLLTSYYASS	LVIIWGILAM	KPHFLKINVS	240 300
	BENESCHEDI B	PWLFGTVILK YTKTLLLPVV	INVENTION	TTOTANGUTA	KEPSYKDED	PDMOPTAVIIA	360
75	LOLLAYTALG	ILIMRLKLFL	TPHMCVNASL	ICSRQLFGWL	FCKVHPGAIV	FAILAAMSIQ	420
	GSANLOTOWN	IVGRESNLPO	RELIEWIKYS	TKPDAVFAGA	MPTMASVKLS	ALRPIVNHPH	480
		KIVYSMYSRK			BSWCVRRSKP	GCSMBEIMDA	540
			_	ALKADRAAKD			
80	Seq ID NO:	500 DNA sec	quence				
	Nucleic Ac	id Accession Lence: 127.	1 #: NM_001	276.1			
	marinh sedi	wence: 127.	/0				
85	1	11	21	31	41	51	
03	AGTOGAGTOO	GACAGGTATA	TAAAGGAAGT	ACAGGGCCTVI	GGGAAGAGGG	CCTGTCTWGG	60
		CAGGAGCCGT					120

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		GTGTGAAGGC	GTCTCAAACA	GGCTTTGTGG	TCCTGGTGCT	CCTCCAGTGC	180
	TGCTCTGCAT	ACAAACTGGT	CTGCTACTAC	ACCAGCTOGT	CCCAGTACCG	GGAAGGCGAT	240
	GCCAATATAA	TCCCAGATGC GCAACGATCA	CATCGACACC	TOGGAGTOGA	ATGATGTGAC	GCTCTACGGC	300 360
5	ATGCTCAACA	CACTCAAGAA	CAGGAACCCC	AACCTGAAGA	CTCTCTTGTC	TGTCGGAGGA	420
	TOGAACTTTG	GGTCTCAAAG CAGTACCGCC	ATTTTCCAAG	ACCCATGGCT	PERMIT	GGACCTTGCC	480 540
	TGGCTCTACC	CTGGACGGAG	AGACAAACAG	CATTITACCA	CCCTAATCAA	GGAAATGAAG	600
10	GCCGAATTTA	TAAAGGAAGC AGGTCACCAT	CCAGCCAGGG	AAAAAGCAGC	TCCTGCTCAG	CGCAGCACTG	660 720
10	CATTTCATTA	GCATCATGAC	CTACGATTTT	CATGGAGCCT	GGCGTGGGAC	CACAGGCCAT	780
	CACAGTCCCC	TGTTCCGAGG	TCAGGAGGAT	GCAAGTCCTG	ACAGATTCAG	CAACACTGAC	900
	CCC2/CCPTCC	GCTACATGTT	CACTUTACUT	TOTTOTGAGA	CTGGTGTTGG	AGCCCCCAATC	960
15	TCAGGACCGG	GAATTCCAGG	CCGGTTCACC	AAGGAGGCAG	GGACCCTTGC	CTACTATGAG	1020
	ATCTGTGACT	TCCTCCGCGG GCAACCAGTG	AGCCACAGTC	CATAGAACCC	TOGGCCAGCA	ALCCARGOTG	1080
	CAGTACCTGA	AGGATAGGCA	GCTGGCAGGC	GCCATGGTAT	GGGCCCTGGA	CCTGGATGAC	1200
20	TTCCAGGGCT	CCTTCTGCGG	CCAGGATCTG	CGCTTCCCTC	TCACCAATGC	CATCAAGGAT	1260 1320
20	CCCCCTCTGG	CTCCAGCTGG	COGGGAGOCT	GATCACCTGC	CCTGCTGAGT	CCCAGGCTGA	1380
	GCCTCAGTCT	COCTOOCTIG	GGGCCTATGC	AGAGGTCCAC	AACACACAGA	TTTGAGCTCA	1440
	GCCCTGGTGG	TAGTACACAC	TTGTTGATGA	TTAATGGAAA	AGTGAGGCAT TGTTTACAGA	TOCCCAAGCC	1560
25	TGGCAAGGGA	ATTTCTTCAA	CTCCCTGCCC	CCTAGCCCTC	CTTATCAAAG	GACACCATTT	1620
	TGGCAAGCTC	TATCACCAAG	GAGCCAAACA	TCCTACAAGA	CACAGTGACC	ATACTAATTA	1680 1740
	ACTTCCCCTT	CCTAATTCCA	CAGCTGCTCA	ATAAAGTACA	AGAGTTTAAC	AGTGTGTTGG	1800
30	CGCTTTGCTT	TOCTTCCTCT	TIGAGCCCCC	ACTAGACCCA	CTGGACTCAC	CICCCCCATC	1860
30	ATGTT	rocrector	GAGCCTTGGG	MCCCCTGMGC	TIGCHGHGHI	GANOSCUGUU	1920
	Can TD NO.	501 Protein					
0.5	Protein Ac	ession #: 1	P_001267.1				
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	i	Ī	1	i	i	ì	
		AATATTÖGGS					120
40	KSVPPFLRTH	NNDVTLYGML GFDGLDLAWL	VPGRRDKOHF	TTLIKENKAR	FIKEAOPGKK	OLLLSAALSA	180
	GKVTIDSSYD	IAKISQHLDF	ISIMTYDFHG	AWRGTTGHHS	PLFRGQEDAS	PDRFSNTDYA	240
	VGYMLRLGAP	ASKLVMGIPT TLGOOVPYAT	FGRSFTLASS	DEGUVERY	PGIPGRPTKE	AGTLAYYEIC	300 360
		PLINAIKDAL		QUOVINORI QI	DIGUIDIO I	***************************************	300
45							
	Nucleic Ac:	502 DNA sec Ld Accession	#: NM 006	474.1			
	Nucleic Ac:		#: NM 006	474.1			
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50	Nucleic Act Coding sequ	ld Accession pence: 181.	1 #: NM_006 .669	31 	1	ì	50
50	Nucleic Ac: Coding sequ 1 GCTGCCTAGG	Id Accession pence: 181. 11 GTCTGGAAAG CCACCGTCGC	#: NM_006	31 CTCCCTCTCC GCTGGGCCTG	GGGGCTCCTG TGGCCGCGGT	CTCCCACCCC GCTTTTAATT	60 120
	Nucleic Ac: Coding sequ 1 GCTGCCTAGG TCCGGCCCCC	Id Accession pence: 181. 11 GTCTOGAAAG CCACCOTCGC TCAGAATCTT	1 #: NM_006 .669 21 CTCGGGCACC GCTCCTCCAG GCTGCTCGGC	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA	GGGGCTCCTG TGGCCGCGGT GCAACAACTC	CTCCCACCCC GCTTTTAATT AACGGGAACG	120 180
50 55	Nucleic According sequents GCTGCCTAGG TCCGCCCCCCCTTCCCCCAGC	Id Accession ience: 181. 11 GTCTOGAAAG CCACCGTCGC TCAGAATCTT TGTCAGCTCT	#: NM_006 .669 21 CTCGGGCACC GCTCCTCCAG GCTGCTCGGC	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA TTGGGAAGCG	GGGGCTCCTG TGGCCGCGGT GCAACAACTC CGTCGCTCTG	CTCCCACCCC GCTTTTAATT AACGGGAACG GGTCCTGGCA	120
	Nucleic Act Coding sequ Coding	Id Accession nence: 181. 11 GTCTGGAAAG CCACCGTCGC TCAGAATCTT TGTCAGCTCT GCACAGGCCA GCACGGCCA CAGGTGCCGA	#: NM_006 .669 21 CTCGGGCACC GCTCCTCCAG GCTGCTCGGC GCTGCTCGGC GCTGCTGGCT GCCAGAAGAT AGATGATGTG	31 - CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA TTGGGAAGC GACACTGAGA GTGACTCCAG	GGGGCTCCTG TGGCCGCGGT GCAACAACTC CGTCGCTCTG CTACAGGTTT GAACCAGCGA	CTCCCACCC GCTTTTAATT AACGGGAACG GGTCCTGGCA GGAAGGCGGC AGACCGCTAT	120 180 240 300 360
	Nucleic Act Coding sequence Coding sequence C	Id Accession ience: 181. II GTCTOGAAAG CCACCGTCGC TCAGAATCTT TGTCAGCTCT GCACAGGCCA CACAGGCCA TGACAGCTCA TGACAACTCT	#: NM_006 .669 21 CTCGGGCACC GCTCTCCCAG GCTGCTCGGC GCTGCTCGGT GCCAGAAGAT GCCAGAAGAT GGTGGCAACA	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA TTGGGAAGCG GACACTGAGA GTGACTCCAGA AGTGTCAACA	GGGGCTCCTG TGGCCGCGGT GCAACAACTC CGTCGCTCTG CTACAGGTTT GAACCAGCGA GTGTAACAGG	CTCCCACCC GCTTTAATT AACGGGAACG GGTCCTGGCA GGAAGGCGGC AGACCGCTAT CATTCGCATC	120 180 240 300 360 420
	Nucleic According sequences of the control of the c	Id Accession Lence: 181. II GTCTGGAAAG CCACCGTCGC TCAGAATCTT TGTCAGCTCT CGCACGGCCA CAGGTGCCGA TGACAACTCT CAACTTCTTCAGA TGCCACACCAC TGACAACTCT CAACTTCCAGA	1#: NM_006 669 21	31 CTCCCTCTCC GCTGGGCCTG CCCAGGAGA TTGGGAAGC GACACTGAGA GTGACTCCAG ASTGTCAACA CACGCGCAAG GRGAAAGTGG	GGGGCTCCTG TGGCCGCGGT GCACACACTC CGTCGCTCTG CTACAGGTTT GAACCAGGGA GTGTAACAG AACAAGTCC ATGGAGGACAC	CTCCCACCCC GCTTTTAATT AACGGGAACG GGTCCTGGCA GGAAGGCGCC AGACCGCTAT CATTCGCATC AAGCGCCACA ACGCCACAACA	120 180 240 300 360 420 480 540
55	Nucleic According sequences of the control of the c	Id Accession Lence: 181. II GTCTGGAAAG CCACCGTCGC TCAGAATCTT TGTCAGGTCT GCACAGGCCA CAGGTGCCA TGACAACTCT CAACTTCAGA TGGCAACACT TGACAACTCT CAACTTCAGA	1#: NM_006 669 21 CTCGGGCACC GCTCCTCCAG GCTGCTCGGC GCTCTTCGTT GCCAGAAGAT AGATGATOTG GGTGGCAACA AAGCACACTC TCACTCCACG	31 CTCCCTTCCC GCTGGGCCTG CCCCAGGAGA TTGGGAAGCG GACACTGAGA GTGACTCCA AGTGTCAACA CACGGCAAG GAGAACTG	GGGGCTCCTG TGGCCGCGGT GCAACAACTC CCTCGCTCTG CTACAGGTTT GAACCAGGGA GTGTAACAGG AACAAAGTCA ATGGAGACAC TCATAGTTGG	CTCCCACCCC GCTTTAATT AACGGGAACG GGTCCTGGCA GGAAGGCGGC AGACCGCTAT CATTCGCATC AAGCGCCACA AGACAACA GGTCTTACTA	120 160 240 300 360 420 480 540 600
55	Nucleic Act Coding sequing and act processed and act act act act act act act act act act	id Accession ence: 181. 11	#: NM_006 669 21	31 CTCCCTCTCC GCTCGGCCTG CCCAGGAGA TTGGGAGCG GACACTGAGA GTGTCAACA CACGGCGAG CACGGCGAG GAGAAACTGG CTGGTTGGAA GTGGTTGATATSC	GOOGCTCCTG GCACAACTC CCTCGCTCTG CTACAGGTTT CTACAGGTTTA AACCAGCGA AACAAGTCC ATGGAGACAC CATAGTTGG GAAAATGTCC	CTGCCACCC GCTTTAATT AACGGGAACG GGTCCTGGCA GGAAGGCGGC AGACCGCTAT CATTCGCATC AAGCGCCACA ACAGACAACA GGTCTTACTA GGGAAGGTAC	120 180 240 300 360 420 480 540
55	Nucleic Act Coding sequence Coding sequence	Ld Accession Lence: 181. 11 11 GTCTOGAAAG CCACCOTCGC CCACCTCGC CCACGTGCCCA CAGGTGCCCA CAGGTGCCCA CAGGTGCCCA CAGGTGCCCA CAGGTGCCCA CAGGTGCCCA CAGGTGCCGA TGGCCACCAG TGGCGCGCGGAGGG GAGGTGGAGGG GAGGTGGAGGG GAGGTGGAGGG GTGGCCCTGT	#: NM_006 669 21 CTCGGGCACC GCTCCTCGG GCTCCTCGG GCTCTTCGGT GCCAGAAGAT AGATGATGT GGTGGCAACA AGATGATGT TCACTCCACC AACAGTGACC AACAGTGACC CCCTGAGGTCC CCCTGAGGTCC CCCTGAGGTCC CCCTGAGGTC	31 CTCCCTCTCC GCTGGGCCTG GCCCAGGAGA TTGGGAAGCG GACACTGAGA GTGACTCCAG CAGGCAAG GAGAAACTGG CTGGTTGGAA GTGGTTATGG GCTTGCCAAC	GGGGCTCCTG GGACACACTC GCTGGCTCTG CTACAGGTTT CAACAGGTT CAACAGGAAAATCC CATCATAGTTGG GAAAAATTCC GAAAATTCC GTGCTTTAAA GATGACCCTG	CTCCCACCC CCTCTTAATT AACGGAACG GGTCCTGCA GGACGGCGC AGACCGCTAT CATTCGCATC AAGGCAACA ACGACAACA GGTCTTACTA GGGAAGGTTAC AAAAGACCGT GGAACATTTG	120 180 240 300 360 420 480 540 600 660 720 780
55	Nucleic Act Coding sequence of the Coding seq	id Accession Lence: 181. 11 GTCTOGAAAG CCACCOTCGC TCAGAATCTT TGTCAGCTCT GCACAGCCCA TGACAACTCT CAACTTCAGA TGGCCACCAGA TGGCCACAGA ATGGTTTGTC ATTGGTGG ATGGTTTGTC CACTTGGTAGA TGACAACTCT CAATTGGTAGA ATGGTTTGTC	#: NM_006 669 NM_006 669 CTCTCTCAG GCTGCTCCAG GCTGCTCGGC GCTGTTCGTT GCCAGAAGAT AGATGATGT GTGACCAACACT TCACTCCACG AACAGTGACC GTTACGCCC CCCTGAGCTC CCTTGAGCTT	31 CTCCCTCTCC GCTGGGCCTG GCCCAGGAGA TTGGGAAGCG GACACTGAGA GTGACTCCAG CAGGCAAG GAGAAACTGG CTGGTTGGAA GTGGTTATGG GCTTGCCAAC	GGGGCTCCTG GGACACACTC GCTGGCTCTG CTACAGGTTT CAACAGGTT CAACAGGAAAATCC CATCATAGTTGG GAAAAATTCC GAAAATTCC GTGCTTTAAA GATGACCCTG	CTCCCACCC CCTCTTAATT AACGGAACG GGTCCTGCA GGACGGCGC AGACCGCTAT CATTCGCATC AAGGCAACA ACGACAACA GGTCTTACTA GGGAAGGTTAC AAAAGACCGT GGAACATTTG	120 180 240 300 360 420 480 540 600 660 720
55	Nucleic Ac Coding seq 1 GCTGCCTAGG TCCGCCCCC TTCCCCAGG ATGTGGAAGG GAAGGACCCA GCTCTAACG GCCTCTAACG GCCTCTAACG TTCGCCTAA GCCATGGCT TCGCCCTAA TCCGCCCTAA	dd Accession Lence: 181. 11 GTCTOGRAAG CCACCOTCGC TCAGAGTCTT TOTCAGCTCT GCACAGCCCA CAGGTCCGA TGGCCACACTC CACCTCAGA TTGGCCACCA ATGGTTTGCA ATGGTTGTG GAGCTGAAG GTGGCCACT CAGTTGAGA TCATTGGTG CAGTTGAGA TCATTGGTG CAGTTGACA TGGTTGATA TGGTTGTC TCATTGGTAG TGAGTTTCATA TGGTTCTATAGTTCATC TGGTTCTTAA	##: NM_006 669 NM_006 21 CTCGGGGACC GCTGCTCAG GCTGCTCAG GCTGCTCAG GCTGTCAGC GCTGAGACAA AGATGATOTG TCACTCCAC AACACAGT GTTACGCCT GCTTACGCCT GCTTACGCCT ACTTTC ACTTTC ACTTTC ACTTTC ACTTTC ACTTTC ACTTTC ACTTTC ACTTTC ACTTTC	31 CTCCCTCTCC GCTGGGCCTG GCCCAGGAGA TTGGGAAGCG GACACTGAGA GTGACTCCAG CAGGCAAG GAGAAACTGG CTGGTTGGAA GTGGTTATGG GCTTGCCAAC	GGGGCTCCTG GGACACACTC GCTGGCTCTG CTACAGGTTT CAACAGGTT CAACAGGAAAATCC CATCATAGTTGG GAAAAATTCC GAAAATTCC GTGCTTTAAA GATGACCCTG	CTCCCACCC CCTCTTAATT AACGGAACG GGTCCTGCA GGACGGCGC AGACCGCTAT CATTCGCATC AAGGCAACA ACGACAACA GGTCTTACTA GGGAAGGTTAC AAAAGACCGT GGAACATTTG	120 180 240 300 360 420 480 540 600 660 720 780
55 60 65	Nucleic Act Coding sequence of the coding sequence of the codecec	Ld Accession Lence: 181. 11 TCTGGAAAG CCACCOTCGC TCAGAATCTT TOTCAGCTCT CCACGTCCCA TGACTCCCA TGACTCCACA TGACTCTCAGA TGGCCACCAG TGACTTCAGA TGGCCACCAG GACGCCTGT CACTTCAGA TGGCCACCAG TGACTTGTC TCATTGGTG GACTGAACT TCATTGGTG TGACTTCATA 503 Protein 503 Protein	#: NM_006 669 21 1 CTCGGGCACC GCTCCTCCAG GCTCTCGTG GCCAGAAGAT AGATGATCGTG GGTGGCAACA AAGCACACACA AACACTCCACC AACAGTGACC CCCTGAGCTC GGTGACTTC ACTTTC	31 CTCCCTCTCC GCTGGGCCTG GCCCAGGAGA TTGGGAAGCG GACACTGAGA GTGACTCCAG CAGGCAAG GAGAAACTGG CTGGTTGGAA GTGGTTATGG GCTTGCCAAC	GGGGCTCCTG GGACACACTC GCTGGCTCTG CTACAGGTTT CAACAGGTT CAACAGGAAAATCC CATCATAGTTGG GAAAAATTCC GAAAATTCC GTGCTTTAAA GATGACCCTG	CTCCCACCC CCTCTTAATT AACGGAACG GGTCCTGCA GGACGGCGC AGACCGCTAT CATTCGCATC AAGGCAACA ACGACAACA GGTCTTACTA GGGAAGGTTAC AAAAGACCGT GGAACATTTG	120 180 240 300 360 420 480 540 600 660 720 780
55	Nucleic Act Coding sequence of the coding sequence of the codecec	Id Accession ence: 181. 11 TOTTIGNAME CCACCITCGE TOTAGATCT TOTAGATCT TOTAGATCT CCACAGCCA TAGCAACTCT CCACAGCCA TAGCAACTCT CCACAGCACA TAGCAACTCT TCATTIGNAGC TCA	#: NN_006 21 CTCGGGCACC CCTCGGGCACC GCTGCTCGGC GCTGCTCGGC GCCAGAGAT AGAGATAGTT AGAGAGAT AGAGAGAT CTTACGCCAC ANCATCGTT GTTACGCCT GCTGACCTTC CCTGAGCTT CACTCCTC ACCTTACGCCT ACCTTACGCCT ACCTTACGCCT ACCTTACGCCT ACCTTACGCCT ACCTTACGCCT ACCTTACGCCT ACCTTACGCTT 1 Sequence #P_006465.1	31 CTCOTCTGC CCCAGGAGA TTGGGAGAGA TTGGGAGAGA GTGACTCAG AGTGTCAACA CACCEGCAGE GAGAAACTGC GTGGTTGGAAC GTGGTTTGCAAC GTGGTTTGCAAC GTGGGGAGAAC GTGGGAACA GTGGGAACA CGTTTGCCAAC	GGGGCTCCTG TGGCCGCGGT TGGCCGCGGT GCAACACTC CTCCACGGTTT GMACCAGCGA AMACAAGTC TCATAGTTGG GMACATGC GMACATGC TCATAGTTGG GMACATGC GTGCTTTAAA GATGACCCTG ATTRACCGAG	CTCCCACCC GCTTTEANT AACGGAACG GGTCCTIGCA GGAAGGCGGC AGACCACA AAGCCCACA AAGCCCACA ACAGACAACA GGTCTTACTA GGAAGGTACA AAAAGACACT GGAACATTG GGAACATTG GAACACTTTG	120 180 240 300 360 420 480 540 600 660 720 780
55 60 65	Nucleic Act Coding sequence of the coding sequence of the codecec	Ld Accession Lence: 181. 11 TCTGGAAAG CCACCOTCGC TCAGAATCTT TOTCAGCTCT CCACGTCCCA TGACTCCCA TGACTCCACA TGACTCTCAGA TGGCCACCAG TGACTTCAGA TGGCCACCAG GACGCCTGT CACTTCAGA TGGCCACCAG TGACTTGTC TCATTGGTG GACTGAACT TCATTGGTG TGACTTCATA 503 Protein 503 Protein	#: NM_006 669 21 1 CTCGGGCACC GCTCCTCCAG GCTCTCGTG GCCAGAAGAT AGATGATCGTG GGTGGCAACA AAGCACACACA AACACTCCACC AACAGTGACC CCCTGAGCTC GGTGACTTC ACTTTC	31 CTCCCTCTCC GCTGGGCCTG GCCCAGGAGA TTGGGAAGCG GACACTGAGA GTGACTCCAG CAGGCAAG GAGAAACTGG CTGGTTGGAA GTGGTTATGG GCTTGCCAAC	GGGGCTCCTG GGACACACTC GCTGGCTCTG CTACAGGTTT CAACAGGTT CAACAGGAAAATCC CATCATAGTTGG GAAAAATTCC GAAAATTCC GTGCTTTAAA GATGACCCTG	CTCCCACCC CCTCTTAATT AACGGAACG GGTCCTGCA GGACGGCGC AGACCGCTAT CATTCGCATC AAGGCAACA ACGACAACA GGTCTTACTA GGGAAGGTTAC AAAAGACCGT GGAACATTTG	120 180 240 300 360 420 480 540 600 660 720 780
55 60 65	Nucleic According sequence of the control of the co	Id Accession Lence: 181. 11 GRITIGAANAG CCACCOTTCGC TOCAGANTCTT TOTCAGANTCT TOTCAGATCT CCACCGCCC CAGGTGCCA TOGCCACCAC CAGGTGCCA TOGCCACCAC ATGGTTTOTC TOGCCACCAC GAGGTGCCA TOGCCACCACCAC TOGCCACCACCAC TOGCCACCACCAC TOGCCACCACCAC TOGCCACCACCAC TOGCCACCACCAC TOGCCACCACCACCAC TOGCCACCACCAC TOGCCACCACCACCAC TOGCCACCACCACCAC TOGCCACCACCACCAC TOGCCACCACCACCAC TOGCCACCACCACCAC TOGCCACCACCACCACCAC TOGCCACCACCACCACCACCAC TOGCCACCACCACCACCACCACCAC TOGCCACCACCACCACCACCACCACCACCACCACCACCACCA	18: NN_006 669 21	31 CTOCOTTOTOC GEOGRAPHICA CONTROL	GGGGCTCCTG TGGCCGCGGT TGGCACAACTC CGTCGCTCTG GCAACAACTC CGTCGCTCTG GAACAACTC GTGTAACAGG ATGTAACAGG AACAAGTCC ATGGAACAC TCATAGTTGG GAAAAATGTC ATGTTTMA GATGACCCTG ATTAACCGAG 41	CTCCCACCC GCTTTAATT ACCGGAATA ACCGGAATA GGAAGGOGC AGACCGCTAT CATTOCCATC ACAGACAACA ACAGACAACA ACAGACAACA ACAGACACACA AAAAGACCCT GAAAGACCTT 51	120 180 240 300 360 420 540 600 720 780 840
55 60 65 70	Nucleic Actording sequence of the control of the co	Id Accession and	in #: NN_006 The	31 CTCCCTTCTCC GCGCGGGGGGGGGGGGGGGGGGGGG	GOGGETCCTG TGGCGGGT GGCACCAACTC CGTCGCTCTG CTRCAGGTTT GAMCCAGCGA GTGTAACAGG AACAAATCC GTGCTACAGG GAAAATGTC GTGCTTAAACGGG ATTAACCGGG ATTAACCGGG 41 VAMEGABDUV VAMEGABDUV VAMEGABDUV	CTCCCACCC GCTTTAATT ACCGGAATA ACCGGAATA GGAAGGOGC AGACCGCTAT CATTOCCATC ACAGACAACA ACAGACAACA ACAGACAACA ACAGACACACA AAAAGACCCT GAAAGACCTT 51	120 180 240 300 360 420 540 600 660 720 780 840
55 60 65	Nucleic According sequence of the control of the co	Id Accession Lence: 181. 11 STYTOGRANG CORROCTOGE TORRANGTOT TOTAGRANGT T	il: NN_006 669 21	31 CTCCCTTCTCC GCGCGGGGGGGGGGGGGGGGGGGGG	GOGGETCCTG TGGCGGGT GGCACCAACTC CGTCGCTCTG CTRCAGGTTT GAMCCAGCGA GTGTAACAGG AACAAATCC GTGCTACAGG GAAAATGTC GTGCTTAAACGGG ATTAACCGGG ATTAACCGGG 41 VAMEGABDUV VAMEGABDUV VAMEGABDUV	CTCCCACCC GCTTTAATT ACCGGAATA ACCGGAATA GGAAGGOGC AGACCGCTAT CATTOCCATC ACAGACAACA ACAGACAACA ACAGACAACA ACAGACACACA AAAAGACCCT GAAAGACCTT 51	120 180 240 300 360 420 540 600 720 780 840
55 60 65 70	Nucleic Actoring segment of the control of the cont	Id Accession Length 181. 111 TITING AND CONCOMENT 181. TITING AND CONCOMENT 181. TITING ACTIC CONCOMENT 181. TITING ACTIC CONCOMENT 181. CONCOMENT 1	18: NN_006 669 21 1	31 CTCOCTETEC CCCCCCCCCCCCCCCCCCCCCCCCCCCC	GOGGETCCTG TGGCGGGT GGCACCAACTC CGTCGCTCTG CTRCAGGTTT GAMCCAGCGA GTGTAACAGG AACAAATCC GTGCTACAGG GAAAATGTC GTGCTTAAACGGG ATTAACCGGG ATTAACCGGG 41 VAMEGABDUV VAMEGABDUV VAMEGABDUV	CTCCCACCC GCTTTAATT ACCGGAATA ACCGGAATA GGAAGGOGC AGACCGCTAT CATTOCCATC ACAGACAACA ACAGACAACA ACAGACAACA ACAGACACACA AAAAGACCCT GAAAGACCTT 51	120 180 240 300 360 420 540 600 720 780 840
55 60 65 70 75	Nucleic Act Coding seg 1 1 CTOCTTAGG CTOCTTAGG CTOCTTAGG CTOCTTAGG CTOCTTAGG CTOCTTAGG CAGAGCCA GTTOCCATCA AAGTCTGGAGCA AAGTCTGGAGCA AAGTCTGGAGCA CTOCTGGAGCA CTOCTGGAGCA CTOCTGGAGCA CTOCTGAGCA CTOCTGGAGCA STCTCAGCAGCT 1 MINUSALLEV RSGLITLVAT VEROGLSTUT Seq ID NO: Seq ID	II	18: NN_006 669 21 CTCGGGGCACC GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCAG GCTCCAG ATCATCGT CCCTAGCCCC GCTAGCCTC GCTAGCTCC GCTAGCT GCTAGCT GCTAG	31 CTCOCTETEC CCCCCCCCCCCCCCCCCCCCCCCCCCCC	GOGGETCCTG TGGCGGGT GGCACCAACTC CGTCGCTCTG CTRCAGGTTT GAMCCAGCGA GTGTAACAGG AACAAATCC GTGCTACAGG GAAAATGTC GTGCTTAAACGGG ATTAACCGGG ATTAACCGGG 41 VAMEGABDUV VAMEGABDUV VAMEGABDUV	CTCCCACCC GCTTTAATT ACCGGAATA ACCGGAATA GGAAGGOGC AGACCGCTAT CATTOCCATC ACAGACAACA ACAGACAACA ACAGACAACA ACAGACACACA AAAAGACCCT GAAAGACCTT 51	120 180 240 300 360 420 540 600 720 780 840
55 60 65 70	Nucleic Act Coding seg 1 1 CTOCTTAGG CTOCTTAGG CTOCTTAGG CTOCTTAGG CTOCTTAGG CTOCTTAGG CAGAGCCA GTTOCCATCA AAGTCTGGAGCA AAGTCTGGAGCA AAGTCTGGAGCA CTOCTGGAGCA CTOCTGGAGCA CTOCTGGAGCA CTOCTGAGCA CTOCTGGAGCA STCTCAGCAGCT 1 MINUSALLEV RSGLITLVAT VEROGLSTUT Seq ID NO: Seq ID	IL Accession Lead Acc	1 8: NN_006 669 21 21 21 CTC0900CACC CTC0900CACC GCTC0TCCAG GCTC0TCCAG GCTC0TCCAG GCTCTCCAG GCTCTCCAG GCTCACACA AACAATCACC GCTCACACA AACAATCACC GCTCACACC GCTC	31 CROOCITICO COCCOSCICIO COCCOSTICIO CO	GOOGCTCCTG GOOGCTCCTG TGGCCGCGT GOCACCACTC CUTCGCCTCTG CUTCGCCTCTG GACCAGCAG GACCAGCAG ACCAGCAG ACCAGCAG ACCAGCAG ACCAGCAG ACCAGCAGCAG ACCAGCAGCAG ACCAGCAGCAG ACCAGCAGCAG ACCAGCAGCAG ACCAGCAGCAGCAG ACCAGCAGCAGCAG ACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	CTCCCACCC CCTTTTATT AACOSGAAC GOTCTTGGCA GOTCCTGGCA GOTCCTGGCA GOTAGCGGCA AACOSCACA AACOSCACA AACOSCACA AACOSCACA GOTAGCTGCACA AACOSCACA GOTCTGCACTA G	120 180 240 300 360 420 540 600 720 780 840
55 60 65 70 75	Nucleic Act Coding seg 1 1 CTOCTTAGG CTOCTTAGG CTOCTTAGG CTOCTTAGG CTOCTTAGG CTOCTTAGG CAGAGCCA GTTOCCATCA AAGTCTGGAGCA AAGTCTGGAGCA AAGTCTGGAGCA CTOCTGGAGCA CTOCTGGAGCA CTOCTGGAGCA CTOCTGAGCA CTOCTGGAGCA STCTCAGCAGCT 1 MINUSALLEV RSGLITLVAT VEROGLSTUT Seq ID NO: Seq ID	II	18: NN_006 669 21 CTCGGGGCACC GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCTCCAG GCTCCAG GCTCCAG ATCATCGT CCCTAGCCCC GCTAGCCTC GCTAGCTCC GCTAGCT GCTAGCT GCTAG	31 CTCOCTETEC CCCCCCCCCCCCCCCCCCCCCCCCCCCC	GOGGETCCTG TGGCGGGT GGCACCAACTC CGTCGCTCTG CTRCAGGTTT GAMCCAGCGA GTGTAACAGG AACAAATCC GTGCTACAGG GAAAATGTC GTGCTTAAACGGG ATTAACCGGG ATTAACCGGG 41 VAMEGABDUV VAMEGABDUV VAMEGABDUV	CTCCCACCC GCTTTAATT ACCGGAATA ACCGGAATA GGAAGGOGC AGACCGCTAT CATTOCCATC ACAGACAACA ACAGACAACA ACAGACAACA ACAGACACACA AAAAGACCCT GAAAGACCTT 51	120 180 240 300 360 420 540 600 720 780 840
55 60 65 70 75	Nucleic Act Coding seq I I I CODING	Id Accessio. 11 11 17 18 17 17 18 17 17 17 18 17 17 17 18 17 17 18 17 18 17 18 18 18 18 18 18 18 18 18 18 18 18 18	1 #: NN_006 669 21 21 21 21 CTCGGGCACAC GCTGCTCCAG GCTGCTCCAG GCTGCTCCAG GCTGCTCCAG GCTGCTCAG GCTGCAAGAT AAGATGATCT TCACTCCAG AACAGTGAC AACAGCACCCC AACAGTGAC AACAGCACCCCC AACAGTGAC AACAGCACCCCC AACAGTGAC AACAGCACCCCC AACAGTGAC AACAGCACCCCC AACAGTGAC AACAGCACCCCC AACAGTGAC AACAGCACCCCC AACAGTGAC AACAGCACCCCC AACAGTGAC AACAGCACCCCC AACAGCACCCCC AACAGCACCCCC AACAGCACCCCC AACAGCACCCCC AACAGCACCCCC AACAGCACCCCCC AACAGCACCCCCC AACAGCACCCCCC AACAGCACCCCCC AACAGCACCCCCC AACAGCACCCCCCC AACAGCACCCCCCC AACAGCACCCCCCC AACAGCACCCCCCCC	31 CTOCCTUTICC GCT003GCT0 CCCCAGGGAA TT00GAAGC0 GCACCTGAG GGAAACT03 CACGGGCAA GGGAAACT03 CTOGTT00AA GTOGTTATAC GCT00GGAAA GTTTGCAA 31 DTETTGLEGG IMQE05F8AT VVMRNMSGRY Quence	GOGGETCCTG GOGGET GOGGET GOGGET GOGACACACTC COTCOCTCTG COTCOCTCTG GOACCACAC ANDROA ANDROATCC ANDROA ANDROATCC GOGGET GOGGET GOGGET ANDROA ANDROATCC GOGGET ANDROA ANDROATCC GOGGET ANDROA ANDROATCC ANDROA ANDROATCC ANDROA	COCCAGOCO COTTETANT ANCOSCANA COCCAGO CONTRACT C	120 180 240 300 420 480 540 600 720 840
55 60 65 70 75 80	Nucleic Act Coding sequ I I GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGTAGE GCTGGGTGGTGGGAGE GCTGGGTGGGAGE GCTGGGGTGGGAGE GCTGGGGTGGGAGE GCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	II decession ence : 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 #: NN_006 669 21 11 CTOGGGCACC GCTCGTCGGC GCTCGTCGGC GCTGTTCGGC GCTGTGGCACA AGCACACT TCACTCCACA AACAGTGACC AACAGTGACC CGTGACTGGC GCTGGCGCACACAC CGTGGCACACAC CGTGGCACACAC AACAGTGACC AACAGTGACC AACAGTGACC CGTGACTTC CGTGACCC CGTGACTTC CGTGACC CGTGACCC CGTGACC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACC CGTGACCC CGTGACCC CGTGACCC CGTGACCC CGTGACC C	31 CTOCCITICCE GTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GOGGCTCACACACACACACACACACACACACACACACACACA	CTOCCAGOCC CCTTTANT ANCOGRAGO COTTTANT ANCOGRAGO COTTCTOCA CAT	120 160 240 300 420 460 520 660 720 6840
55 60 65 70 75	Nucleic Act Coding sequ I I CODING C	Id Accession In Control of the Cont	is: NN_oose 669 21 1 CTCOGGGCACC CTCCTCCAC GCTGCTCCACC GCTGCTCCACC GCTGCTCCACC GCTGCTCCACC GCTGCTCCACC GCTGCTCCACC ACCACC ACCACC ACCACC ACCACC ACCACC	31	GOOGCTCCTO TOGCCDCCCCTO TOGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	COCCAGOCC COTTITATT AAACOSCAAC COCCAGOCC COTTITATT COCCAGOCC COCCA	120 120 120 120 120 120 120 120
55 60 65 70 75 80	Nucleic Act Coding sequ I I CODING C	Id Accession ence: 181. 11 11 9TCTGGAAAG CCACCTTCCC TOCAGATCTC TOCAGCTTCC TAGAATCT TOTAGACTCT CAGATTCAGA TOGACATCT CAGATTCAGA TOGACATCT CAGATTCAGA TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACATCT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGACT TOGAC TOGACT TOGAC TOGACT TOGAC TOGACT TOGAC TOGA	is: NN_oose 669 21 1 CTCOGGGCACC CTCCTCCAC GCTGCTCCACC GCTGCTCCACC GCTGCTCCACC GCTGCTCCACC GCTGCTCCACC GCTGCTCCACC ACCACC ACCACC ACCACC ACCACC ACCACC	31	GOOGCTCCTO TOGCCDCCCCTO TOGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	COCCAGOCC COTTITATT AAACOSCAAC COCCAGOCC COTTITATT COCCAGOCC COCCA	120 240 330 360 420 600 540 660 720 840

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	TGTCTGTGCT GCCCAACTGT TGAAAGATGG	GCTGGATGGA GGATTTGGAA GATGCCTATT	AAACTGGCAT GCTACAACCC	TATTGATTAT	GGAATCCGTC	TCAATAGGAG GCGTCTTTAC	360 420 480
5	TGACCTTGAA TGACCTTGAA TGATGTCCAT TACAGGAAAT	CARATTETA CACATTAGAC GATGACCCAG GGCTTTGTGG GTCATGACCT	TCAAGTATGG GTTGCTTGGC GAAGATACTG TGAAGTTTCT	TCAGCGTATT TGATTATGTT TGGAGATGAG AAGTGATGCT	CACCTGAGTT GAAATATATG CTTCCAGATG TCAGTGACAG	TTTTAGATTT ACAGTTACGA ACATCATCAG CTGGAGGTTT	540 600 660 720 780
10	TACTACTTCT AAAAAAGGA CTCACTGTTA TAGGGAAAAT	TATGTTGCAA ACTOGAAATA TGATCAAAAC TTATTAACAT TGGAAAATAT	AAAACTTTTT ACACAGTGTT TTATTTATTA AGGAAACTTT	AGCTGGAAGA TATGTTGGAA TTTTTCTAAA AAACGAGAAA	TTTAGCCACT TCTTTTGGAA TGTGAAAGCA ATGAAACCTC	TATAAAAAA CTCCTTTGAT ATACATAATT TCATAATCCC	940 900 960 1020 1080
15	TTTGTGGTAT TCTATGTACA TCATTGATTA TGTTTTATGC	AATAACAAGC ATGTATATAT GTTTTGTATT TTCTACAAAA ATTATTTAAG TAAATATCCT	GTACCTATAT ATACTTTTTA ACATGATTTT CCTGTCTCTA	GTATTTGCAT AATCTTGAAC AAACAGCTGT TTGTTGGAAT	TTGAAATTTT TTTATAAACA AAAATATTCT TTCAGGTCAT	GGAATCCTGC TTTTCTGAAA ATGATATGAA	1140 1200 1260 1320 1380
20	Seq ID NO: Protein Ace	505 Protein dession #: 1	n sequence Sos sequence				
25	EGGHLATYKO	11 - LWEDTQGWGF LEARKIGPH HAKBCGGVFT DYVEIYDSYD	VCAAGWMAKG DPKQIFKSPG	RVGYPIVKPG FPNBYEDNQI	PNCGFGKTGI CYWHIRLKYG	IDYGIRLNRS QRIHLSFLDF	60 120 180 240
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35	Nucleic Ac Coding sequ	id Accession	n #: №M_007 902				
	GAATTOGCAC	11 TGCTCTGAGA	21 ATTTGTGAGC	31 AGCCCCTAAC	41 AGGCTGTTAC ATGGGAAGAC	TTCACTACAA	60 120
40	ACCACAGAGA GTGAATTTGA GATTTCATGT	GATCATCTTA GGATGGAATT AGCACGGTCT AGGCGGCCAT CTGTGCTGCT	GGCAAATACA CTCGCAACTT GGATGGATGG	AGCTCACCTA ACAAGCAGCT CTAAGGGCAG	TGAACGAGCA CGCACAAGCT AGAGGCAGCC AGTTGGATAC	GCCGGTGTGT AAGGCGGTGT AGAAAAATTG CCCATTGTGA	180 240 300 360 420
45	ATAGGAGTGA TCTTTACAGA ACCAAATCTG TAGATTTTGA	CAACTGATGA AAGATGGGAT TCCAAAGCGA CTACTGGCAC CCTTGAAGAT TGTCCATGGC	ATTTTTAAAT ATTAGACTCA GACCCAGGTT	ACARCCACA CTCCAGGCTT AGTATGGTCA GCTTGGCTGA	CCCAAATGAG GCGTATTCAC TTATGTTGAA	TGTGGTGGCG TACGAAGATA CTGAGTTTTT ATATATGACA	420 480 540 600 660 720
50	TCATCAGTAC GAGGTTTCCA ATACAAGTAC AAAAAAAAA TTGATCTCAC	AGGAAATGTC AATCAAATAT TACTTCTACT AAGGATGATC TGTTATTATT	ATGACCTTGA GTTGCAATGG GGAAATAAA AAAACACACA AACATTTATT	AGTTTCTANG ATCCTGTATC ACTTTTTAGC GTGTTTATGT TATTATTTT	TGATGCTTCA CAAATCCAGT TGGAAGATTT TGGAATCTTT CTAAATGTGA	GTGACAGCTG CAAGGAAAAA AGCCACTTAT TGCAACTCCT AAGAAATACA	780 840 900 960 1020
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60	TAAATATTGT	TATGCATTAT TGCAATAAAT 507 Protein	ATCCTTCGGA	CTCTATTGTT ATTC	GGAATTTCAG	GTCATTTTCA	1380
65		ession #: 1		31	41	51	
70	EGGHLATYKQ ERWDAYCYNP DLEDDPGCLA	LWEDTQGWGF LEAARKIGPH HAKECGGVPT DYVEIYDSYD SKSSQGKNTS	VCAAGWMAKG DPKRIFKSPG DVHGFVGRYC	RVGYPIVKPG PPNEYEDNQI GDELPDDIIS	PNXXPGKTGI CYWHIRLKYG	IDYGIRLNRS QRIHLSFLDF	60 120 180 240
75	Nucleic Act	508 DNA sed d Accession ence: 129.	#: NM 001	044.1			
80	AAAGCCCAGG	11 AGCGGGAGGG CCCGGGCGGC GAGTAAGAGC	CAGACCAAGA	GGGAAGAAGC	ACAGAATTCC	TCAACTCCCCA	60 120 180
85	CTAAGGAGCC ACGGAGTGCA AGGATCGGGA	CAATGCCGTG GCTCACCAGC GACCTGGGGC CAACGTCTGG	GGCCCGAAGG TCCACCCTCA AAGAAGATCG	AGGTGGAGCT CCAACCCGCG ACTTTCTCCT	CATCCTTGTC GCAGAGCCCC GTCCGTCATT	AAGGAGCAGA GTGGAGGCCC GGCTTTGCTG	240 300 360 420

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	TGTACTGGGG GCTGTGCTGG	AAGCTGGTCA	GCCCCTGCTT	TCTCCTGTTC	GTGGTCGTGG	1740
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	TGGAGCGTGT ACTACCCCAG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	CCTATCCCCG	3000
45	GACCEGACEC ATGCAGGGCC CCCACAGGAG CGTGTACTAC	CCCACAGGAG	CGTGTACTAC	CCCAGGACGC	ATGCAGGGCC	3060 3120
43	CCCACAGGAC COTOTACTAC	CCCAGGATGC	CAGCCTGCAG	ACCARCAGGAG	TGCCTGCCCT	3180
	TGAGCCGTGA CCTCCAGGAA	GGGACCCCAC	TGGAATTTTA	TTTCTCTCAG	GTGCGTGCCA	3240
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50	ATCAAAACAA ATTCAAGAAT	GCAGTATCCG	CGAGCCTGCT	TGCTGATATT	GCAGTTTTTG	3360 3420
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	TOGGTOGGCC TOCCTACGTG	CTGCCCGAGG	GCAGGGGCCG	TGCAGGGCCA	GTCATGGCTG	3540
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22	GGGAGGGACA CAGAGGACGG	CTTCCCCATC	GCCTTCTGGC	CGCTGCAGTC	AGCACAGAGA TOGOGETOTO	3720 ·
	GCGGCTTCCC CATTGCCTTC GTTGTTGAAG ACAGCACAGA	CA COCCACTTC	COCATOGOCT	TCTGGGGAGG	GGCTCCGTGT	3840
	AGCAACCCAG GTGTTGTCCG	TGTCTGTTGA	CCAATCTCTA	TTCAGCATCG	TGTGGGTCCC	3900
	TAAGCACAAT AAAAGACATC	CACAATGGAA	алалалала	GAATTC		
60	Seg ID NO: 509 Protein					
	Protein Accession #: 1					
	Process Accession W. 1					
	1 11	21	31	41	51	
65	l	1		OT TOO TO THE	DO ON TO DO	60
	MSKSKCSVGL MSSVVAPAKE ETWGKKIDFL LSVIGFAVDL	PHANGPRENE	VIOLGGGGREATA	OPTIGOLITIES	MPLEVMELAL	120
	GOFNREGAAG VWKICFILKG	VGFTVILISL	YVGPFYNVII	ANALHYLESS	FTTELPWINC	180
=-	NNSWNSPNCS DAHPGDSSGD	SSGLNDTFGT	TPAABYFBRG	VLHLHQSHGI	DDLGPPRWQL	240
70	TACLVLVIVL LYFSLWKGVK	TSGKVVWITA	TMPYVVLTAL	LLRGVTLPGA	IDGIRAYLSV	300
	DFYRLCEASV WIDAATQVCF GFVVFSFLGY MAQKHSVPIG	SLGVGFGVLI	AFSSYNKFTN	NCYRDAIVTT	SINSLISISS	360 420
	DSAMGGMESV ITGLIDEFOL	LHRHRELPTI	FIVLATELIA	LFCVTNGGIY	VPTLLDHFAA	480
	GTSILFGVLI EAIGVAWFYG	VGOFSDDIOO	MTGQRPSLYW	RLCWKLVSPC	PLLFVVVVSI	540
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		TOGOGGCCTT	CTGCCCGGCC GCGCCTGCGC		TGGAACTCCT	OGGCTTCCAG	660
	CTCCTGGGC	TAGAGATGGC	TCTGGGTCCC	GGGCGGGAGT	ACCGGGCTCT	GCAGCTGCAT	720
10	CTGCACTGGG	GGGCTGCAGG	TOSTCOGGGC	TCGGAGCACA	CTGTGGAAGG	CCACCGTTTC	780
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	GGTGACTCTC	GGCTA CAGCT	GAACTTOOGA	GCGACGCAGC	CTTTGAATGG	GCGAGTGATT	1200
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20	GTGAGCTACC	GCCCAGCAGA	GGTAGCCGAG	ACTOGAGCCT	AGAGGCTGGA	TCTTGGAGAA	1440
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25	Seq ID NO:	511 Protein	sequence				
25	Protein Acc	ession #: 1	_				
	1	11	21	31	41	51	
	MADICPRONIL	PLLIPAPAPG	LTVOLLLSLL	LLMPVHPQRL	PRMOEDSPLG	GGSSGEDDPL	60
30	GEEDLPSEED	SPREEDPPGE	EDLPGEEDLP	GEEDLPEVKP	KSEEEGSLKL		120
		RDKEGDDQSH	WRYGGDPPWP		QSPVDIRPQL RALQLHLHWG	AAFCPALRPL	180 240
	ELIGITATION	PELRLRNNGH HVVHLSTAFA	SVQLTLPPGL	GLAVIAAFLE	EGPEENSAYE		300
	EEGSETOVPG	LDISALLPSD	FSRYFOYEGS	LTTPPCAQGV	INTVFNQTVM	LSAKQLHTLS	360
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	GLLPAVTSVA	FLVQMRRQHR	RGTKGGVSTR	PASVABIGA			
	Seq ID NO:	512 DNA sec	mence				
40	Nucleic Ac	id Accession Lence: 13!	1 #: Eos 8	equence			
40	Couring Bed						
	1	11	21	31	41	51	
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	TTCAAGGAGA		GAGAGAGGAA	GATGCTGGTA	TAATOGGTA		2400 2460
85	CTCTTCACTG	COTTYNIACAA	CCTCCTGATG	ATGACCTGTG	GGCCCCAGGG	CAACAGGACC	2520
05	ATOTOTO AOO	TOTOCOCOCO	actagcaga.	ATTYXTTCAGC	ATGITGTA CCA	GTGGGTGTAC	2580
	ACTGCAAGCA	TGGTGTTCAT	GCTGGTGTTT	GGCGTCACCA	AAGGCTTCGT	CTTCACCAAG	2640

WO 02/086443 GCCAGCCTTG CTGTAGGCTT CTTCATTCTG TTAGGCATTT TCCACAGAGG AGTCCAGGAG CTCAAGAAGG TYGAGAATGT CAGCCGGTGCA CCCTGGTTCA CCCACATCAC CTCCTCCATG 2940 3000 CAGGGCCTGG GCATCATTCA CGCCTATGGC AAGAAGGAGA GCTGCATCAC CTATACTTCA TOCARAGGOO TOTCATTOTO ATACATCATO CAGOTGAGOG GACTGOTCCA AGTGTGTGTG 3120 CGAACGGGAA CAGAGACGCA AGCCAAATTC ACCTCCGTGG AGCTGCTCAG GGAATACATT 3180 10 TOGACCIGIG TICCIGAATG CACICATCCC CICAAAGIGG GGACCIGICC CAAGGACIGG
CCCAGCIGIG GGGAGATCAC CITCAGAGAC TATCAGAIGA GATACAGAGA CAACACCCCC 3240 3300 CTTGTTCTCS ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCGG GATTGTTGGA AGAACAGGTT COGGAAAGTC ATCGTTAGGA ATGGCTTTGT TTCGTCTGGT GGAGCCAGCC 3420 AGTGGCACAA TCTTTATTGA TGAGGTGGAT ATCTGCATTC TCAGCTTGGA AGACCTCAGA 3480 ACTIGACICA TCTTEATURA TORGOTOGIAT ATCHICATTC TURGUTUGU ARRACTICAS 486 ACCARACTEG GETIGATOCO ACQARATICA GEOGRAFITO TAGGATOCHI TAGGATACA 5340 TIGGATCCCT TURGAGICA CACCAGIATAS ANDCITIGAG ARGITICITAGA GRADATIC 1500 STARBARRAC CANTANTORA ACTICICAGIA NATTACAGA CARAGITICA ARRAMICA 5340 GRADACTICT CAGTRAGGGA ACTICICAGIA NATTACAGA CARAGITICA ARRAMICA 5340 GRADACTICT CAGTRAGGGA ACTICICAGIA NATURACAG CAGARATICA ARRAMICA 5340 15 GANACTIC CAGMAGGGA ACUTACIC CITYGRAFAG CAGAGACT TECCAMAT TUAAAARCA CITYCCTTGA TRAACCACC GOTCHATGA ATTCCAMGA TAGACCCT 3786 GTTCAGAACA CATCAAAGA TGCCTTCAAG GOTCGCCT TGCTGACCAT GOCCACCG 3846 CTCAACACG TCTCAACTG CGATCACGTC CTOUTTATG ANANTGGGAA GGTGATTGA 3900 TTTGACAAGC CTGAAGTCCT TGCAGGAAG CAGATTCTG CATTTGGGAT GTTAATGACA 20 GCAGAAGTCA GATTGTAG 25 Seq ID NO: 513 Protein sequence

Protein Accession #: Bos sequence

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1	ALAMAINYRT	AIRLKVALST	LVFENLVSFK	TLTHISVGEV	LNILSSDSYS	LFEAALFCPL	240
	PATIFILMVF	CAAYAFFILG	PTALIGISVY	VIFIPVQMFM	AKLNSAFRRS	AILVTDKRVQ	300
35	TMNEFLTCIR	LIKMYAWEKS	FINTIQUIRR	RERKLLEKAG	FVQSGNSALA	PIVSTIAIVL	360
		KLTAPVAFSV					420
	PSYITOPEDP	DTVLLLANAT	LIWEHEASRK	STPKKLONOK	RHLCKKQRSE	AYSBRSPPAK	480
	GATGPEEOSD	SLKSVLHSIS	FVVRKLCRYP	BAQLLAWRWP	AVFVGRIIRG	YRPHGFSAKD	540
	KDESRRLLTW	POBVDRTORA	AKYLCKILGI	CGNVGSGKSS	LLAALLGOMO	LQKGVVAVNG	600
40	TLAYVSOOAW	IFHGNVRENI	LFGEKYDHQR	YQHTVRVCGL	QKDLSNLPYG	DLTEIGERGL	660
	NLSGGGRORI	SLARAVYSDR	QLYLLDDPLS	AVDAHVGKHV	FEECIKKTLR	CKTVVLVTHQ	720
	LOFLESCDEV	ILLEDGEICE	KGTHKELMEE	RGRYAKLIHN	LRGLQFKDPE	HLYNAAMVBA	780
	FKESPAEREE	DAGIICYLLS	LFTVFLFLLM	IGSAAFSNWW	LCLWLDKGSR	MTCGPQGNRT	840
	MCEVGAVLAD	IGQHVYQWVY	TASMVFMLVF	GVTKGFVFTK	TTLMASSSLH	DTVFDKILKS	900
45	PMSFFDTTPT	GRIMNRFSKD	MDBLDVRLPF	HAENFLOOFF	MVVFILVILA	AVPPAVLLVV	960
	ASLAVGFFIL	LRIFHRGVOB	LKKVENVSRS	PWFTHITSSM	QGLGIIHAYG	KKESCITYTS	1020
	SKGLSLSYII	OLSGLLOVCV	RTGTETQAKF	TSVELLREYI	STCVPECTHP	LKVGTCPKDN	1080
	PSCGEITFRD	YOMRYRDNTP	LVLDSLNLNI	QSGQTVGIVG	RTGSGKSSLG	MALFRLVEPA	1140
		ICILSLEDLR					1200
50		KLQABVTENG					1260
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Seq ID NO: 514 DNA sequence Nucleic Acid Accession #: 231560 Coding sequence: 1-966

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			GCCCATGAAT				180
			CCCCAAGATG				240
	GCCGAGTGGA	AACTTTTGTC	GGAGACGGAG	AAGCGGCCGT	TCATCGACGA	GGCTAAGCGG	300
65	CTGCGAGCGC	TGCACATGAA	GGAGCACCCG	CATTATAAAT	ACCGGCCCCG	GCGGAAAACC	360
	AAGACGCTCA	TGAAGAAGGA	TAAGTACACG	CTGCCCGGCG	GGCTGCTGGC	CCCCGGCGGC	420
	AATAGCATGG	CGAGCGGGGT	CGGGGTGGGC	GCCGGCCTGG	GCGCGGGGGT	GAACCAGCGC	480
	ATGGACAGTT	ACGCGCACAT	GAACGGCTGG	AGCAACGGCA	GCTACAGCAT	GATGCAGGAC	540
	CAGCTGGGCT	ACCCCCCAGCA	CCCGGGCCTC	AATGCGCACG	GCGCAGCGCA	GATGCAGCCC	600
70	ATGCACCGCT	ACGACGTGAG	CGCCCTGCAG	TACAACTCCA	TGACCAGCTC	GCAGACCTAC	660
	ATGAACGGCT	CGCCCACCTA	CAGCATGTCC	TACTCGCAGC	AGGGCACCCC	TGGCATGGCT	720
	CTTGGCTCCA	TOGGTTCGGT	GGTCAAGTCC	GAGGCCAGCT	CCAGCCCCCC	TGTGGTTACC	780
	TCTTCCTCCC	ACTCCAGGGC	GCCCTGCCAG	GCCGGGGACC	TCCGGGACAT	GATCAGCATG	840
	TATCTCCCCG	GCGCCGAGGT	GCCGGAACCC	GCCGCCCCCA	GCAGACTICA	CATGTCCCAG	900
75			GCCCGGCACG				960
	ATGTGAGGGC	CGGACAGCGA	ACTGGAGGGG	GGAGAAATTT	TCAAAGAAAA	ACGAGGGAAA	1020
	TGGGAGGGGT	GCAAAAGAGG	AGAGTAAGAA	ACAGCATGGA	GANANCCCCCC	TACGCTCAAA	1080

80 Seq ID NO: 515 Protein seq Protein Accession #: CAA83435

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	KTLMKKDKYT	LPGGLLAPGG	NSMASGVGVG	AGLGAGVNOR	MDSYAHMNOW	SNGSYSMMOD	180

	LGSMGSVVKS	086443 NAHGAAQMQP EASSSPPVVT AINGTLPLSH	SSSHSRAPCQ	YNSMTSSQTY AGDLREMISM	MINGSPTYSMS YLPGAEVPBP	YSQQGTPGMA AAPSRLHMSQ	240 300
5	Nucleic Ac:	516 DNA sec id Accession Lence: 29!	#: U91618				
10	CATGCTACTC	11 TTGTTAGAAG CTGGCTTTCA GCAGATTTCT AAGATGACTC	GCTCCTGGAG TGACCAATAT	GCATACATCA	GATTCAGAAG AAGATTAGTA	AGGAAATGAA	60 120 180 240
15	AGCTGAGGAA TGCTTTAGAT TCACAGCAGG TGACAAAAAT	ACAGGAGAAG GGCTTTAGCT GCTTTTCAAC GGAAAGGAAG AATAAACCCA	TTCATGAAGA TGGAAGCAAT ACTGGGAGTT AAGTCATAAA	GGAGCTTGTT GTTGACAATA AATCCAGGAA GAGAAAAATT	GCAAGAAGGA TACCAGCTCC GATATTCTTG CCTTATATTC	ARCTTCCTAC ACAAAATCTG ATACTGGAAA TGAAACGGCA	300 360 420 480 540
20	AGAGAATAAA ATTATATTTG ATTGAATGTG	TCATTTATTT TGTGAAAATG TTTTTCTGCA AAAAAAAAAA	ACATGTGATT TGACAAACAC CTAATAGAAA	GTGATTCATC ACTTATCTGT TTAGACTAAG	ATCCCTTAAT	TAAATATCAA	600 660 720
25	Protein Ace	517 Protein cession #: 8	AAB50564				
30	1 MMAGMKIOLV	11 CMLLLAFSSW	21 SLCSDSEREM	31 KALEADFLIN	41 MHTSKISKAH	51 VPSWKMTLLN	60
	VCSLVNNLNS	PAEETGEVHE NDKNGKEEVI	EELVARRKLP KRKIPYILKR	TALDGFSLEA	MLTIYOLHKI	CHSRAFQHWE	120
35	Nucleic Ac:	518 DNA sec id Accession sence: 109.	#: NM_006 .2940				
	1	11	21	31	41	51	
40	ACCTARAACC	TTGCAAGTTC	AGGRAGAAAC	CATCTGCATC	CATATTGAAA	ACCTGACACA	60
	ATGTATGCAG	CAGGCTCAGT	GTGAGTGAAC	TGGAGGCTTC	TCTACAACAT	GACCCAAAGG	120 180
	GARCTYCCTAT	GTCCTATTTG TCCTGGGAGC	TGGAGTACAG	CTTCABGACA	ATGGGTATAA	TGGATTGCTC	240
	ATTICCA ATTA	ATCCTCAGGT	ACCTCACAGA	CAGAACCTCA	TOTCRARCAT	TANGGARATG	300
45	ATAACTGAAG	CTTCATTTTA	CCTATTTAAT	GCTACCAAGA	GAAGAGTATT	TTTCAGAAAT	360
	ATAAAGATTT	TAATACCTGC AGGCAAATGT	CACATGGAAA	GCTAATAATA	ACAGCAAAAT	AAAACAAGAA	420 480
	TACACCCTAC	AATACAGAGG	GTGTGGAAAA	GAGGGAAAAT	ACATTCATTT	CACACCTAAT	540
	TTCCTACTGA	ATGATAACTT	AACAGCTGGC	TACGGATCAC	GAGGCCGAGT	GTTTGTCCAT	600
50	GAATGGGCCC	ACCTCCGTTG AAAATCAAAT	GGGTGTGTTC	GATGAGTATA	ACANTGACAA	ACCTTTCTAC	660 720
	GTGTGTG131	AAGGTCCTTG	CCCCCAAGAA	AACTGTATTA	TTAGTAAGCT	TTTTAAAGAA	780
	GGATGCACCT	TTATCTACAA	TAGCACCCAA	AATGCAACTG	CATCAATAAT	GTTCATGCAA	840
55	AGTTTATCTT	CTGTGGTTGA AGATGTGCAG	ATTTTGTAAT	GCAAGTACCC	ACAACCAAGA	AGCACCAAAC	900 960
55	TTTCACCACA	CCTTTCCCCAT	GAATGGGGACT	GAGCTTCCAC	CTCCTCCCAC	ATTCTCGCTT	1020
	GTACAGGCTG	GTGACAAAGT	GGTCTGTTTA	GTGCTGGATG	TGTCCAGCAA	GATGGCAGAG	1080
	GCTGACAGAC	TOCTTCAACT	TGCCAGTTTC	GEAGAATTTT	GAGAGATCAG	AGCCCAGCTA	1200
60	CACCAAATTA	ACAGCAATGA	TGATCGAAAG	TTGCTGGTTT	CATATCTGCC	CACCACTGTA	1260
	TCAGCTARAA	CAGACATCAG GAAAAGCTTA	CATTTGTTCA	GGGCTTAAGA	AAGGATTTGA	GGTGGTTGAA	1320 1380
	CTTCTTGGCA	ATTGCTTACC	CACTGTGCTC	AGCAGTGGTT	CAACAATTCA	CTCCATTGCC	1440
65	CTGGGTTCAT	CTGCAGCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500
05		CAGATATATC GAGACATTTT	CCAGCAACAT	AGCATGATTG	ATGCTTTCAG	TAGAATTTCC	1560
	AAACCTCACC	ATCAATTGAA	AAACA CAGTG	ACTGTGGATA	ATACTGTGGG	CAACGACACT	1680
	ATGTTTCTAG	TTACGTGGCA ACTACACAAA	GGCCAGTGGT	CCTCCTGAGA	TTATATTATT	TGATCCTGAT	1740
70	TGGATTCCAG	GAACAGCTAA	GCCTGGGCAC	TGGACTTACA	CCCTGAACAA	TACCCATCAT	1860
	TOTOTOCA NO.	COCTOBBACE	GACAGTGACC	TOTOGGGGGGG	CCAACTCAGC	TOTOCCCCCA	1920
	GCCACTGTGG	AAGCCTTTGT TGAAACAGGG	GGAAAGAGAC	AGCCTCCATT	CCACTITICAC	TGTGATGATT	1980
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100
75	GTTATAAAAA	ATGATGGAAT	TTACTCGAGG	TATTTTTTCT	CCTTTGCTGC	AAATGGTAGA	2160
	CCAGGGAGTC	AAGTGCATGT ATGCTATGTA	TOTACCAGGE	TACACAGCATAA	ACCCURACE	TCAGATGAAT	2280
	GCTCCAAGGA	AATCAGTAGG	CAGAAATGAG	GAGGAGCGAA	AGTGGGGCTT	TAGCCGAGTC	2340
80	AGCTCAGGAG	GCTCCTTTTC AAATTATTGA	AGTGCTGGGA	GTTCCAGCTG	GCCCCCACCC	TGATGTGTTT	2400 2460
30	TGGACAGCAC	CTGGAGAAGA	CTTTGATCAG	GGCCAGGCTA	CAAGCTATGA	AATAAGAATG	2520
	AGTARAGGTC	TACAGAATAT	CCAAGATGAC	TTTAACAATG	CTATTTTAGT	AAATACATCA	2580
	AAGCGAAATC	CTCAGCAAGC CTGAACATCA	TGGCATCAGG	GAGATATTTA	CGTTCTCACC	CCAGATTTCC	2640 2700
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	CCTCTGTTTA	TTCCCCCCAA	TTCTGATCCT	GTACCTGCCA	GAGATTATCT	TATATTGAAA	2820 2880
	GUAGTTTTAA	CAGCAATGGG	TTTGATAGGA	ATCATTIGCC	TIATTATAGT	TOTGACACAT	2660

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	CATACTTTAA	GCAGGAAAAA	GAGAGCAGAC	ANGAAAGAGA	ATGGAACAAA	ATTATTATAA	2940
		AAAGTGTCTT					3000
		AAGTCAAATT					3060
		GATTTTTACA					3120
5		TGGCTATGAA					3180
		GGGTAAAGTC					3240
		AGCAGAGAAA					3300
	TCATTTAGTT	ACTITGATTA	ATTTTTTTTT	TCTCCTTATC	TGTGCAGTAC	AGGTTGCTTG	3360
		GATCATGCTA					3420
10		TGTTATATAT					3480
		AGAGGTAACC					3540
		AGGICTATIG					3600
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Seq ID NO: 519 Protein sequence Protein Accession #: NP_006527.1

			_				
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		GCGKEGKYIH					180
		IKVTRCSSDI					240
25	MEMOSLESVV	EFCNASTHNO	EAPNLONOMC	SLRSANDVIT	DSADFHHSFP	MNGTELPPPP	300
	TESLVOAGDK	VVCLVLDVSS	KNAEADRLLO	LQQAAEFYLM	QIVEIETFVG	IASFDSKGEI	360
	RAOLHOINSN	DDRKLLVSYL	PTTVSAKTDI	SICSGLKKGF	EVVEKLNGKA	YCSVMILVTS	420
		PTVLSSGSTI					480
		FOOHIQLEST					540
30	FDPDGRKYYT	IMPITMLTER	TASLWIPGTA	KPGHNTYTLN	NTHHSLQALK	VTVTSRASNS	600
	AVPPATVEAF	VERDSLHFPH	PVMIYANVKO	GFYPILNATV	TATVEPETGD	PVTLRLLDDG	660
	AGADVIKNDG	IYSRYFFSFA	ANGRYSLKVH	VNHSPSISTP	AHSIPGSHAM	YVPGYTANGN	720
	IOMNAPRKSV	GRNEBERKWG	FSRVSSGGSF	SVLGVPAGPH	PDVFPPCKII	DLEAVKVEEE	780
	LTLSNTAPGE	DFDQGQATSY	EIRMSKSLON	IODDFMMAIL	VNTSKRNPQQ	AGIREIFTFS	840
35	POISTNGPEH	OPNGETHESH	RIYVAIRAND	RNSLQSAVSN	IAQAPLFIPP	NSDPVPARDY	900
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	CTCCTGCATG	CCCAACAAGC	CTGCTCCCGT	GGGGCCTGCT	ATCCACCTGT	TOGGGACCTG	180
	CTTGTTGGGA	GGACCCGGTT	TCTCCGAGCT	TCATCTACCT	GTGGACTGAC	CAAGCCTGAG	240
	ACCTACTGCA	CCCAGTATGG	CGAGTGGCAG	ATGAAATGCT	GCAAGTGTGA	CTCCAGGCAG	300
	CCTCACAACT	ACTACAGTCA	CCGAGTAGAG	AATGTGGCTT	CATCCTCCGG	CCCCATGCGC	360
50	TOGTGGCAGT	CCCAGAATGA	TGTGAACCCT	GTCTCTCTGC	AGCTGGACCT	GGACAGGAGA	420
	TTCCAGCTTC	AAGAAGTCAT	GATGGAGTTC	CAGGGGCCCA	TGCCCGCCGG	CATGCTGATT	480
	GAGCGCTCCT	CAGACTTCGG	TAAGACCTGG	CGAGTGTACC	AGTACCTGGC	TGCCGACTGC	540
		TOCCTCGGGT					600
	CAGTCCCTGC	CTCAGAGGCC	TAATGCACGC	CTAAATGGGG	GGAAGGTCCA	ACTTAACCTT	660
55	ATGGATTTAG	TGTCTGGGAT	TCCAGCAACT	CAAAGTCAAA	AAATTCAAGA	GGTGGGGGAG	720
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	CCTCCCAGCG	CCTACTATGC	TGTGTCCCAG	CTCCGTCTGC	AGGGGAGCTG	CTTCTGTCAC	840
	GGCCATGCTG	ATCGCTGCGC	ACCCAAGCCT	GGGGCCTCTG	CAGGCCCCTC	CACCGCTGTG	900
	CAGGTCCACG	ATGTCTGTGT	CTGCCAGCAC	AACACTGCCG	GCCCAAATTG	TGAGCGCTGT	960
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	AACTGTGAGC	GGTGTCAGCT	GCACTATTTC	COGAACCGGC	GCCCGGGAGC	TTCCATTCAG	1200
	GAGACCTGCA	TCTCCTGCGA	GTGTGATCCG	GATGGGGCAG	TGCCAGGGGC	TCCCTGTGAC	1260
65	CCAGTGACCG	GGCAGTGTGT	GTGCAAGGAG	CATGTGCAGG	GAGAGCGCTG	TGACCTATGC	1320
	AAGCCGGGGCT	TCACTGGACT	CACCTACGCC	AACCCGCAGG	GCTGCCACCG	CTGTGACTGC	1380
	AACATCCTGG	GGTCCCGGAG	GGACATGCCG	TGTGACGAGG	AGAGTGGGCG	CTGCCTTTGT	1440
	CTGCCCAACG	TOGTGGGTCC	CAAATGTGAC	CAGTGTGCTC	CCTACCACTG	GAAGCTGGCC	1500
	AGTGGCCAGG	GCTGTGAACC	GTGTGCCTGC	GACCCGCACA	ACTOCCCTCA	GCCCACAGTG	1560
70	CAACCAGTTC	ACAGGGCAGT	GCCCTGTCGG	GAAGGCTTTG	GTGGCCTGAT	GTGCAGCGCT	1620
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	ATCCGAGCAG	TTCTCAGCAG	CCCCGCAGTC	ACAGAGCAGG	AGGTGGCTCA	GGTGGCCAGT	2040
		COCT CAGGCG					2100
	GAGACGTTGT	CCCTTCCGAG	AGACCTGGAG	AGTCTTGACA	GAAGCTTCAA	TGGTCTCCTT	2160
80	ACTATGTATC	AGAGGAAGAG	GGAGCAGTTT	GAAAAAATAA	GCAGTGCTGA	TCCTTCAGGA	2220
	GCCTTCCGGA	TGCTGAGCAC	AGCCTACGAG	CAGTCAGCCC	AGGCTGCTCA	GCAGGTCTCC	2280
	GACAGCTCGC	GCCTTTTGGA	CCAGCTCAGG	GACAGCCGGA	GAGAGGCAGA	GAGGCTGGTG	2340
	COCCAGGCGG	GAGGAGGAGG	AGGCA CCGGC	AGCCCCAAGC	TIGTGGCCCT	GAGGCTGGAG	2400
	ATGTCTTCGT	TGCCTGACCT	GACACCCACC	TTCAACAAGC	TCTGTGGCAA	CTCCAGGCAG	2460
85	ATGGCTTGCA	COCCAATATO	ATGCCCTGGT	GAGCTATGTC	CCCAAGACAA	TGGCACAGCC	2520
	TOTGGCTCCC	GCTGCAGGGG	TOTCCTTCCC	AGGGCCGGTG	GGGCCTTCTT	GATGGCGGGG	2580
	CAGGTGGCTG	AGCAG CTGCG	GGGCTTCAAT	GCCCAGCTCC	AGCIGACCAG	GCAGATGATT	2640
	CAUCIGOCIO		00001101011				

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		GCCGCTCCCA					2760
	CAGGTCCGGG	ACTTCCTAAC	AGACCCCGAC	ACTGATGCAG	CCACTATCCA	GGAGGTCAGC	2820
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5	GAGATCCAGG	CCATTGCAGC	CAGGCTCCCC	AACGTGGACT	TGGTGCTGTC	CCAGACCAAG	2940
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	CTGCAGGAAG	CTCAGGACAC	CATGCAAGGC	ACCAGCCGCT	CCCTTCGGCT	TATCCAGGAC	3120
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10	AAGCMGCTGG	GTGACTTCTG	GACACGGATG	GAGGAGCTCC	GCCACCAAGC	CCGGCAGCAG	3240
	GGGGCAGAGG	CAGTCCAGGC	CCAGCAGCTT	GCGGAAGGTG	CCAGCGAGCA	GGCATTGAGT	3300
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	GAGCTGTTTG	GGGAGACCAT	GGAGATGATG	GACAGGATGA	AAGACATGGA	GTTGGAGCTG	3480
15	CTGCGGGGCA	GCCAGGCCAT	CATGCTGCGC	TCGGCGGACC	TGACAGGACT	GGAGAAGCGT	3540
		TCCGTGACCA					3600
		TCCAGCCCGT					3660
		GAATGCTTTC					3720
••		GGTGTGTAGC					3780
20		CACTTGACAG					3840
		AAGGAAGCTG					3900
		ACCAAGCACA	AAAACTTAAC	AAAAGTGATG	TAAAAATGAA	AAGCCAAATA	3960
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25							
23	Seq ID NO:	521 Protein	n sequence				

Seq ID NO: 521 Protein sequence Protein Accession #: NP_000219.1

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						VRCOSLPORP	180
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	VSQLRLQGSC	FCHGHADRCA	PKPGASAGPS	TAVQVHDVCV	COHNTAGPNO	ERCAPFYMIR	300
35	PWRPAEGODA	HECORCIOCNG	HSETCHFDPA	VFAASQGAYG	GVCDNCRDHT	EGKNCERCQL	360
	HYFRNRRPGA	SIQETCISCE	CDPDGAVPGA	PCDPVTGQCV	CKEHVQGERC	DLCKPGFTGL	420
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Seq ID NO: 522 DNA sequence Nucleic Acid Accession #: NM_001944.1 Coding sequence: 84..3083

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		CCAATCAGTT					1200
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YTPDMNREDV DYAIRKAPQV WSWVTPLKPS KINTGMADIL VVFARGARGD FHAFDGRGGI LAHAFGPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY KYYDINTFRI SADDIRGIOS LYGDPKENOR LPNPENSEPA LCDPNISEPA VITUNKIPP FKORFPHIKV SERKTSVAL ISSIMPTLPS GIEAAYEIEA RNQVPLPKUD KYWLISNIRP EPNYYRSIHS FGPPNYKKI DAAVEMPPRY RTYFPUNOV WKYDEROOM DGYVPKLTK NEGGIGANID AVEYSKNKYY YFFOGSNOFE YDFLLORITK TLKSNSWFGC

Seq ID NO: 526 DNA sequence

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GGGAAACGTT TTCCTGAGGA TTTAGCACAG CAAAACTTAA TTATATCAAA CACAGAAGCA 2220 2280 COTTOGRADACT ATAGACTICTG CTCTGCCAAT GGATTTATGA CCCAAACTAC CAACAACTCT AGCCAAGGTT TTTGTGGTAC TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAAACCATT GARATGATGA AAGGAGGAAA CCAGACCTTG GAATCCTGCC GGGGGGCTGG GCATCATCAT 2460 55 ACCOMPGACT COMPCAGGGG AGGACACACG GAGGTGGACA ACTGCAGATA CACTTACTOG 2520 CACTOCICACA CONTRACTOR ACCOCCUTOTO CONCARGRAT CONTRACROS ACACACTOST 2580 TAAABATTAA ACATABAAGA AATTGCATCG ATGTAATCAG AATGAAGACC GCATGCCATC CCAAGATTAT GTCCTCACTT ATAACTATGA GGGAAGAGGA TCTCCAGCTG GTTCTGTGGG 2700 CTGCTGCAGT GAAAAGCAGG AAGAAGATGG CCTTGACTTT TTAAATAATT TGGAACCCAA 2760 60 ATTTATTACA TTMOCAGAGA CATUCACHAA GAGATMATUT CACAGTUCTA CAATTAGGTC TTTGTCAGAC ATTCTGAGO TTTCCCMANAA TAATATTUTA AASTTCAATT TCAACAGTGA TGTATATGAT GATTTTTTC TCAATTTGA ATTATUCTAC TCACCAATTA ATTATTATA AGCCAGTUT TGCTAACTT TTCCAARAMA TGMAAMATUT TAAAACAGAC AACTGGTAMA 2820 2880 TOTCARACTO CAGCACTOGA ATTRAGGTOT CTARAGORTO TGOTOTTTTT TTTTTTTACG 3060 65 GATATTITAG TAATAAATAT GCTGGATAAA TATTAGTCCA ACAATAGCTA AGTTATGCTA ATATCACATT ATTATGTATT CACTITAGT GATAGTTTAA AAAATAAACA AGAAATATTG 3120 3180 AGTATCACTA TOTGAAGAAA GTTTTTGGAAA AGAAACAATG AAGACTGAAT TAAATTAAAA ATGTTGCAGC TONTAAAGAA TTGGGACTCA CCCCTACTGC ACTACCAAAT TCATTTGACT TIGGAGGCAA AATGIGTIGA AGIGCCCTAT GAAGIAGCAA TITICTATAG GAATATAGIT 3360 70 GGAAATAAAT GTGTGTGTGT ATATTATTAT TAATCAATGC AATATTTAAA ATGAAATGAG 3420 AACAAAGAGG AAAATGGTAA AAACTTGAAA TGAGGCTGCC GTATAGTTTG TCCTACAATA 3480 GAAAAAAGAG AGAGCTTCCT AGGCCTGGGC TCTTAAATGC TGCATTATAA CTGAGTCTAT GAGGAAATAG TTCCTGTCCA ATTTGTGTAA TTTGTTTAAA ATTGTAAATA AATTAAACTT 3600 TTCTGGTTTC TGTGGGAAGG AAATAGGGAA TCCAATGGAA CAGTAGCTTT GCTTTGCAGT 3660 75 CTGTTTCAAG ATTTCTGCAT CCACAAGTTA GTAGCAAACT GGGGAATACT CGCTGCAGCT 3720 GOOGTTCCCT GCTTTTGGT AGCAAGGGTC CAGAGATGAG GTGTTTTTTT CGGGGAGCTA 2780 ATAACAAAA CATTTTAAA CTTACCTTA CTGAAGTTAA ATCCTCTATT GCTGTTTCTA TTCTCTCTTA TAGTGACCAA CATCTTTTTA ATTTAGATCC AAATAACCAT GTCCTCCTAG 3900 GAGG CTAGAGGGAG CTGAGGGGAG GATCTTACTG AAAGCACCCT GGGGAGATTG 3960 ATTGTCCTTA AACCTAAGCC CCACAAACTT GACACCTGAT CAGGTCTGGG AGCTACAAAA 80 4020 TTTCATTTTT CTCCTCACTG CCCTTCTTCT GAGTGGCATT GGCCTGAATC AAGGAAAGCC 4080 AGGCCTTOTG GGCCCCCTTC TTTCGGCTTT CTGCTAAAGC AACACCTCCA GCAGAGATTC 4140 COTTAGTGA CTCCAGGTTT TOCACCATCC TTCAGGGTGA ATTAGTTTT AATCAGTTTG CTTTCTCCAG AGAAATTTTA AAATAATAGA AGAAATAGAA ATTTTGAATG TATAAAAGAA 4260 85 AAAGATCAAG TIGTUATTII AGAACAGAGG GAACTITOGG AGAAAGCAGC CCAAGTAGGT TATTIGTACA GITCAGAGGGC AACAGGAAGA TUCAGGCCII CAAGGGCAGG GAAGGGCATAA AAGGAATATG GGTUGGAGTA AAAGCAACAT COTCIGCTIC ATACTITITC CTACGCTTG 4320 PCT/US02/12476

240

PCT/US02/12476

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Seq ID NO: 527 Protein sequence Protein Accession #: NP_077741.1

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Seq ID NO: 528 DNA sequence Nucleic Acid Accession #: NM_001941.2 Coding sequence: 64..2754

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			GGCAGAGTTA			240
TCTGCAGACC	TCATCCGGTC	AAGTGATCCT	GATTTCAGAG	TTCTAAATGA	TGGGTCAGTG	300
TACACAGCCA	GGGCTGTTGC	GCTGTCTGAT	ANGAAAAGAT	CATTTACCAT	ATGGCTTTCT	360
GACAAAAGGA	AACAGACACA	GAAAGAGGTT	ACTGTGCTGC	TAGAACATCA	GAAGAAGCTA	420
TOGRAGACAA	GACACACTAG	AGAAACTGTT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
ATTCCTTGCT	CTATGCAAGA	GAATTCCTTG	GGCCCTTTCC	CATTGTTTCT	TCAACAAGTT	540
			TTCTACTCAA			600
AAAGAACCTT	TAAATTTGTT	TTATATAGAA	AGAGACACTG	GARATCTATT	TTGCACTCGG	660
CCTGTGGATC	GTGAAGAATA	TGATGTTTTT	GATTTGATTG	CTTATGCGTC	AACTGCAGAT	720
GGATATTCAG	CAGATCTGCC	CCTCCCACTA	CCCATCAGGG	TAGAGGATGA	AAATGACAAC	780
CACCCTGTTT	TCACAGAAGC	AATTTATAAT	TTTGAAGTTT	TGGAAAGTAG	TAGACCTGGT	840
ACTACAGTGG	GGGTGGTTTG	TGCCACAGAC	AGAGATGAAC	CGGACACAAT	GCATACGCGC	900
CTGAAATACA	GCATTTTGCA	GCAGACACCA	AGGTCACCTG	GGCTCTTTTC	TGTGCATCCC	960

	AGCACAGGGG	TAATCACCAC	AGTCTCTCAT	TATTTGGACA	GAGAGGTTGT	AGACAAGTAC	102
	TOATTOATAA	TOABAGTACA	AGACATGGAT AGATTCAAAT AAATGCATTC	GGCCAGTTTT	TTGGATTGAT	AGGCACATCA	108
	1 CONTRACTOR	DATE CO CONTROL	ACAMMCAAAM	CATAMECCAC	COLCUMBORO	A CRABBATICE	114
	ACTIGIATOR	THACAGIANC	MONTICADAL	GATIOTICAC	CONCILIONS	ACAMANAGCI	120
-	TATGUUGCAT	TTGTAGAGGA	MANTGCATTC	MIGIGORIA	TCTTACGAAT	ACCIAINGRA	
5	GATAAGGATT	TAATTAACAC	TGCCAATTGG	AGAGTCAATT	TTACCATTTT	AAAGGGAAAT	126
	GAAAATGGAC	ATTTCAAAAT	CAGCACAGAC	AAAGAAACTA	ATGAAGGTGT	TCTTTCTGTT	132
	GTABAGCCAC	PERSONNEL	CAGCACAGAC AGAAAACCGT	CARGTGRACC	TOGGADATTOG	AGTAAACAAT	138
	Chaccoccan	THEOGRACACA.	TATTCCCAGA	CTYCACACCCT	TORRODO	CPTGGTPACA	144
	GAAGCGCCAT	TIGCINGNON	TATTCCCAGA	GIONCHOCCI	TONNCHONGC	CITOGITACA	144
10	GTTCATGTGA	GGGATCTGGA	TGAGGGGCCT GGGGTCAAAG	GAATGCACTC	CIGCAGCCCA	ATATGTGCGG	150
10	ATTAAAGAAA	ACTTAGCAGT	GGGGTCAAAG	ATCAACGGCT	ATAAGGCATA	TGACCCCGAA	156
							162
	ammonamora a a	mman acame	AATCATAACT TATTACAGTC	SOUTH A SATISTICS	TOGATAGGGA	COTTONANCT	168
	ATTOATOAAA	LITCAGGGIC	MITCHIANCI	TOURINGE	10001100000	GOT TOWNSCT	174
	CCCAAAAATG	AGTIGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	
	ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	180
15	GAATATGTAG	TCATTTGCAA	ACCAAAAATG TCCATTTTAT	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	186
	GATGAACCTG	TOCATOGRAGO	TCCATTTTAT	TTCAGTTTGC	CCAATACTTC	TCCAGAAATC	192
	MORNON CROWN	COLOCOPORO	CAAAGTTAAT	CATACACCTC	COCCUPATION	ATATCAGAAA	198
	MOTHORCIGI	GONGCCICAC	CUUUATIUM	ARTHUMOUTO	*********	0000001100	204
	AATGCTGGAT	TTCAAGAATA	TACCATTCCT	ATTACTGTAA	MIGHCAUGGC	COGCCAMOCI	204
	GCAACAAAAT	TATTGAGAGT	TACCATTCCT TAATCIGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	210
20							216
	AMACCACHOC	TOTATO CTOT	ATTGCTAACT TTTAGCACAG	TTACTATOTC	CACTTTTTCC	TGCAACTAAA	222
	ALMOCACIOC	1011110101	WALLOCTION OF	CINDINITOIO	CONTRACTOR OF	Changenacch	228
	GGGAAACGTT	TTOCTGAMGA	TITAGCACAG	CHANCLING	TIATATCANA	CACAGANGCA	
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTTATGA	CCCAAACTAC	CARCARCICI	234
	AGCCAAGGTT	TTTGTGGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAAACCATT	240
25	GRANTGATGA	AAADDADDAA	CCAGACCTIG	GAATOCTGCC	GGGGGGGCTGG	GCATCATCAT	246
	A GOODLE ON	COTOGRACIO	AGGACACACG	CACCORCOCACA	DOTOC DODGE	CACHEACTCO	252
	ACCCIGGACT	CCIGCAGGGG	AGGMCACACG	CMGG1GGMCM	MCIGCHONIA	CACITACICO	258
	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC AGATTATGTC	GGTGAAAAAT	TUCATCUATU	TAATCAGOOT	258
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	264
							270
30	A B MA A MITTON	33000333000	TATTACATTA GTCAGACATT	CCACAACCAT	CONCREGACIO	ATRATOTORO	276
50	WINNITIOS	MCCCMUTT	INTINONIAN	ocnonnocn:	GCACAGAGAG	manage the	282
	AGTGCTACAA	TTAGGTCTTT	GTCAGACATT	CIGGAGGITI	CCAAAAATAA	TWITTGIWANG	
							288
	CCAATTTATA	TTTTTAAAGC	CAGTTGTTGC CAAACTCCAG	TTATCTTTTC	CAAAAAGTGA	AAAATGTTAA	294
	ANGRONCANO	TOTAL A STOT	CARACTICCAC	CACTGGAATT	ADDOTOTOTA	ANGCATCTGC	300
35	MICHOROPO	1001111111	ATTTTAGTAA		0010101010	ma anaan a ca	306
22	TCTTTTTTT	TITTACGGAT	ATTITAGTAA	TAAATATGCT	GGMTMAMTAT	TAGTCCAACA	300
	ATAGCTAAGT	TATGCTAATA	TCACATTATT ATCACTATGT	ATGTATTCAC	TTTAAGTGAT	AGTTTAAAAA	312
	ATAAACAAGA	AATATTGAGT	ATCACTATGT	GAAGAAAGTT	TTGGAAAAGA	AACAATGAAG	318
							324
	ACTOMITTAL	Manage Course	ar again 111m	amanman nam	COCCEDENTAL	CONTRACTOR	330
40	ACCADATTCA	TITGACTITG	GAGGCAAAAT AATAAATGTG	GIGITOMAGI	GCCCINION	GINGCAMIII	336
40	TCTATAGGAA	TATAGTTGGA	AATAAATGTG	TGTGTGTATA	TTATTATTAA	TCAATGCAAT	
							342
	TACTIFICATOR	TACALTACAA	AAAAGAGAGA GAAATAGTTC	GCTTCCTAGG	CCTGGGCTCT	TARATGCTGC	348
	1001110100	A GEOGRAPHICA C	CARAMAGNEC	CONTROCT ARE	TOTOTALATER	OTTOTALANTE	354
	ATTATANCEG	MOTOTALONG	CADDLINGLIC	CIGICCANII	IGIGIANITI	GITIAAAA	360
40	GTAAATAAAT	TAAACTTTTC	TGGTTTCTGT	GGGAAGGAAA	TAGGGAATCC	AATGGAACAG	
45	TAGCITTGCT	TTGCAGTCTG	TTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	366
	CARTACTOCC	TGCAGCTGGG	TTTCAAGATT	TTTTGGTAGC	AAGGGTCCAG	AGATGAGGTG	372
		GOLGOOD AND	ACAAAAACAT	TOTALLACTE	ACCUPATE CTG	DAGTTABATC	378
	77777777000	GGMGCIMMIN	TCTCTTATAG TTAGAGGCTA	TITAMANCIT	MOCTITACIO	The care of the care	384
	CTCTATTGCT	GTTTCTATTC	TCTCTTATAG	TGACCAACAT	CTITTIAATT	TAGATCCAMA	304
	TAACCATGTC	CTCCTAGAGT	TTAGAGGCTA	GAGGGAGCTG	AGGGGAGGAT	CITACIGAAA	390
50							396
	GTCTGGGAGC	TETELLACION	CATTTTTCTC	CTCACTGCCC	TTCTTCTGAG	TGGCATTGGC	402
	OTOLOGO AG	CO A DOCCORCO	CATTTTTCTC CCTTGTGGGC	COCOMMOTEM	COCCEPTECEC	CTABBOCARC	408
	CIGNATCANG	GACAGGCCAGG	CC1131000C	CCCCTTCTTT	COOCTITICTO	Laconat Man	
							414
	AATTTTTAAT	CAGTTTGCTT	TCTCCAGAGA GATCAAGTTG	AATTTTAAAA	TAATAGAAGA	AATAGAAATT	420
55	TTGAATGTAT	AAAAGAAAAA	CATCABGTTG	TCATTTTAGA	ACAGAGGGAA	CTTTGGGGAGA	426
-		A COMA CICIONA M	TIGTACAGIC	10100000110	ACCORD CAMCO	3000000000	432
	Muchoccun	MOINGGIANI	GAATATGGGT TGCCTTTTCC	ACAGOOCHAC	20220101100	OTTO CONTRACTOR	438
	GGGCAAGGAG	AGGCCACAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCUT	CIGCITCATA	
	CTTTTTTCCTA	GGCTTGGCAC	TGCCTTTTCC	TTTCTCAGGC	CANTGGCAAC	TGCCATTTGA	444
	GTCCGGTGAG	GGATCAGCCA	ACCTCTTCTC	TATGGCTCAC	CITATTTGGA	GTGAGARATC	450
60	ANGGAGACAG	AGCT/GACT/GC	ATGATGAGTC CATTCATGGG	TGAAGGCATT	TOCAGGATGA	GCCTGAACTG	456
00	ANGUNUNCAG	MOCTONCIOC	MIGNIGACIC	LOUDIGGCALL	1000000100	1000000000	462
	GTTGTGCAGA	NCMMCNAGG	CATTCATOOG	MATIGITATA	TICCTICIOC	MOCCCICCII	402
	CTGGGCACTA	AGAAGGTCTA	TGAATTAAAT	GCCTATCTAA	AATTCIGATT	TATTCCTACA	468
	TTTTCTGTTT	TCTAATTTGA	CCCTAAAATC	TATGTGTTTT	AGACTTAGAC	TTTTTATTGC	474
	ccccccccc	TTTTTTTTTC	CCCTAAAATC AGACGGAGTC	TOGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	480
65							486
05	9010004101	CIGCICIOIO C	TACAGGCGCC ACTGTGTTAG	G1 00000011	000000000000000000000000000000000000000	TO THE TOTAL THE	492
	GCCTCCTGAG	TAUCTGGGAC	TACAGGCGCC	CACCACCACG	CCGGCIAAI	IIIIIIIIIII	498
	TTTAATAGAG	ACGGGGTTTC	ACTGTGTTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCGTG	
							504
	CARCAMARCO	CTTTALLOTO	GTCTTCTTTT ATCTTGAAAT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	510
70		************	3000000111	1000110011	PAGE CROSSOC	3.033.000.00	516
70	TOATCATACG	MATTGGATCA	MICTIGIONI	ACTUARCON	MONCAGICO	NONHOCCAGO	
	GGGAGAAAGA	ACTCAGGGCA	CAAAATATTG	GTCTGAGAAT	GGAATTCTCT	GTAAGCCTAG	522
	TTGCTGAAAT	TTCCTGCTGT	AACCAGAAGC	CAGTTTTATC	TAACGGCTAC	TGAAACACCC	528
	ACTOTOTOTOT	COTCACTOOC	TCACTCACCG	ATCARARCCT	GCTACCTCCC	CARGACTITA	534
	CON COCCOO	ENANGEM NO	CAAAGAGCAA	CONCERNOON	THE CONTRACTOR	ATTABANCETC	540
75	CARGIGOCCIA	CONCLUST.	CONCRUCION CON	COMMISSION	OGEOGRAPITE	manageric :	546
13	TARCUATUTO	TITGTTCITT	GAACATGCTG AATGAAAATT	MAACCACCT	COTCIGCATG	INTUUCUIAA	546
	TTTGTAATTC	TTTTCTCTCA	AATGAAAATT	TAATTTTAGG	GATTCATTTC	TATATTTTCA	552
							558
	CARGRADATA	TATTTTTALA	COTTOCATOR	THYCCCCAGT	GAATGATTTA	GAATTTTTT	564
	mont a ami T	CACATACAGA	GCTTTCATTT TTTCTTACTT	mpaga acces	CCACCORCEC	33337000000	570
90	TGTAAATATA	CHUAATUITT	LITCITACTT	LINIMUGAA	CAGCIGICI	MANAGEMET	
80	GGGGTTTGTT	TIGCAATGIT	TTANACAGAG	TTTTAGTATT	GCTATTAAAA	GAAGTTACTT	576
	TOCTTTTAAA	GARACTTOGC	TGCTTAAAAT	AAGCAAAAAT	TGGATGCATA	AAGTAATATT	582
	TACACATOTO	GGGAGATGTA	TGCTTAAAAT ATAAAACAAT	APPRACTIGG	Takah Jahan Salah	THETHETATT	588
	magagaratic	PART PARTIES	GATGATCACT	Trockharen	ATVICTOR	CECCCAECCE	594
	TAGAGATTAA	ATANTTCTAA	GATGATCACT	TIGGARATT	MIGCITATEG	CIGGCATGGA	
0.5	AATAGAAATA	CTCAATTATG	TCTTTGTTGT ATTAATATAT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	600
85	ATTATCAAAT	TGTCGACATC	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCACTATTIT	606
-	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAATT	TTGATCGGGT	612
	Amma a a a com-	mpagaagers	GTTATAATTG	CAGAGTATOG	CATGARTICS	ACACTGACAC	618
	ALTANAAGTA	LINGUISITG	GITALAAITG	COMMINITO	CUTOUUTUGI.	**CACTOUCHC	010

5	GGCATATTG CAAGATGATC AGTGTGCTCC AGCCTTACAT CATTATTTTT ACCGGATACA	086443 CTTTGAGGAC CAGTCTTGAT CAACCATALA CCTACAAACG TTTAATATAG GTGTATGTCT TTTCACGTGT GGACACTAGA	TCTGCCACTT GGTGCTCTGT TTAAGACTGA GTTGAACCAA TCAAGAATGT CCTTCAGTAT	ACAGGATAGA GCTTCACAGT TCATTTCAAA AATTTCAATT TCATTGGATT TCATTTGGTT	TAATGCCIGA GAATCTTTTC AATCTATTAG CCAGTAACTT TITGTTTGTA GAATATTOGG	ACTITATIGA CCCATGCAGG CTATATCAAA CTATTGTAAC ATAGTAAAAT TCATAATGGT	6240 6300 6360 6420 6480 6540 6600
10	TTCTGTGTGA GAACAATGCC ATAGAACACT GTAGTTGGAT	CCTTTGAAAG AGCCTCATGG GCCTGCACAT ATACTACCGA CCCGAAACAT	GCTACTTATT GGTTGTTGAA AGTAAAAGAA ACAATATCTA	TCCTCTCTTA TCATTAAATT TTATAAGTGT	GCTTTCTCAT AGTTAATATA GAGGTAGTTG	TAAAATCAAT CCTAAAGTAC GTAAAATTAT	6720 6780 6840 6900
15	Seq ID NO: Protein Acc	529 Proteir cession #: 1	sequence				
20	ADLIRSSDPD KTRHTRETVL	11 RGAVCLHLLL FRVLNDGSVY RRAKRRWAPI	TARAVALSDK PCSMQENSLG	PEPLFLQQVE	KRKQTQKEVT SDAAQNYTVF	VLLEHQKKVS YSISGRGVDK	60 120 180
25	EPLNLFYIER PVFTEAIYNF TGVITTVSHY EAFVEENAFN KPLNYEENRQ KENLAVGSKI	DTGNLFCTRP EVLESSRPGT LDREVVDKYS VEILRIPIED VNLEIGVNNE NGYKAYDPEN	VDREBYDVFD TVGVVCATDR LIMKVQDMDG KDLINTANWR APFARDIPRV RNGNGLRYKK	LIAYASTADG DEPDIMHTRL QFFGLIGTST VMFTILKGNE TALMRALVTV LHDPKGWITI	YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDESPE DEISGSIITS	SPGLFSVHPS NAPTFRQNAY ETNEGVLSVV CTPAAGYVRI KILDREVETP	240 300 360 420 480 540
30	EPVHGAPFYF TKLLRVNLCE KRFPEDLAQQ MMKGGNOTLE	AIDKDDRSCT SLPNTSPEIS CTHPTQCRAT NLIISNTEAP SCRGAGHHHT TYNYEGRGSP	RLWSLTKVND SRSTGVILGK GDDRVCSANG LDSCRGGHTE	TAARLSYQKN WAILAILLGI FMTQTTNNSS VDNCRYTYSE	AGFQEYTIPI ALLFSVLLTL QGFCGTMGSG WHSFTOPRLG	TVKDRAGQAA VCGVPGATKS MKNGGQETIE EKLHRCNONE	660 720 780 840
35	DIGITAL	111111111111111111111111111111111111111	A0070CCDEA	Quantitative.	TODAY TELEV		
	Seq ID NO: Nucleic Ac:	530 DNA sec id Accession	guence 1 #: NM_016	583.2			
40	Coding sequ	lence: 728	342				
	1	11 AGAGAGAGGA	21 -	31 	41 CCTCTAAGAA	51 GTCCRGATAC	60
45	TAAGAGCAAA CCATGGCCCA ATCCAGCCCT ATGGCCTGCT	GATGTTTCAA GTTTGGAGGC GCCCTTGAGT GTCTGGGGGC	ACTGGGGGCC CTGCCGTGC CCCACAGGTC CTGTTGGGCA	TCATTGTCTT CCCTGGACCA TTGCAGGAAG TTCTGGAAAA	GACCCTGCCC CTTGACAAAT CCTTCCGCTC	TTAGCCCAGA TTGAATGTGA GCCCTCAGCA CTGGACATCC	120 180 240 300 360
50	TARAGCTCCA TGGACATCAC TTGGTGACTG	TOGGCTGAAC TGTGCAGAGC AGTGAATACG TGCAGAAATC CACCCATTCC	TTAGCTGTGA CCTGGAAGCC	GAGATAAGCA TGCAAATTTC	GGAGAGGATC TCTGCTTGAT	CACCTGGTCC GGACTTGGCC	420 480 540 600 660
55	AGTTGGTTCA CCCTGGTGCA AAGCCTTCCA GCCCATGTGC TCCCACCAGG	TCAAGGTCTT GGGCAACGTG TGACATTGTT GGAAGGGGCT TGGAAGATGA CGTGTGTAAC	TGCCCTCTGG AACATGCTGA GGCCTCTGCT CACAGTTGCC ATCCCATGTG	TCAATGAGGT TCCACGGACT GAGCTGCTTC TTCTCTCCGA	ACAGTTTGTC CCAGTGCTCA GGAACCTGCC	TTGGACATCA ATCAAGGTCT CAGATGGCTG CCCTCTCCTT	780 840 900 960 1020
60	Seq ID NO:	AAAAAAAAA 531 Protein cession #: 1	sequence				
65	1 MFOTGGLIVF	11 YGLLAQTNAQ	21 FGGLPVPLDO	31 TLPLNVNPAL	41 PLSPTGLAGS	51 LTNALSNGLL	60
70	SGGLLGILEN VOSPDGHRLY	LPLLDILKPG VTIPLGIKLQ LLDGLGPLPI	GGTSGGLLGG VNTPLVGASL	LEGKVTSVIP	GLENIIDIKV AEILAVRDKO	TDPQLLELGL ERIHLVLGDC	120 180 240
75	Nucleic Ac	532 DNA sec id Accession Lence: 115.	#: NM_004	363.1			
	1	11	21	31	41	51 	
80	TOCTGGAACT	AGGGAGGAAG CAAGCTCTTC CCCCTCCCCA CCTTCTGGAA	TCCACAGAGG	AGGACAGAGC	AGACAGCAGA	GACCATGGAG	60 120 180 240
85	TTCAATGTCG TTTGGCTACA GTAATAGGAA	CAGAGGGGAA GCTGGTACAA CTCAACAAGC CCCTGCTGAT	GGAGGTGCTT AGGTGAAAGA TACCCCAGGG	GTGGATGGCA CCCGCATACA	ACCOTCAAAT GTGGTCGAGA	CCAGCATCTT TATAGGATAT GATAATATAC	300 360 420 480

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			TGTGAATGAA	GAAGCAACTG	GCCAGTTCCG	GGTATACCCG	540
	GAGCTGCCCA	ACCOUNTMENT	CTCCAGCAAC	SACTOTABAC	CYGTYYGAGGA	CARGGATGCT	600
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5	TTCAATGTCA	CAAGAAATGA	CACAGCAAGC	TACAAATGTG	AAACCCAGAA	CCCAGTGAGT	780
	GCCAGGCGCA	GTGATTCAGT	CATCCTGAAT	GTCCTCTATG	GCCCGGATGC	CCCCACCATT	840
	TCCCCTCTAA	ACACATCTTA	CAGATCAGGG	GAAAATCTGA	ACCTCTCCTG	CCACGCAGCC	900 960
	GAGCTCTTTA	TOTOGRACAT	CACTGTGAAT	AATAGTGGAT	CCTATACGTG	CCAAGCCCAT	1020
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	CCCAAACCCT	TCATCACCAG	CAACAACTCC TCAGAACACA	AACCCCGTGG	AGGATGAGGA	TGCTGTAGCC	1140 1200
	CTCCCGGTCA	GTOCCAGGCT	GCAGCTGTCC	AATGACAACA	GGACCCTCAC	TCTACTCAGT	1260
	GTCACAAGGA	ATGATGTAGG	ACCCTATGAG	TGTGGAATCC	AGAACGAATT	AAGTGTTGAC	1320
15	CACAGCGACC	CAGTCATCCT	GAATGTCCTC	TATGGCCCAG	ACGACCCCAC	CATTTCCCCC	1380
	CONCORRACNO	ACTAPPOPPO	AGGGGTGAAC GCTGATTGAT	GGGAACATCC	AGCARCACAC	ACARGAGCTC	1500
	TTTATCTCCA	ACATCACTGA	GAAGAACAGC	GGACTCTATA	CCTGCCAGGC	CAATAACTCA	1560
20	GCCAGTGGCC	ACAGCAGGAC	TACAGTCAAG	ACANTCACAG	TCTCTGC3GA	GCTGCCCAAG	1620 1680
20	COCTCCATCT	CCAGCAACAA	CTCCAAACCC	CTGTGGGGGG	TABATOCTCA	GAGCCTCCCA	1740
	GTCAGTCCCA	CCCTCCACCT	GTCCAATGGC	AACAGGACCC	TCACTCTATT	CAATGTCACA	1800
	AGAAATGACG	CAAGAGCCTA	TGTATGTGGA	ATCCAGAACT	CAGTGAGTGC	AAACCGCAGT	1860
25	GACCCAGTCA	CCCTGGATGT	CCTCTATGGG GAACCTCAAC	CCGGACACCC	CCATCATTTC	TRACCCAGAC	1920 1980
23	CCGCAGTATT	CTTGGCGTAT	CAATGGGATA	CCGCAGCAAC	ACACACAAGT	TCTCTTTATC	2040
	COTABBATCS	CCCCLLATER	TRACGGGGGCC	TATGCCTGTT	TTGTCTCTAA	CITGGCTACT	2100
	GGCCGCAATA	ATTCCATAGT	CARGAGCATC CGGCATCATG	ACAGTCTCTG	CATCTGGAAC	TTCTCCTGGT	2160
30	TAGCAGCCCT	GGGGGAGTGT	CTTCATTTCA	GGAAGACTGA	CAGTIGUETT	GCTTCTTCCT	2280
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35	ACTGCACTCC	AGTCTGGCAA	CAGAGCAAGA	CTCCATCTCA	AAAAGAAAAG	AAAAGAAGAC	2580
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45	Seq ID NO: Protein Acc	533 Protein	n sequence NP_004354.1 21	31 1	ī	Ĭ-	60
	Seq ID NO: Protein Acc	533 Protein	n sequence NP_004354.1 21 TASLLTFWNP	31 PTTAKLTIES	TPPNVAEGKE	VLLLVHNLPQ	60 120
45 50	Seq ID NO: Protein Acc	533 Protei: cession #: ! 11 WCIPHQRLLL ERVDGNRQII NEEATGOFRV	n sequence NP_004354.1 21 TASILTFWNP GYVIGTQQAT YPELPKPSIS	31 PTTAKLTIES PGPAYSGREI SNMSKPVEDK	TPFNVABGKE IYPNASLLIQ DAVAFTCEPE	VLLLVHNLPQ NIIQNDTGFY TQDATYLWWV	120 180
	Seq ID NO: Protein Acc 1 MESPSAPPHR HLFGYSWYKG TLHVIKSDLY	533 Protei: cession #: 1 11 WCIPHQRLLL ERVIGINRQII NEEATGQFRV	n sequence NP_004354.1 21 TASLLTFWNP GYVIGTQQAT YPELPKPSIT	31 PTTAKLTIES PGPAYSGREI SMNSKPVEDK ASYKCTONP	TPFNVABGKE IYPNASLLIQ DAVAFTCEPE USARRSDSVI	VLLLVHNLPQ NIIQNDTGFY TQDATYLWWV LNVLYGPDAP	120 180 240
50	Seq ID NO: Protein Acc 1 MESPSAPPHR HLFGYSWYKG TLHVIKSDLV NNQSLPVSPR TISPLWTSYR	533 Protei: cession #: 1 11 WCIPHQRLLL ERVDGNRQII NEEATGQFRV LQLSNGNRTL LQLSNGNRTL SGENLNLSCH	n sequence NP_004354.1 21 TASLLTFWNP GYVIGTQQAT YPELPKPSIS TLPNVTRIDT AASNPPAQYS	31 PTTAKLTIES PGPAYSGREI SNNSKPVEDK ASYKCETQNP WFVNGTFOOS	TPFNVABGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT	VLLLVHNLPQ NIIQNDTGFY TQDATYLHWV LWVLYGPDAP VNNSGSYTCQ	120 180
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50	Seq ID NO: Protein Acc 1 - MESPSAPPHR HLFGYSWYKG TLEVIKSDLV NNOSLPVSPR TISPLNTSYR ARMSDTGLMR QSLPVSPRLQ QSLPVSPRLQ SPSYTTYRPG	533 Protei: cession #: 1 11 WCIPMORLLL ERVDGMRQII MEEATGGPRV LQLEMGMRTL SGEMINISCH TTVTTITVYA LSNDMRTLTL LYNDMRTLTL LYNDMSCHAA	n sequence NP_004354.1 21 TASLLTFWNP GYVIGTQQAT YPELPKPSIS AASNPPAQYS EPPKDFITSN LSVTRNDVGP LSVTRNDVGP LSVTRNDVGP	31 PTTAKLTIES PGPAYSGREI SMNSKPVEDKA ASYKCETON HFVNGTFOOS NSNPVEDEDA YECGIQNELS IDCHIQOHTO	TPPNVABGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILN ELFISNITEK	VLLLVHNLPQ NIIQNDTGFY TQDATYLHHV LNVLYGPDBY VNNSGSYTCQ WTTYLHHVMN VLYGPDDFTI NSGLYTCQAN	120 180 240 300 360 420 480
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50 55	Seq ID NO: Protein Acc 1 MESPSAPPHR HLPGYSWYKG TLEVIKSDLV NNOSLPVSPR ARMSDTGLMR QSLPVSPRLQ QSLPVSPRLQ QSLPVSPRLQ RSASGHSRTT LEVERELILLE	533 Protei: cession #: 1 11 WCIPMORLLL ERVDGMRGGII MEEATGQFRV LQLAMGHRTL LGHDMRTLTL UNLSLSCHAA VKTITVSAEL WOMBFLITVSAEL	n sequence MP_004354.1 21 TASLLTFWNP GYVIGTQQAT YPELPKPSIS TLFNUTRNDT EPPKPFITSN LSVTRNDVGP LSVTRNDVGP LSVTRNDVGP LSVTRNDVGP LSVTRNDVGP LSVTRNDVGP LSVTRNDVGP LSVTRNDVGP LSVTRNDVGP LSVTRNDVGP LSVTRNDARAYV	31 PTTAKLTIES PGPAYSGREI SNISKPVEDK ASYKCETONP MYNNSTPOOS MSNPVEDEDA MYROSTOME LOGNIQOSTO KPVEDKDAVA COIONSYSAN	TPPNVABGKE IYPNASILIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILN ELFISNITEK PTCEPEAQNT RSDPVILVUL	VLLLVHNLPQ NIIQNDTGFY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWVNN VLYGPDDPTI NSGLYTCQA TYLWWVNGQS YGPDTPIISP	120 180 240 300 360 420 480
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50 55 60 65 70 75	Seq ID NO: Protein Acc No:	533 Proteinesson #: 1 11 VICTIVICATION V	n sequence NF_004334.1 I SALLTFWNP GYVIGTOONT THENTITONT THENTITONT SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPPROFITS SPROFITS	31	TPRIVABGIE ITPRIVABGIE TPRIVAGIG ITPR	VILLUMNIEG NIIONTGEY TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT ACTITITIAN TOTAL TODATTIANT TODATT	120 180 300 360 420 480 560 660 120 180 360 360 480 480 660 660
50 55 60 65 70	Seq ID NO: Protein Acc No:	533 Proteinession #: 1 11 WOITHORLLL ENUDERNOIT REATORPH R	n Bequence FP_004354.1 21 TASLLTPWNP GYVIOTOONT TLENVTRENT TLENVTRENT TLENVTRENT TLENVTRENT PROPRIETE LSYTENDAP REPREPTIES SINNS SUPPAOYSH PROPRIETE ACAACTCAAC GYTGGGCAT ACAACTCAAC GYTGGGCAT ACAACTCAAC GYTGGGCAT ACAACTCAAC GYTGGGCAT ACAACTCAAC GYTGGGCAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCAGGAAAT ACAACTCAAC GCACACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAACTCAAC ACAACTCAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAAC ACAACTCAACTCAAC ACAACTCAACTCAAC ACAACTCAACTCAACTCAAC ACAACTCAACTCAACTCAACTCAACAC ACAACT	31	TPRIVABGIE ITPRIVABGIE TPRIVAGIG ITPR	VILLUMNIEG NIIONTGEY TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT ACTITITIAN TOTAL TODATTIANT TODATT	120 180 240 300 420 480 600 660 660 600 120 120 130 420 420 420 420 420 460 660
50 55 60 65 70 75	Seq ID NO: Protein Acc 1 Nospeap Print III, Nospeap Print III, Protein Acc III, Nospeap Print III, Protein Acc III, Nospeap Print III, Protein III, Nospeap IIII, Nospeap IIIIII, Nospeap IIII, Nospeap IIIIIIII, Nospeap IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	533 Proteinession #:1 11 11 12 MCIPHORELLE REVIDENCIA ENVIRONMENTAL LORNOMETICL LORNOM	n Bequence MP_00434.1 21 1 TASILTPREY GTYLOTOONS TOTYLOTOONS TLENVIRNIT AASEPPAOTS LOFFERDON MPACTOR	31	TPRIVABGIE ITPRIVABGIE TPRIVAGIG ITPR	VILLUMNIEG NIIONTGEY TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT ACTITITIAN TOTAL TODATTIANT TODATT	120 180 300 360 420 480 560 660 120 180 360 360 480 480 660 660
50 55 60 65 70 75 80	Seq ID NO: Protein Acc. Separate Separa	533 Proteinession # 1 1	n sequence P_00434.1 21 ASILTTONIP YPELFRES TENTINE ASSIPPACES SIPPACES SIPPACES SIPPACES SIPPACES TOTALIS TOTALIS COLORADA COLORADA COLORADA AGATOCHAC AGATO	31	TPRIVABGIE ITPRIVABGIE TPRIVAGIG ITPR	VILLUMNIEG NIIONTGEY TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT TODATTIANT ACTITITIAN TOTAL TODATTIANT TODATT	120 180 300 360 420 480 560 660 120 180 360 360 480 480 660 660
50 55 60 65 70 75	Seq ID NO: Protein Acc. Separate Separa	533 Proteinession #:1 11 11 12 MCIPHORELLE REVIDENCIA ENVIRONMENTAL LORNOMETICL LORNOM	n sequence P_00434.1 21 ASILTTONIP YPELFRES TENTINE ASSIPPACES SIPPACES SIPPACES SIPPACES SIPPACES TOTALIS TOTALIS COLORADA COLORADA COLORADA AGATOCHAC AGATO	31	TPRIVABGIE ITPRIVABGIE TPRIVAGIG ITPR	VILLUMNIEG NIIONTGEY TODATTIANT TOTAL TOTAL TODATTIANT	120 180 300 360 420 480 560 660 120 180 360 360 480 480 660 660

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	MAKDNSTVRC	FOGLLIFGNV	IIGCCGIALT MKSSRKILLA	AECIFFVSDQ	HSLYPLLEAT	DNDDIYGAAN	60 120			
	ELKOMI-ERVO	MMSDDMMDDO	WEDNGVIKTW	DRIMIODNCC	GVNGPSDWOK	YTSAFRTENN	180			
5	DADYPWPRQC	CAMMITKELT	NLEACKLGVP	GFYHNQGCYE	LISCPMNRHA	WGVAWFGFAI	240			
3	LCWTFWYLLG TMFYWSRIEY									
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	Nucleic Acid Accession #: NMM_002638.1 Coding sequence: 120473									
10										
	1	11	21	31	41	51				
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15			GTATGGCCTT		CAAACACCTT		120 180			
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	TCAATGGACA	AGATCCCCTT	AAAGGACAAG	TTTCAGTTAA	AGGTCAAGAT	AAAGTCAAAG	300			
			CCCCCTAACC				360 420			
20	TCAAGAAGTG	CTGTGAAGGC	TCTTGCGGGA	TGGCCTGTTT	CGTTCCCCAG	TGAAGGGAGC	480			
	COOFFICE	TOTACCTOTO	CCGTCCCCAG	ACCTACAGGC	CCCATCTGGT	CCTAMGTOCC	540 600			
			TTTCCAATAA		ATTUAGGATG	CCCACGGCIG	600			
25										
25	Seq ID NO:	537 Protein	n sequence							
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	1	11	21	31	41	51				
30	MRASSFLIVV	VFLIAGTLVL	EAAVTGVEVK	GODTVKGRVP	FNGQDPVKGQ	VSVKGQDKVK	60			
	AQEPVKGPVS	TKPGSCPIIL	IRCAMLNPPN	RCLKDTDCPG	IKKCCEGSCG	MACEVEO				
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25	Nucleic Ac:	id Accession	n #: NM 001	793.2						
35	Coding sequ	uence: 71	2560							
	1	11	21	31	41	51				
		or compress	GAACACCCCC	one common	GGCAGCTGCT	TCACCCCTCT	60			
40	CTCTGCAGCC	ATGGGGCTCC	CTCGTGGACC	TCTCGCGTCT	CTCCTCCTTC	TCCAGGTTTG	120			
	CTGGCTGCAG	TGCGCGGCCT	CCGAGCCCTC	CCGGGCGGTC	TTCAGGGAAGG CTGGGGAAAG	CTGAAGTGAC	180 240			
	CTGCCCTGGG	GGAGGCGCGG CAAGAGCCAG	CTCTGTTTAG	CGGCCAGGCG	GATGACTICA	CTGTGCGGAA	300			
4.5	TGGCGAGACA	GTCCAGGAAA	GAAGGTCACT	GAAGGAAAGG	AATCCATTGA	AGATCTTCCC	360			
45	ATCCANACGT	ATCTTACGAA	GACACAAGAG TCCCCCAGAG	AGATTGGGTG	GTTGCTCCAA		420 480			
	AGACACCAAG	ATTTTCTACA	GCATCACGGG	GCCGGGGGCA	GACAGCCCCC	CTGAGGGTGT	540			
	CTTCGCTGTA	GAGAAGGAGA	CAGGCTGGTT TTGGCCACGC	GTTGTTGAAT	AAGCCACTGG	ACCGGGAGGA	600 660			
50	CCCCATGAAC	ATCTCCATCA	TCGTGACCGA	CCAGAATGAC	CACAAGCCCA	AGTITACCCA	720			
	GGACACCTTC	CGAGGGAGTG	TCTTAGAGGG	AGTCCTACCA	GGTACTTCTG	TCATGCAGGT	780 840			
	GACAGCCACG	GATGAGGATG	ATGCCATCTA ACCCACACGA	CACCTACAAT	ACCATTCACC	GGAGCACAGG	900			
	CACCATCAGC	GTCATCTCCA	GTGGCCTGGA	CCGGGAAAAA	GTCCCTGAGT	ACACACTGAC	960			
55			ATGGGGACGG		ACGGCAGTGG CAGAAGTACG	CAGTAGTGGA	1020			
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	CAACTCACCA	GCGTGGCGTG	CCACCTACCT	TATCATGGGC	GGTGACGACG	GGGACCATTT	1200			
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	GCTGAAGCTC	CCAACCTCCA	CAGCCACCAT	AGTGGTCCAC	GTGGAGGATG	TGAATGAGGC	1380			
	ACCTGTGTTT	GTCCCACCCT	CCAAAGTCGT	TGAGGTCCAG TGACAAGGAG	GAGGGCATCC	CCACTGGGGA TCAGCTACCG	1440 1500			
	CATCCTGAGA	GACCCAGCAG	GGTGGCTAGC	CATGGACCCA	GACAGTGGGC	AGGTCACAGC	1560			
65	TGTGGGCACC GGTCTTGGCC	CTOGACCGTG ATGGACAATG	AGGATGAGCA	GTTTGTGAGG CACCACTGGC	AACAACATCT	ATGAAGTCAT	1620 1680			
	ACTGATTGAT	GTCAATGACC	ATGGCCCAGT	CCCTGAGCCC	CGTCAGATCA	CCATCTGCAA	1740			
	CCAAAGCCCT	GTGCGCCAGG	TGCTGAACAT	CACGGACAAG	GACCTGTCTC	CCCACACCTC	1860			
70			CAGATGACTC TGTCCCTGAA				1920			
	GCACCTTTCT	CTGTCTGACC	ATGGCAACAA	AGAGCAGCTG	ACGGTGATCA	GGGCCACTGT	1980			
	GTGCGACTGC	CATGGCCATG	TOGARACCIG	CCCTGGACCC	TOGRAGOGAG		2040			
	GAGAAAGAAG	COGRAGATCA	AGGAGCCCCT	CCTACTCCCA	GAAGATGACA	CCCGTGACAA	2160			
75	CGTCTTCTAC	TATGGCGAAG	AGGGGGGTGG CCAGGCCGGA	CGAAGAGGAC	CAGGACTATG		2220			
	CATCATCCCG	ACACCCATGT	ACCUTCCTOS	GCCAGCCAAC	CCAGATGAAA	TOGGCAACTT	2340			
	TATAATTGAG	DECCTORAGG	CGGCTAACAC	AGACCCCACA	GCCCCGCCCT	ACGACACCCT	2400			
80	CTCCGCCTCC	GACCAAGACC	GCAGCGGCTC AAGATTACGA	TTATCTGAAC	GAGTGGGGCA	GCCGCTTCAA	2460 2520			
50	GAAGCTGGCA	GACATGTACG	GTGGCGGGGA	GGACGACTAG	GCGGCCTGCC	TGCAGGGCTG	2580			
	GGGACCAAAC	GTCAGGCCAC	AGAGCATCTC AGTGGCCGTA	CANGGGGTCT	CAGTTCCCCC	TATGAGTCTG	2640 2700			
	ACGTTAGAGT	GGTTGCTTCC	TTAGCCTTTC	AGGATGGAGG	AATGTGGGCA	GTTTGACTTC	2760			
85	AGCACTGAAA	ACCTOTOGAC	CTGGGCCAGG TCAACCCTGT	CTTGCCTCAG	AGGCCAAGTT	TCCAGAAGCC	2820 2880			
	TACAGTGGAC	TTTCTCTCTG	GAATGGAACC	TTCTTAGGCC	TOCTOGTGCA	ACTTAATTTT	2940			

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	TTTTTTTAAT	GCTATCTTCA	AAACGTTAGA	GANAGITCIT	CAAAAGTGCA	GCCCAGAGCT	3000		
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5	TAAAGAAACT	TTTCCCAGAA	AAAAA						
	Seq ID NO:	539 Protei	sequence						
10		cession #: 1	_						
10	1	11	21 	31	41 	51			
	MGLPRGPLAS	PPPTGACMPG		FREAEVILEA			60		
	QEPALFSTON	DDFTVRNGET LKSNKDRDTK	VQERRSLKER	NPLKIPPSKR	I LEKKHERDAV	VAPISVPENG	120		
15	YELFGHAVSE	NGASVEDPMN	ISIIVTDOND	HKPKFTODTF	RGSVLEGVLP	GTSVMQVTAT	240		
	DEDDALYTYN	GVVAYSIHSO	BPKDPHDLMP	TIHRSTGTIS	VISSGLDREK	VPEYTLTIQA	300		
	TOMOGDGSTT	TAVAVVEILD GDDGDHFTIT	ANDNAPHPDP	OKYEAHUPEN	AVGHEVQRLT	WTDLDAPNSP	360 420		
	PTSTATIUUH	VECVNEAPVF	VPPSKVVKVO	RGIPTGEPVC	VYTAEDPDKE	NOKISYRILE	480		
20	DPAGNLAMDP	DSGQVTAVGT	LDREDEQFVR	NNI YEVMVLA	MDNGSPPTTG	TGTLLLTLID	540		
	VNDHGPVPEP	RQITICNQSP	VRQVLNITEK	DLSPHTSPFQ	AQLIDDSDIY	WTAEVNEEGD	600		
	TVVLSLKKFL	KQDTYDVHLS LVLLLLVRKK	PRINCENT	TVIRATVCDC	VGRRGGGRRD	ODVDITOLHR	720		
	GLEARPEVVL	RNDVAPTIIP	TPMYRPRPAN	PDBIGNFIIE	NLKAANTDPT	APPYDTLLVF	780		
25	DYEGSGSDAA	SLSSLTSSAS	DQDQDYDYLN	ENGSRFKKLA	DMYGGGBDD				
	Seq ID NO:	540 DNA se	guence						
	Nucleic Ac	id Accession	1 #: Eos se	quence					
10	Courne sed	Jencer I	-						
	1	11	21	31	41	51			
	NTG NG GTGC	AAAGACCCCG	ACAGGGGGGGG	GOOGGTOOGA	ggrammarc	cogggggggg	60		
	CGGGGCTCCC	CCTACCGGCC	AGACCCG33G	AGAGGCGCGC	GGAGGCTGCG	AAGGTTCCAG	120		
5	AAGGGCGGGG	AGGGGGGGCCC	GOGCGCTGAC	CCTCCCTGGG	CACCGCTGGG	GACGATGGCG	180		
	CTGCTCGCCT	TGCTGCTGGT GAGATCCAGA	CGTGGCCCTA	CCGCGGGGGG	GGACAGACGC ACCCTCACA	TACACTGACT	300		
	TOTCATOTT	GTGAGAGAGA	AAACACTITC	GAGTGCCAGA	ACCCAAGGAG	GIGCAAATGG	360		
	ACAGAGCCAT	ACTGCGTTAT	AGCGGCCGTG	AAAATATTTC	CACGITTITT	CATGGTTGCG	420		
10	AAGCAGTGCT	CCGCTGGTTG	TGCAGCGATG	GAGAGACCCA	AGCCAGAGGA	GAAGCGGTTT	480 540		
	CTCCTGGAAG	CACCTATCAA	CTCATCAGG	TTCABAGAAT	ATGCTGGGAG	CINCIGCAAT	600		
	AGCTGTGGTG	GGCTGTGGCT	GGCCATCCTC	CTGCTGCTGG	CCTCCATTGC	AGCCGGCCTC	660		
5	AGCCTGTCTT	GA							
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	Seq ID NO: 541 Protein sequence Protein Accession #: Eos sequence								
	Seq ID NO: Protein Ac	541 Protein Session #:	sequence Sos sequence	9					
	Seq ID NO: Protein Act	541 Protein Session #: 1	sequence Sos sequence 21	31	41	51			
50	Protein Ac	ression #: :	Sos seguence 21	31	1	Ī	60		
0	Protein Acc	11 AGGRRAPEGG	21 RGSPYRPDPG	31 RGARRLERFQ	KGGEGAPRAD	PPWAPLGTMA			
0	Protein Ac	11 AGGRRAPEGG PRVWTDANLT KIFPEFFMVA	21 RGSPYRPDPG ARQRDPEDSQ KQCSAGCAAM	31 RGARRLERFQ RTDEGENRVW ERPKPEEKRF	KGGEGAPRAD CHVCERENTF LLEEPMPFFY	PPWAPLGTMA BOONPRRCKW	120		
_	Protein Ac	11 	21 RGSPYRPDPG ARQRDPEDSQ KQCSAGCAAM	31 RGARRLERFQ RTDEGENRVW ERPKPEEKRF	KGGEGAPRAD CHVCERENTF LLEEPMPFFY	PPWAPLGTMA BOONPRRCKW	120		
-	Protein Acci 1 	11 AGGRRAPRGG PRWYDANLT KIFPRFFMVA FKEYAGSMGE	21 RGSPYRPDPG ARQRDPEDSQ KQCSAGCRAM SCGGLWLAIL	31 RGARRLERFQ RTDEGENRVW ERPKPEEKRF	KGGEGAPRAD CHVCERENTF LLEEPMPFFY	PPWAPLGTMA BOONPRRCKW	120		
-	Protein Acc	11 AGGRRAPRGG PRUWTDANLT KIFPRFFMVA FKEYAGSMGE 542 DNA se id Accessio	21	31 RGARRLERFQ RTDEGDNRVW ERPKPEEKRF LLLASIAAGL	KGGEGAPRAD CHVCERENTF LLEEPMPFFY	PPWAPLGTMA BOONPRRCKW	120		
_	Protein Acc	11	21	31 RGARRLERFQ RTDEGDNRVW ERPKPEEKRF LLLASIAAGL	KGGEGAPRAD CHVCERENTF LLEEPMPFFY	PPWAPLGTMA BOONPRRCKW	120		
5	Protein Acc	11 AGGRRAPRGG PRUWTDANLT KIFPRFFMVA FKEYAGSMGE 542 DNA se id Accessio	21	31 RGARRLERFQ RTDEGDNRVW ERPKPEEKRF LLLASIAAGL	KGGEGAPRAD CHVCERENTF LLEEPMPFFY	PPWAPLGTMA BOONPRRCKW	120		
5	Protein Act MRLQRPRQAP LLALLLYVAL TEPYCVIAAV LEGPPINSSV Seq ID NO: Nucleic Ac Coding sequence 1	11	21	31 RGARRLERFQ RTDEGONRVW ERPKPEEKRF LLLASIAAGL	KGGEGAPRAD CHVCERENTF LLEEPMPFFY SLS	PPWAPLGTMA PCQNPRRCKW LKCCKIRYCN	120		
5	Protein Act	11	21	31 GARRLERFO RGARRLERFO RTDEGINRW ERPREEERF LLLASIAAGL 3292.2 31 AggCCOGGCC	KGGBGAPRAD CHVCERENTF LLBEPMPFFY SLS	PPWAPLGTMA POMPRESW LKCCKIRYCN 51 GCATGGCGGG	120		
5	Protein Act MRLQRPRQAP	11	21	31 RGARRLERFO RTDEGENRVW ERPKPEERFF LLLASIAAGL 5292.2 31 AGGCCOGGCC GCCGGCGGCGC CGGCTGGCGCGCGCC	KGGBGAPRAD KGGBGAPRAD CHVCBRENTF LLEEPNPPFY SLS 41 GGTGCGCAGA GAGGAGAAG CCGCCCAGGGG	PPWAPLOTMA PONPRECKW LKCCKIRYCN 51 GCATGGCGGG AAGAGGCGCG AAGAGGGGGGG	120 180 180		
55	Protein Act	11	ZOS SEQUENCI Z1	31 RGARRIERFPQ RTDEGDINRW ERPKPEEKRF LLLASIAAGL 5292.2 31 AGGCCCGGCC GCCGCCGCCC GCCGCCGCCC	KGGEGAPRAD CHVCERENTF LLBEPMPFFY SLS 41 0GTGCGCAGA GAGGAGAAG GCCAGCATOG	PPWAPLGTMA PCONPRECSW LKCCKIRYCN 51 GCATGGCGGG AAGAGGCGGG AAGAGGCGAGGT TGGGGACCAT	120 180 180 120 180 240		
55	Protein Act MRLQRPRQAP LALLLWVAL MRLQRPRQAP LALLLWVAL TEPYCVIAAV LEGPPINSSV Seq ID No: Nucleic Ac Coding seq GCTCGCTGGG GCGGGGCCCG GGAGAAGATG GGTACCCTG TAYGGGCTTOG	11	21	31 RGARRLERFO RTDEGINEW ERPREEERF LILASIAAGL 5292.2 31 AGGCCCGGCC GCCGGCCGGCC CACCGCCTGGCG CACCGCCTGGCG GGCCTGGCTG	KGGBGAPRAD CHVCBRENTF LLBEPNPFFY SLS 41 GGTGCGCAGA GAGGAGAAGG CCGGCAGCG GCCATCATCG GCATCATCG	PPWAPLOTHA BOONPRECKW LKCCKIRYCN 51 GCATGGCGGG AGGGCGACGAT TGGGGACCAT GCTCGCCGGG	120 180 180 120 180 240 300		
55	Protein Act I MRLQRPRQAP LLALLUVAL TEPYCVIAAV LEOPPINSSV Seq ID NO: Nucleic Ac Coding seq I GCTC3CTGGG GGAGAAGATG GGGGGGCTG GCTGGGGGCTG GCTGGGGGTC	11 AGGRAPRGG PRIVITDANLT KIFPRFPNVA FKEVAGSNGE 542 DNA se id Accessio uence: 53 11 COGCOGCTCC AACCGGCGCA CAGCGGCACCA GGCARCTGGCGCGCA GGCACCACCA	21	31 RGARRLERFO RTDEGINEW ERPKPEERFF LLLASIAAGL 5292.2 31 AGGCCOGGCC CGCCTCGGCC CACCGCCTG GGCCTGCTC CGTCTTCTCC GGCCGTCGCCC	41 	PPMAPLGTMA BOONPERCON LKCCKIRYCN 51 GCATGGCGGG AAGAGGCGGG AGGGCGACGAT GCTGGCGGG CGTTTGCTTGCTA	120 180 120 120 180 240 360 420		
i5 i0	Protein Act MRLQRPRQAP LEALLLYVAL TEPYCVIAW LEADPINSOV Seq ID NO: Nucleic Ac Coding seq: GCTCGCTGGG GGGGAGCCG GAGAAGATC GCTGGCCCG GATGGCCCG GCTGGCCCG GCTGGCCCG GCTGGCCCG GCTGGCCCG GCTGGCCTGC GCTGGCCTGC GCTGGCCTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	11	ZOS SEQUENCE 21 RESPYRPIPE RESPYRPIPE ROSCILLA ROCCIONA ROCCIO	31 RGARRLERFO RTDEGDIRVM ERFERSERF LLLASIANGL 5292.2 31 AGGCCCGGCC GCCCGGCCG GCCCGCCC GGCCTGGCCG GGCCTGCCC GGCCTGCCCG GGCCTGCCC GGCCTGCCC GGCCTGCCC GGCCTGCCC GGCCTGCCC GGCCTGCCC GGCCTGCCC	41. OGTECGCAGA ANGARGANG ANGARGANG ANGARGANG CONCENTOR ANGARGANG ANGARG ANGARGANG ANGARG ANGARGANG ANGARG	PPMAPLOTMA BOONPRRCW LKCCKIRYCN 51 GCATGGCGGG AGGGCGAGGG TGGGGACCAT GCTGGCGGG GCTCTGCTA TGCTGGAGGTT TCCGGCGTTC	120 180 120 180 240 300 420 480		
i5 i0	Protein Act I	11 AGGRAPROS AGGRAPAROS AGGRAPAROS AGGRAPAROS AGGRAFATANLT AGGRAFATAN	20 sequence 21 1 RESPYRPDEG XXCSAGCAM XXCSAGCAM XXCSAGCAM XXCSAGCAM XXCSAGCAM 21 10 COSTAGCAC XXCSAGCAC XX	31 RGARRLERFO RTDBGDNRW ERPKPEERK LLLASIAAGL 5292.2 31 AGGCCOGGCC GCCGGCGGCC CAGCGGCGCC CAGCGGCGCC CAGCGGCCC CAGCGGCCC CGCCTTCTCC CGCCTTCTCC CGGCGGGCCC CGGCGGCGCC CGGCGGCCC CGGCGGCCC CGGCGGCCC CGGCGCGCCC CGGCGCGCCC CGGCGCGCCC CGGCGCGCCC CGGCGCGCCC CGGCGCGCCC CGGCGCCCCC CGCCTCCCCC	41.	PPMAPLGTMA BOONPERCON LKCCKIRYCN 51 GCATGGCGGG AGGGCGAGGG GCCTCGCCGGG TCGCGGGGT TCCGGCGTT TCTTCCCCAC	120 180 120 180 240 300 420 480 540		
5 0	Protein Act I	11 AGGRAPAGG PRWYDANLY KIEPBERWYA SHE KEYAGSIMGE 542 DNA sedd Accessio Lucnoc 53 1 CCGCGGCTCC AAGGGGGGG CTGCCGCCA AGGGACTCC AGGGACACA CAAGGGGACACA AGGCACACACA CAAGGGACACACA ATGGGGGCGCCA ATGGTGGGGG	20 sequence 21 21 21 22 23 24 25 25 25 27 27 27 27 27 27 27 27 27 27 27 27 27	31 RCARPLERFO RTDEQDIRW ERPKFESKF LLLASTANGL 5292.2 31 AGGCCCGGCC GCCGGCCGGC GCCGGCCGGC GGCGGCGG	41.	PPMAPLOTMA BOON PRECKM LKCCKIRYCN 51	120 180 120 180 240 360 420 480 660		
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COCCOMICA ACAPAGOOAG GAGGOOGAGE GGCEGCCGGA GGAGCATGC Ser ID NO: 543 Protein sequence Protein Accession #: XP 035292.2 MAGAGPERRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLORNI TLLNGVAIIV GTIIGSGIFV TPTGVLKBAG SPGLALVVWA ACGVFSIVGA LCYAELGTTI SKSGGDYAYM 120 10 LEVYGSLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL PPTCPVPEEA AKLVACLCVL LLTAVKCYSV KAATRVQDAF AAAKLLALAL IILLGFVQIG KGDVSNLDPN PSFEGIKLDV 180 240 GNIVLALYSG LPAYGGWNYL NEVTERMINE YRNLEMAIII SLEIVTLVYV LTNLAYFITL 300 STROMLSSEA VAVDPGNYHL GVMSWIIPVF VGLSCPGSVN GSLFTSSRLF FVGSREGHLP SILSMIHPOL LTPVPSLVPT CVMTLLYAPS KDIPSVINFF SFFNWLCVAL AIIGMIWLRH 420 15 RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWWEN KPKWLLOGIF STTVLCOKLM OVVPOET Sed ID NO: 544 DNA sequence Nucleic Acid Accession #: NM 005268.1 20 Coding sequence: 168..989 TANABAGCAA AAGAATTOGC GGCCGCGTCG ACACGGGCTT CCCCGAAAAC CTTCCCCGCT 25 TOTGGRITATG ARATTCARGO IGCTTGCIGA GTCCTATTGC CGGCTGCIGG GAGCGGGGAG
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC IGACGCGTGG GTCCACCATG AACTGGAGTA 120 180 TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240 TOTATOTA CTTCATCTTC COCCTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT 360 30 TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420 CATGCCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTCAG GAGAAGAGGC 480 ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT 600 TICTCHATGE GITCCACTCA TECTACCCCA ANTATATCCE CCCTCCTGTG GTCAAGTGCC 660 35 ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 220 TTTTCACCCT CTTCATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTCGAGC TCATCTACT GGTGAGCAAG AAAGCACAA GAGTGCATG GAGAAGGAAA GACTCACTCTTTCTT CAAACAAGAA GACCTCCTTT 780 840 CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCCTCC TCTCTTACCA GACCGCCCCC 960 4∩ GAGACCATGT GAAGAAACC ATCTTGTGAG GGGCTGCCTG GACTGGTCTG GCAGGTTGGG CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1020 1080 CATGRIGATAG GOGCAGGCAA GAGRAGAGGAT TCAGROGCTC TGGGRAGCCAG TTCCTAGTCC 1140 TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA GCTCGGTTTC CTTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC 45 Seq ID NO: 545 Protein sequence Protein Accession #: NP 005259.1 50 MNNSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVTA ERUWSDDHKD FDCNTRQPGC SNYCFDEFFP VSHYRLWALQ LILVTCPSLL VYMNVAYREV QEKRHREANG ENSGRLYLNP GKKRGGLWYT YVCSLYFKAS VDIAFLYVFH SFYPKYLLPP VYKCHADPCP NIVDCFISKP 120 SEKNIFTLEM VATABICILL NEVELIYEVS KECHECLAAR KACAMCTCHH PHGTTSSCKO 55 DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL Seq ID NO: 546 DNA sequence Nucleic Acid Accession #: NM 002391.1 Coding sequence: 26..457 60 31 CGGGCGRAGE AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCCTCC TCACCCTCCT CGCCCTGCTG GCGCTCACCT CCGCGGTCGC CAARAAGAAA GATAAGGTGA AGAAGGGCGG 120 65 CCCGGGGAGC GAGTGCGCTG AGTGGGCCTG GGGGCCCTGC ACCCCCAGCA GCAAGGATTG 180 COGOCITGGGT TICOGOJAGG GCACCIGGOG GGCCCAGACC CAGCGCATCC GGTGCAGGGT GCCCTGCAAC TIGAAGAAGA AGTTTGGAGC GGCCCAGAAC ACAAGTTC AGAACTAGGGT TGCGTGTGATA GGGGGCAAG GCACCAAAGT CGCCAAAGA ACAAGTTCAAAAA 240 300 CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCCA AGACCAAAGC 420 70 ARAGGCCARA GCCARGRANG GGRAGGGANA GGRCTAGROG CCRAGGCTGG ATGCCRAGGR 480 GOCCOTGGTG TOACATGGGG COTGGCCACG COCTCCCTCT CCCAGGCCCG AGATGTGACC 540 CACCAGRACC TECTOSCONIC TORTAGEST TARTCANCA TOCCCONICCE TOTCCCTCTC 600 ACTOCCCAGO CCCACOCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660 TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTCTTCCTCC CCACAATTCC 75 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCCCC CAATAAAAGC TCTTCTTTTT 780

Seq ID NO: 547 Protein sequence Protein Accession #: NP_002382.1 1 11 21

Sen ID NO: 548 DNA sequence

TABTAT

WO 02/086443 Nucleic Acid Accession #: NN 006783.1

	Nucleic Acid Accession #: NM_006783.1 Coding sequence: 1786								
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10	DESCRIPTION OF SECOND	GCTATGACCA TCTCCACCCC GCAAGTTCAG ACAAGGTTCG	CTTTTTCYYG	CTCTCCCACA	TYCCGGCTGTG	GGCCCTCCNG	240 300 360		
	TTTTTCCGAA	ACAAGGTTCG TCATCTTTGA CCTGGGTGTT	AGCAGCCITT	ATGTATGTGT	TTTACTTCCT	TTACAATGGG	420 480 540		
15	ATTTGCATGC AGATCAAAGA CAGAATGAAA	GGCCAACAGA TGCTTAACGT GAGCACAGAC TGAATGAGCT	GAAGACCGTG GGCAGAGTTG GCAAAAAAAT	TITACCATTT TGCTACCTGC CACCCCAATC	TEATGATTTC TGCTGAAAGT ATGCCCTAAA	GEGTETTAGG GGAGAGTAAG	600 660 720 780		
20	AGCTAA								
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30	KNVCYDHFFP IKKHKVRIEG FISRPTEKTV	VSHIRLWALQ SLWNIYTSSI FTIFMISASV SGQNAITGFP	LIFVSTFALL FFRIIFEAAF ICMLLHVAEL	VAMHVAYYRH MYVFYFLYNG	TTRKFRRGE YHLPWVLKOG	KRNDFKDIED IDPCPNLWDC	120 180 240		
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	Nucleic Ac:	550 DNA sec d Accession	: #: NM_002	571.1					
35	Coding sequ	ience: 99!	587						
	1	11	21	31	41	51			
	CATCCCTCTG	GCTCCAGAGC	TCAGAGCCAC	CCACAGCCGC	AGCCATGCTG	TGCCTCCTGC	60		
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-10	ACATCTCCCT	CATGGCGACA	CTGAAGGCCC	CTCTGAGGGT	CCACATCACC	TCACTGTTGC	240		
	AGAAGAAGGT	GGACAACCTG	AAGACTGGGA	ATCCAAAGAA	GTTCAAGATC	AACTATACGG	360		
45	TGGCGAACGA	GGCCACGCTG CACCCCCATC	CTCGATACTG	ACTACGACAA	TTTCCTGTTT	CTCTGCCTAC	420 480		
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60	WENNSCVEKK	VLGEKTGNPK	KFKINYTVAN	EATLLDTDYD	NFLFLCLQDT	EDNLEIVLHR TTPIQSMMCQ	60 120		
00		EINQGFIRAF		PDPXCMREAC	RF				
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65	Coding sequ	ience: 27	1967						
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	ACTIGOGICI	CGCCCTCCGG	CCAAGCATGG	GGCTTCCCAG	GCTGGTCTGC	OCCTTCTTGC	60		
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80	TUGTTAAAGA GGAACCACAT	AGACAAAGAT GAAGGAGTCC	ACCCAGTTTT	CCGTCCCTCT	TTTCTACCOG	ACAGAAAAAG	720 780		
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WO 02/086443 TTCMGTTGCR TGACCTGAAA CGGGAGGCAG GAGGCGGCTA TCGCTGCGTG GCGTCTGTGC 1260 GGATGGCATT CANGGAGAGG AAGGTGTGGG TGAAAGAGAA TATGGTGTTG AATCTGTCTT GTGAAGGGTC AGGGCACCCC CGGCCCACCA TCTCCTGGAA CGTCAACGGC ACGGCMAGTG 1440 AACAAGACCA AGATCCACAG CGAGTOCTGA GCACOCTGAA TGTOCTCGTG ACCCCGGAGC 1500 TOTTGGAGAC AGGTGTTGAA TGCACGGCCT CCAACGACCT GGGCAAAAAC ACCAGGATCC
TCTTCCTGGA GCTGGTCAAT TTAACCACCC TCACACCAGA CTCCAACACA ACCACTGGCC 1560 1680 TOAGCACTTC CACTGOCAGT COTCATACCA GAGCONACAG CACCTOCACA GAGAGAAAGC TGCCGGAGCC GGAGAGCCGG GGCGTGGTCA TCGTGGCTGT GATTGTGTGC ATCCTGGTCC 1746 10 TOGCOGTOCT GOSCOCTOTC CTCTATTICC TCTATAGAA OGGCAAGCTG CCGTGCAOGC 1 90 0 GCTCAGGGAA GCAGGAGATC ACGCTGCCCC CGTCTCGTAA GACCGAACTT GTAGTTGAAG 1860 TTAACTCAGA TAAGCTCCCA GAAGAGATGG GCCTCCTGCA GGGCAGCAGC GGTGACAAGA 1920 TRANSTOCKS ASSOCIATED STATEMENT OF THE S 1980 2040 15 CCTCCAAAGG GACTAGAGAG AAGCCTCCTG CTCCCCTCAC CTGCACACCC CCTTTCAGAG GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCCGCTTT TCAGGGACCA 2100 2160 GTCCACCACC ATCTCCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCCAGTCTC CCGACCGGT AGGAGAGTTT CTTGCAGAAC GTGTTTTTTC TTTACACACA TTATGGCTGT 2280 AAATACCTGG CTCCTGCCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTGG TTTCCTGCCC 2340 20 CARACGCTGG CTTCCACCAT CCAGGTGCAC CACTGAAGTG AGGACACACC GGAGCCAGGC 2400 GCCTGCTCAT GTTGAAGTGC GCTGTTCACA CCCGCTCCGG AGAGCACCCC AGCGGCATCC
AGAAGCAGCT GCAGTGTTGC TGCCACCACC CTCCTGCTG CCTCTTCAAA GTCTCCTGTG 2460 ACATTITIC TITGGTCAGA AGCCAGGAAC TGGTGTCATT CCTTAAAAGA TACGTGCCGG 2580 GGCCAGGTGT GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GGCGGGCGGA 2640 25 TCACAAAGTC AGGACGAGAC CATCCTGGCT AACACGGTGA AACCCTGTCT CTACTAAAAA 2700 TCACAMARIC AGACCARAC CATCCTGGCT AACAGGTGA AACCCTGTCT CTACTAANAA 2706
TACAMAARA ARTHAGCTAG COTAGTGT GGGCGCCTA TACTCCAGCT ACTCGAAACA
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2940 30 TCCCCGTGTT CACTTGCTCC CATAGCCCTC TTGATGGATC ACGTAAAACT GAAAGGCAGC 3000 GGGGAGCAGA CANAGATGAG GTCTACACTG TCCTTCATGG GGATTANAGC TATGGTTATA 3060 TTAGCACCAA ACTTCTACAA ACCAAGCTCA GGGCCCCAAC CCTACAAGGG CCCAAATGAG AGAATGGTAC TTAGGGATGG AAAACGGGGC CTGGCTAGAG CTTGGGGTGT GCTACATAT GGTGTATATA TAGGTTTTTGT CAGGTGTGTA AATTTGCAAA 3120 3180 35 3300 AAAGCTTAAT TGTCCCAGAA AATCATACAT TGCTTTTTTA TTCTACATGG GTACCACAGG 3360 AACCTGGGGG CCTGTGAAAC TACAACCAAA AGGCACACAA AACCGTTTCC AGTTGGCAGC 3420 AGAGATCAGG GGTTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG CTACCCTACT TTTCAGCAGC AAAACGTCCC GTATGACGCA GCACGAAGGG CCTGGCAGGC 40 TGTTAGCAGG AGCTATGTCC CITCCTATCG TTTCCGTCCA CTT Seq ID NO: 553 Protein sequence Protein Accession #: NP 006491.1 45 31 41 61 GLPRIVCAPL LAACCCCPRV AGVPGEABQP APELVEVEVG STALLKCGLS QSQGNLSHVD WFSVHKEKRT LIFRVRQGQG QSEPGEYEQR LSLQDRGATL ALTQVTPQDE RIFLCQGKRP RSQEYRIQLR VYKAPEEPNI QVNPLGIPVN SKEPEEVATC VGRNGYPIPQ VIWYKNGRPL 180 50 KEEKNRVHIQ SSQTVESSGL YTLQSILKAQ LVKEDKDAQF YCELNYRLPS GNHMKESREV 240 TYPYPYPTEK VKLEVEPYGM LKEGDRVEIR CLADGNPPPH FSISKONPST REAEEETTHD 300 NGVLVLEPAR KENSGRYEGO ANNLDTMISL LSEPCELLVN YVSDVRVSPA APERCEGSSL TLTCERESSC DLEPCWLREE TDQVLERGPV LQLHDLKREA GGGYRCVASV PSIPCLMRTQ 420 LVKLAIPGPP WMAFKERKUW VKENMVLNLS CEASGHPRPT ISWNVNGTAS EQDQDPQRVL 480 55 STLMVLVTPE LLETGVECTA SMDLGRNTSI LFLELVNLTT LTPDSNTTTG LSTSTASPHT 540 RANSTSTERK LPEPESRGVV IVAVIVCILV LAVLGAVLYF LYKKGKLPCR RSGKQEITLP 600 PSRKTELVVE VKSDKLPEEM GLLQGSSGDK RAPGDQGEKY IDLRH Seq ID NO: 554 DNA sequence Nucleic Acid Accession #: NM_003183.3 60 Coding sequence: 165..2639 31 65 TOSAGOCTGG COGTAGAATC TTCCCAGTAG GCGGCGCGGG AGGGAAAAGA GGATTGAGGG GCTAGGCCGG GCGGATCCCG TCCTCCCCG ATGTGAGCAG TTTTCCGAAA CCCGTCAGG CGAAGGCTGC CCAGAGAGGT GGAGTCGGTA GCGGGCCCGG GAACATGAGG CAGTCTCTCC 120 180 TATTCCTGAC CAGCOTGGTT CCTTTCGTGC TGGCGCCGCG ACCTCCGGAT GACCCCGGCT TOGGCCCCCA CCAGAGACTC GAGAAGCTTG ATTCTTTGCT CTCAGACTAC GATATTCTCT 300 70 CTTTATCTAA TATCCAGCAG CATTCGGTAA GAAAAGAGA TCTACAGACT TCAACACATG 360 TAGAAACACT ACTAACTTTT TCAGCTTTGA AAAGGCATTT TAAATTATAC CTGACATCAA 420

GTACTGAACO TITTCACAA AATTCAAG TOGGGGGG GGGGGGAA AACGAAGGG AGTACACTGC AAAATGGCAG GACTTCTTCA CTGGACACGT GGTTGGTAGA CCGGACTCTA

GGGTTCTAGC CCACATAAGA GATGATGATG TTATAATCAG AATCAACACA GATGGGGCCG

AATATAACAT AGAGOCACTT TOGAGATTTG TTAATGATAC CAAAGACAAA AGAATGTTAG

TTTATAAATC TGAAGATATC AAGAATGTTT CACGTTTGCA GTCTCCAAAA GTGTGTGGTT

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AATTATTOGT GGTAGCAGAT CATCGCTTCT ACAGATACAT GGGCAGAGGG GAAGAGAGTA

CARCTACAAA TTACTTAATA GAGCTAATTG ACAGAGTTGA TGACATCTAT CGGAACACTT

AGTOTOGACA AGAGGTARAA COTGGTGARA AGGACTAGNA CATGGGRARA AGTTROCCAA

ATGRAGRARA GGATGCTTGG GATGTGRAGA TGTTGGTAGA GCARTTTAGC TTTGATATAG CTGAGGRAGC ATCTRAAGTT TGCTTUGCAC ACCTTTTCAC ATACCRAGAT TTTGATATGG

GAACTCTTGG ATTAGCTTAT GTTGGCTCTC CCAGAGCAAA CAGCCATGGA GGTGTTTGTC

CARAGGCITA THATAGCOCA GITGGGANGA ANANTATCIA TITGANTAGI GGITTGACGA GCACAAAGAA THATGGTANA ACCATCCITA CAAAGGANGC IGACCIGGIT ACAACTCAIG

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PCT/US02/12476

480 540

600

660

720

780

840

960

1020

1080

1200

1260

WO 02/086443

	W O 02/						
	AATTGGGACA	TAATTTTGGA	GCAGAACATG	ATCCGGATGG	TCTAGCAGAA	TGTGCCCCGA	1440
	ATGAGGACCA	GGGAGGGAAA	TATGTCATGT	ATCCCATAGC	TGTGAGTGGC	GATCACGAGA	1500
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		TTTTCAAGAA					1620
5	CACAACACTC	TGATCCTGGC	ATCATGTATC	TYGAACAACYGA	CACCIGCIGC	AACAGCGACT	1680
	GCACGTTGAA	GGAAGGTGTC	CAGTGCAGTG	ACAGGAACAG	TOCTTGCTGT	AAAAACTGTC	1740
	ACTITIONAL	TGCCCAGAAG	DOMODOCAGE	AGCCCATTAA	TOCTA CTTGC	ARAGGCGTGT	1800
	OGT LONGAC	AGGTAATAGC	ACTOROGOGO	COCCECCTO	A A TOCTORA	AATGACACTG	1860
		TCTTGGCAAG					1920
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10	AGCAGCTGGA	CCGCTGTGTG	TOTAATGAAA	CTGACAGCTC	CIGCINIGGIG	TGCTGCAGGG	2040
	ACCTITCTGG	CCGCTGTGTG	CCCTATGTCG	ATGCTGAACA	AAAGAACTIA	TITITONOGA	
		CTGTACAGTA					2100
	AGGATGTAAT	TGAACGATTT	TGGGATTTCA	TIGACCAGCT	GAGCATCAAT	ACTTTTGGAA	2160
1.0	AGTTTTTAGC	AGACAACATC	GTTGGGTCTG	TCCTGGTTTT	CTCCTTGATA	TTTTGGATTC	2220
15	CTTTCAGCAT	TCTTGTCCAT	TGTGTGGATA	AGAAATTGGA	TAAACAGTAT	GAATCTCTGT	2280
	CTCTGTTTCA	CCCCAGTAAC	GTCGAAATGC	TGAGCAGCAT	GGATTCTGCA	TCGGTTCGCA	2340
	TTATCAAACC	CTTTCCTGCG	CCCCAGACTC	CACCCCCCT	GCAGCCTGCC	CCTGTGATCC	2400
	CTTCGGCGCC	AGCAGCTCCA	AAACTGGACC	ACCAGAGAAT	GGACACCATC	CAGGAAGACC	2460
	CCAGCACAGA	CTCCCATATG	GACGAGGATG	GGTTTGAGAA	GGACCCCTTC	CCAAATAGCA	2520
20	COLCUCATION	CAAGTCATTT	GAGGATCTCA	COGACCATOC	GGTCGCCAGA	AGTGAAAAGG	2580
	CINCOLOCIA	TARACTGCAG	CGTCAGAATC	GTGTTAACAG	CAAAGAAACA	GAGTGCTAAT	2640
	TTLOTTOTOL	GCTCTTCTGA	CTTARGUERG	CARAGTATTT	TTATAGATTT	GACCTACAAA	2700
	monamon one	CTTGTATTTT	CTCARCACTO	CONNORMACE	TAGCAGATGC	TOOTCATORG	2760
	TORRICA CONTROL	CTGCAGGTAA	ACAGETCETG	TOTAL	CCCTTCTCT	TTTGAAAAGG	2820
25	TITOWICITE	GTGAATCTAC	MCMOTICITO	COMMUNICATION	CCC11C1CC1	BARAGATOTT	2880
23	TANGGTGAAA	GTGCAAAAGC	TIATITIONS	COMMON	OTTO TITT	VUUVIUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTU	2940
	TTGACCTGTG	TCTTTTATAT	AGAAAATACA	CTGGATTGG	GITATGAATA	COMMONOMORE	3000
	TGTAAATTAA	TCTTTTATAT	TGATAACHGC	ACTGACTAGG	GAMATGATCA	GIIIIIIIII	3060
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20	ATAGTTTTTT	TTTTTTTTT	TTTTTTTTCC	CITCAACTAA	AAACAAAGGA	GATAAATTTA	
30	GTATACATTG	TATCTAAATT	GTGGGTCTAT	TTCTAGTTAT	TACCCAGAGT	TTTTATGTAG	3180
	CAGGGAAAAT	ATATATCTAA	ATTTAGAAAT	CATTTGGGTT	AATATGGCTC	TTCATAATTC	3240
	TAAGACTAAT	GCTCAGAACC	TAACCACTAC	CTTACAGTGA	GGGCTATACA	TGGTAGCCAG	3300
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	TTTTATAAGT	ATCTTCATGT	ATCCCTGTTA	CTGATAGGGA	TACATGTCTT	AGAAAATTCA	3420
35	TTTTATAAGT	ATCTTCATGT	ATCCCTGTTA	CTGATAGGGA TAATCCCAGC	TACATGTCTT	AGAAAATTCA GCTGAGGTTG	3420 3480
35	CTATTGGCTG	GGAGTGGTGG	CTCATGCCTG	TAATCCCAGC	ACTTGGAGAG	AGAAAATTCA GCTGAGGTTG	
35	CTATTGGCTG	ATCTTCATGT GGAGTGGTGG CTCCAGCCTG	CTCATGCCTG	TAATCCCAGC	ACTTGGAGAG	AGAAAATTCA GCTGAGGTTG	
35	CTATTGGCTG	GGAGTGGTGG CTCCAGCCTG	CTCATGCCTG GGTGACAGAG	TAATCCCAGC	ACTTGGAGAG	AGAAAATTCA GCTGAGGTTG	
35	CTATTGGCTG CGCCACTACA Seq ID NO:	GGAGTGGTGG CTCCAGCCTG 555 Protein	CTCATGCCTG GGTGACAGAG m sequence	TAATCCCAGC	ACTTGGAGAG	AGAAAATTCA GCTGAGGTTG	
	CTATTGGCTG CGCCACTACA Seq ID NO:	GGAGTGGTGG CTCCAGCCTG	CTCATGCCTG GGTGACAGAG m sequence	TAATCCCAGC	ACTTGGAGAG	AGAAAATTCA GCTGAGGTTG	
35 40	CTATTGGCTG CGCCACTACA Seq ID NO: Protein Ac	GGAGTGGTGG CTCCAGCCTG 555 Protein cession #: 1	CTCATGCCTG GGTGACAGAG n sequence NP_003174.2	TAATCCCAGC TGAGATCTGC	ACTTGGAGAG CTC	GCTGAGGTTG	
	CTATTGGCTG CGCCACTACA Seq ID NO:	GGAGTGGTGG CTCCAGCCTG 555 Protein	CTCATGCCTG GGTGACAGAG m sequence	TAATCCCAGC	ACTTGGAGAG	AGAAAATTCA GCTGAGGTTG	
	CTATTGGCTG CGCCACTACA Seq ID NO: Protein Act	GGAGTGGTGG CTCCAGCCTG 555 Frotein cession #: 1	CTCATGCCTG GGTGACAGAG n sequence NP_003174.2	TAATCCCAGC TGAGATCTGC	ACITGGAGAG CTC	GCTGAGGTTG	3480
	CTATTGGCTG CGCCACTACA Seq ID NO: Protein Acc	GGAGTGGTGG CTCCAGCCTG 555 Protein cession #: 1 11 VVPFVLAPRP	CTCATGCCTG GGTGACAGAG n sequence NP_003174.2 21 PDDPGFGPHQ	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS	ACTTGGAGAG CTC 41 DYDILSLSNI	GCTGAGGTTG 51 QQHSVRKRDL	3480
40	CTATTGGCTG CGCCACTACA Seq ID NO: Protein Acc 1 	GGAGTGGTGG CTCCAGCCTG 555 Protein cession #: 1 11 VVPFVLAPRP TFSALKRHFK	CTCATGCCTG GGTGACAGAG n sequence NP_003174.2 21 PDDPGFGPHQ LYLTSSTERF	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD	ACTTGGAGAG CTC 41 DYDILSLSNI GNNESEYTAK	GCTGAGGTTG 51 QQHSVRKRDL WQDFFTGHVV	3480 60 120
	CTATTGGCTG CGCCACTACA Seq ID NO: Protein Act 1 MRQSLLFLTS GTSTHVETLL GEPDSRVLAH	GGAGTGGTGG CTCCAGCCTG 555 Protein cession #: 1 11 VVPFVLAPRP TFSALKRHFK IRDDDVIIRI	CTCATGCCTG GGTGACAGAG n sequence NF_003174.2 21 PDDFGFGFHQ LYLTSSTERF NTDGAEYNIE	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLMRFVNDTK	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRMLVYKSE	GCTGAGGTTG 51 QQHSVRKRDL MQDFFTGHVV DIKNVSRLQS	60 120 180
40	CTATTGGCTG CGCCACTACA Seq ID NO: Protein Acc 1 MRQSLLFLTS QTSTHVETLL GEPDSRVLAH PKVCSYLKVD	GGAGTGGTGG CTCCAGCCTG 555 Protein cession #: 1 11 VVPFVLAPRP TFSALKRHFK IRDDDVIIRI NEBLLPKGLV	CTCATGCCTG GGTGACAGAG n sequence NP_003174.2 21 PDDPGFGPHQ LYLTSSTERF LYLTSSTERF DREPFEELVH	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLMFFVNDTK RVKRRADPDP	ACTTGGAGAG CTC 41 DYDILSLSNI GNNESEYTAK DKRMLVYKSE MKNTCKLLVV	SI QQHSVRKRDL WQDFFTGHVV DIKNVSRLQS ADHRPYRYMG	60 120 180 240
40	CTATTGGCTG CGCCACTACA Seq ID NO: Protein Act 1 	GGAGTGGTGG CTCCAGCCTG 555 Frotein cession #: 1 11 VVPFVLAFRP TFSALKRHFK IRDDDVIIRI MEBLLPKGU LIBLIDRVDD	CTCATGCTG GGTGACAGAG m sequence NP_003174.2 21 PDDPGFGPHQ LYLTSSTERF NTDGAEYNIE DREPFEELVH LYRNTSNDNA	TAATCCAGC TGAGATCTGC 31 RLEKLDSLLS SONFKVVVVD PLMRPVNDTK RVKRRADPB GFKGYGIOIE	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRMLVYKSE MKNTCKLLVV QIRILKSPQE	SI QQHSVRKRDL WQDFFTGHVV DIKNVSRLQS ADHRFYRYMS VKPGEKHYNM	60 120 180 240 300
40	CTATTGGCTG CGCACTACA Seq ID NO: Frotein Act I MRQSLLFLTS GEPDSRVLAH PKVCGYLKVD RGEBSTTTNY AKSYENBERD	GGAGTGGTGG CTCCAGCCTG 555 Frotein ession #: 1 11 	CTCATGCCTG GGTGACAGAG sequence NP_003174.2 21 PDDPGFGPHQ LYLINSSTERF NTDGAEYNIE DREPPEELVH LYRNTSWDNA FSFDIAEBAS	TAATCCAGC TGAGATCTGC 31 RLEKLDSLLS SONFKVVVVD PLWRFVNDTK RVKRADPDP GFKGYGIQIE KVCLAHLFTY	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRMLVYKSE MKNTCKLLVV QIRILKSPQE QDFDNGTLGL	SI QQHSVRKRDL WQDFFYGHV DIKNVSRLQS ADHRPYRYMS VKPGEKHYNM AYVGSPRANS	60 120 180 240 300 360
40 45	CTATTGGTG GGCACTACA Seq ID NO: Protein Ac:	GGAGTGGTGG CTCCAGCCTG 555 Protein cession #: 1 11 VVPFVLAPRP TFSALKRHFK IRDDDVIIRI MEBLIPKGLV LIELIDRVDD AMDVMLLEG SPVGKMIYL	CTCATGCCTG GGTGACAGAG sequence NP_003174.2 21 PDDPGFGFHQ LYLTSSTERF NTDGAETNIE DREPFEELVH LYRNTSHENA FSFDIAEEAS FSFDIAEEAS	TAATCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLWRFVNDTK KVKSRADPDP GFKGYGIQIE KVCLAHLFTY	ACTTGGAGAG CTC 41 DYDILSLENI GKNESEYTAK DKRMLVYKLIV QIRILKSPQE QDFDNGTLGL LVTTHELGHM	GCTGAGGTTG 51 QQHSVRKRDL QQHSVRKRDL QQHSVRKRDL	60 120 180 240 300 360 420
40	CTATTGGTG GGCACTACA Seq ID NO: Protein Ac:	GGAGTGGTGG CTCCAGCCTG 555 Protein cession #: 1 11 VVPFVLAPRP TFSALKRHFK IRDDDVIIRI MEBLIPKGLV LIELIDRVDD AMDVMLLEG SPVGKMIYL	CTCATGCCTG GGTGACAGAG sequence NP_003174.2 21 PDDPGFGFHQ LYLTSSTERF NTDGAETNIE DREPFEELVH LYRNTSHENA FSFDIAEEAS FSFDIAEEAS	TAATCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLWRFVNDTK KVKERADPDP GFKGYGIQIE KVCLAHLFTY	ACTTGGAGAG CTC 41 DYDILSLENI GKNESEYTAK DKRMLVYKLIV QIRILKSPQE QDFDNGTLGL LVTTHELGHM	GCTGAGGTTG 51 QQHSVRKRDL QQHSVRKRDL QQHSVRKRDL	60 120 180 240 300 360
40 45	CTATTGGTG GGCACTACA Seq ID MO: Protein Act	GGACTGTGG CTCCAGCCTG 555 Frotein cession #: 1 11 VVPFVLAFRP TFSALKRHFK IRDDDVIIRI NEELLPKGLV LIBLIDRGLV ANDVKMLLEQ SPYGKKNIYL GKYWMPIAV	CTCATGCCTG GGTGACAGAG m sequence MP_003174.2 21 j PDDFGFGFHQ LYLTSSTERF NTDGAETWIE DREPFEELWH LYRMTSWINA FSFDIAERAS NSGLTSTKNY SGDMENNKMF	TAATCCAGC TGAGATCTGC 31	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE MKNYCKLLVV QIRILKSPQE QDFDNGTLGL LVTTHELGER TIESKAGECF	STI 	60 120 180 240 300 360 420
40 45	CTATTGGTG CGCACTACA Seq ID NO: Protein Ac: MRQSLLFLTS QTSTRVETLL GEPDSRVLAH PKVCGYLKVD RGESSTITNY AKSYPNEEKD HGGVCPKAYY ABCAPNEDQG SRVDBGEBECD	GGACTGGTGG CTCCAGCCTG 555 Protein cession #: 1 11 VVPFVLAPRP TFSALKRHFK IRDDDV1IRI NEELLPKGLV LIBLIDRVDD AWDVKMLES SPYGKKNIYL GKYWMYIJAV FGIMYLENDT	CTCATGCCTG GGTGACAGAG n sequence NP_003174.2 21 PDDPGFGPHQ LYLINSTERF NTDGAEVNIE DREPPEELVH IYRNTSMINA FSFDIAESA NSGLTSTKNY SGDRENNKMP CCNSDCTLKE	TAATCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLHEPVNDTK RVKRRADPDP GFKGYGIQIE KVCLAHLFTY GKTILTKEAD SNCSKGSIYK GVGCSDRNSF	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK MKNTCKLLVV QIRILKSRQE QDFDNGTLGL LVTTHELGEN TIESKAGECF CCKNCQFETA	51 QQHSVRKRDL WQDFFTGHVV DIRWYSRLQS ADHRFYRYMS VKSGEKHYNM AYVGSPRAMS FGAEHDPDCL QERSNRVCOM	60 120 180 240 300 360 420 480
40 45	CTATTGCTG CGCCACTACA Seq ID MO: Frotein Aci CTSTMVETLL GEPDSRVLAH PKVCSYLKVD RGGSESTITNY AKSYPNERGD GGGVCPKAYY AECAPNEDQG SRVDBGEBCD TCKGVSYCTG	GGAGTGGTGG CTCCAGCCTG 555 Frotein ession #: 1 11 VVPFVLAFRP TFSALKRHFK IRDDVIIRI NEBLLPKGLV LIBLIDRVDD AWDVMLLEQ SPVGKMILG SPVGKMILG GKYVMYPIAV FGINYLANDT MSSECPPFGM	CTCATGCCTG GGTGACAGAG m sequence MP_003174.2 21 PDDPGFGPHQ LYLINSTERF MTDGAEYNIE DREPFBELVH IYRNTSMINA FSFDIAERA NSGLISTRAN SGUSTENS SGDHENNKMF CCNBOCTIKE AENDTVCLDL	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS SONFKVVVVD PLMRFVMDTK RVKRRADPDP GFKCYGIQIE KVCLAHLFTY GKTLTKEAD SNCSKQSIYK GVQCSDRNSF	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE MKNTCKLLVY QIRILKSRQE QDFDNGTLGL LVTTHELGL LVTTHELGL TIESKAQECF CCNKCQFETA	51 QOHSVEKEDL QOHSVEKEDL QOHSVEKEDL QOHSVEKEDL QOHSVEKEDL QOHSVEKEDL QOHSVEKEDL QERSNEVOSH QUESTION Q	60 120 180 240 360 420 480 540 600
40 45 50	CTATTGCTG CGCCACTACA Seq ID NO: Frotein Act I MRQSLLPLTS QTSTHVETLL GEPDSRVLAH PKVCGTLAH MKSYENEEM KGGVCPKAYY AECAPNEDGG TCKGVSYCTG EVVCCEDLSGE	GGACTGGTGG CTCCAGCCTG CTCCAGCCTG 5:55 Frotein cession #:1 11	CTCATGCCTG GGTGACAGAG BEQUENCE NP_003174.2 21	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLMRFVNDTK RVKRRADPDP GFKCYGIQIE RVCLAHLFTY GKTILTKRAD SNCSKQSIYK GVQCSDRNSF GKCKDGKCIF TVGFCDNGK	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE QDFDNGTLGL LVTTHELGEN TIESKAGECF CCNNCQFETA FCEREQQUES CEKRYQOUS	51 QQHSVEKEDL WQDFFTGHVV DIRKVEKLYS ADREFYEYMS VKSGEKHYMM AYVGSPEANS FGAEDDDGL QERSNEVOL QERSNEVOL QERSNEVOL RECEDING CACCEDING CACCEDING CACCEDING	60 120 180 240 300 360 420 480 540 660
40 45 50	CTATTGCTG CGCCACTACA Seq ID NO: Protein Ac:	GGACTGGTGG CTCCAGCCTG 555 Frotein cession #: 1 11 VVFFVLAFRP TFSALKRHFK IRDDDVIIRI NEBLLPKGLVV LIBLIDEVDD AMDVMMLLEQ SPYGKNEILG SPYGKNEILG KYWMYPIAV PGIMYLANDT NSSECPPFGN CVPYVDARQK NIVGSVLVPS	CTCATGCCTG GGTGACAGAG n sequence pp_003174.2 21 PDDPGFGPHQ LYLTSSTERF NTDAGEYNE IYENTSNENA FSFDIAERA NSGLTSTENA SGGLESNENA CCNSDCTLA AENDTVCLDL NLFREKERFC LIFFIFFSIL	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLHRPVNDTK RVKERADPDP GFKGYGTQTE KVCLAHLPTY GKTLTKERAD SNCSKQSTYK GWQCSDRISK GWQCSDRISK GWQCSDRISK GWQCSDRISK VHCYDKKLDK	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE QHFDNGTLGL LVTTHELGEL LVTTHELGEL TIESKAQECF CCNCOCPET PCEREQQLES CEKRVQDVIE QYESLSLEHP	51 QOHSVEREDL WODFFTGHVV VKSGERIYM AYVCSPEAMS FGAEHDPOLL GERSNEVCON OKKCOEAINNA CACNETINNA CACNETINNA SEVERIFICAL	60 120 180 240 360 420 480 600 660
40 45	CTATTGCTG CGCCACTACA Seq ID NO: Protein Ac. 1	GGATGGTGG CTCCAGCCTG 5:55 Frotein 5:55 Frotein 5:55 Frotein 7:50 Frotein 11 11 12 12 12 13 14 15 15 16 16 16 16 16 16 16 16 16 16 16 16 16	CTCATGCCTG GGTGACAGAG GGTGACAGAG BEQUENCE BP_003174.2 21 PDDPGFGPHQ LYLTSSTERF NTDGAETNIE IYRNTSHINA FSFDIAESA NSGLISTNNY GGDMENNEY CCNSDCTLKE AENDTVCLDL LIFRIFSEL LIFRIFSEL LIFRIFSEL LIFRIFSEL LIFRIFSEL LIFRIFSEL LIFRIFSERA	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLMMFVMDTK GVKCAALPTY GKTLITKEAD GNCSKGSTYK GVQCSDRNSP GKCKGGKCIF TVGFCD90GK VHCVDKKLDK	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE QHENGTLGLLVV QIRILKSPQE QPFONGTLGL LVTTHELGEN TIESKAGEN CCKNVQDYETA FCEREQQUSE CCKNVQDYET QYESLSLEHP TIQEDPSITOS	51 QOHSVEREDL WODFFTGHVV VKSGERIYM AYVCSPEAMS FGAEHDPOLL GERSNEVCON OKKCOEAINNA CACNETINNA CACNETINNA SEVERIFICAL	60 120 180 240 300 360 420 480 540 660
40 45 50	CTATTGCTG CGCCACTACA Seq ID NO: Protein Ac. 1	GGACTGGTGG CTCCAGCCTG 555 Frotein cession #: 1 11 VVFFVLAFRP TFSALKRHFK IRDDDVIIRI NEBLLPKGLVV LIBLIDEVDD AMDVMMLLEQ SPYGKNEILG SPYGKNEILG KYWMYPIAV PGIMYLANDT NSSECPPFGN CVPYVDARQK NIVGSVLVPS	CTCATGCCTG GGTGACAGAG GGTGACAGAG BEQUENCE BP_003174.2 21 PDDPGFGPHQ LYLTSSTERF NTDGAETNIE IYRNTSHINA FSFDIAESA NSGLISTNNY GGDMENNEY CCNSDCTLKE AENDTVCLDL LIFRIFSEL LIFRIFSEL LIFRIFSEL LIFRIFSEL LIFRIFSEL LIFRIFSEL LIFRIFSERA	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLMMFVMDTK GVKCAALPTY GKTLITKEAD GNCSKGSTYK GVQCSDRNSP GKCKGGKCIF TVGFCD90GK VHCVDKKLDK	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE QHENGTLGLLVV QIRILKSPQE QPFONGTLGL LVTTHELGEN TIESKAGEN CCKNVQDYETA FCEREQQUSE CCKNVQDYET QYESLSLEHP TIQEDPSITOS	51 QOHSVEREDL WODFFTGHVV VKSGERIYM AYVCSPEAMS FGAEHDPOLL GERSNEVCON OKKCOEAINNA CACNETINNA CACNETINNA SEVERIFICAL	60 120 180 240 360 420 480 600 660
40 45 50	CRATTGGCTG GGCACTACA Seq ID NO: Protein Act	GGATTGGTGG TOCAGGCTG TOCAGGCTG S55 Protein LI VPPVLAFRP VVPFVLAFRP TFSALKRHFK IRDDDVIIRI NEBLLPKGLV LIBLIDENUD AMDVKMLLEQ SFVCKNNITAV CHYPYDARQK NIVGSULVFS ANGUSTUPFG SPACTEGRLQ SFEDLITHPV	GTCATGCCTG GGTGACAGAG n sequence NF_003174.2 21	TAATCCCAGC TGAGATCTGC 31 RLEKLDSLLS SQNFKVVVVD PLMMFVMDTK GVKCAALPTY GKTLITKEAD GNCSKGSTYK GVQCSDRNSP GKCKGGKCIF TVGFCD90GK VHCVDKKLDK	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE QHENGTLGLLVV QIRILKSPQE QPFONGTLGL LVTTHELGEN TIESKAGEN CCKNVQDYETA FCEREQQUSE CCKNVQDYET QYESLSLEHP TIQEDPSITOS	51 QOHSVEREDL WODFFTGHVV VKSGERIYM AYVCSPEAMS FGAEHDPOLL GERSNEVCON OKKCOEAINNA CACNETINNA CACNETINNA SEVERIFICAL	60 120 180 240 360 420 480 600 660
40 45 50	CHATTGGTG GGCACTACA Seq ID NO: Protein Ac. No: No	CAGATGGTGG CATCAGCCTG 555 Protein cesion #: 1 11 VVPFVLAPR TSFALKRERK IRRDDVIIER IRRD	CTCATGCTG GGTGACAGAG GGTGACAGAG GGTGACAGAG EP_003174.2 21 DDPGPGBHQ LVLTSSTERF NTCAGENIE DREPFELWH ITNYTSWIRM SGDHERNKWF CCNSECTLER AEBITYCLDL NIFLEKKGKPC LIPMIFFSIR LIPMIFFSIR ARSEKAASFK LUPMIFFSIR LUPMIFFSIR	TAATCCCAGE TGAGATCTGC 31 RLEKLDSLLS SONFOVOVOTO RVERFADEDE GFKOYGOTE KVCLAHLFTY GKTLTFKEADEDE GKCKOGKCIF TGAGCGENENG GKCKOGKCIF TGAGCGENENG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE QHENGTLGLLVV QIRILKSPQE QPFONGTLGL LVTTHELGEN TIESKAGEN CCKNVQDYETA FCEREQQUSE CCKNVQDYET QYESLSLEHP TIQEDPSITOS	51 QOHSVEREDL WODFFTGHVV VKSGERIYM AYVCSPEAMS FGAEHDPOLL GERSNEVCON OKKCOEAINNA CACNETINNA CACNETINNA EXCEPTIONS EXCEPTIONS	60 120 180 240 360 420 480 600 660
40 45 50 55	CHATTGGTG CAGCACTACA Seq ID NO: Protein Aci I MROSLLFLTS GEFSRVLAN GEFSRVLAN GEFSRVLAN GEFSRVLAN GESSTTIN AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON	GAGTGGTGG CTCCAGCCTG S55 Protein cesion #: 1 11 11 WPFYLAPRE TSRALKSHK* INDDVIINI MEBLIPKOLV LIELIENKOD ANDVAGLLEG SYCKNITIL GKYWHFIAV FROTEGLEG SYCKNITU MSSECPFON KIVGSTUPS SFEDLITHEN SFEDLITH SFEDLITH SFEDLITH SFEDLITH SFEDLITH SFEDLITH SFEDLITH S	CTCATGCTG GGTGACAGA n sequence NP_003174.2 21 pDPOPOPOPO LITERSTREE NTOCAGENTE NTOCAGENTE NTOCAGENTE NTOCAGENTE SCHEPESLAW SCHEPESLAW SCHEPESLAW SCHEPESLAW ARBOTYCLD ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE ARBOTYCLD LITERSTREE LITERSTRE	TAATCCCAGE TGAGATCTGC 31 RLEKLDSLLS SONFOVOVOTO RVERFADEDE GFKOYGOTE KVCLAHLFTY GKTLTFKEADEDE GKCKOGKCIF TGAGCGENENG GKCKOGKCIF TGAGCGENENG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE QHENGTLGLLVV QIRILKSPQE QPFONGTLGL LVTTHELGEN TIESKAGEN CCKNVQDYETA FCEREQQUSE CCKNVQDYET QYESLSLEHP TIQEDPSITOS	51 QOHSVEREDL WODFFTGHVV VKSGERIYM AYVCSPEAMS FGAEHDPOLL GERSNEVCON OKKCOEAINNA CACNETINNA CACNETINNA EXCEPTIONS EXCEPTIONS	60 120 180 240 360 420 480 600 660
40 45 50	CHATTGGTG CAGCACTACA Seq ID NO: Protein Aci I MROSLLFLTS GEFSRVLAN GEFSRVLAN GEFSRVLAN GEFSRVLAN GESSTTIN AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON	CAGATGGTGG CATCAGCCTG 555 Protein cesion #: 1 11 VVPFVLAPR TSFALKRERK IRRDDVIIER IRRD	CTCATGCTG GGTGACAGG n sequence NP_003174.2 21 pDPOPOPOPO LITERSTREE NTOCAGENTE NTOCAGENTE NTOCAGENTE SCHEPSELME ITRATESMENA FOFDIABAS AGENTYCLDI MELEKAMEN ARSEKAASEK LITMIFFSIL LITMIFFSI	TAATCCCAGE TGAGATCTGC 31 RLEKLDSLLS SONFOVOVOTO RVERFADEDE GFKOYGOTE KVCLAHLFTY GKTLTFKEADEDE GKCKOGKCIF TGAGCGENENG GKCKOGKCIF TGAGCGENENG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG AFKLDGKGRG	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE QHENGTLGLLVV QIRILKSPQE QPFONGTLGL LVTTHELGEN TIESKAGEN CCKNVQDYETA FCEREQQUSE CCKNVQDYET QYESLSLEHP TIQEDPSITOS	51 QOHSVEREDL WODFFTGHVV VKSGERIYM AYVCSPEAMS FGAEHDPOLL GERSNEVCON OKKCOEAINNA CACNETINNA CACNETINNA EXCEPTIONS EXCEPTIONS	60 120 180 240 360 420 480 600 660
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40 45 50 55	CHATTGGTG CAGCACTACA Seq ID NO: Protein Aci I MROSLLFLTS GEFSRVLAN GEFSRVLAN GEFSRVLAN GEFSRVLAN GESSTTIN AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON AKSINABOO TOKKON	GAGTGGTGG CTCCAGCCTG S55 Protein cesion #: 1 11 11 11 11 11 WPFYLAPR TSPALKSHK INDDVIINI MEBLIPKOLV LIBILITKUD ANDIVELLEG SYCKNITIL GKYWHFIAV FROTEGLU SEBULTERV SEBULTERV SEBULTERV SEBULTERV SEBULTERV SEBULTERV	CTCATGCTG GGTGACAGG n sequence NP_003174.2 21 pDPOPOPOPO LITERSTREE NTOCAGENTE NTOCAGENTE NTOCAGENTE SCHEPSELME ITRATESMENA FOFDIABAS AGENTYCLDI MELEKAMEN ARSEKAASEK LITMIFFSIL LITMIFFSI	TAATCCCAGE TGAGATCTGC 31 RLEKLDSLLS SONFKOVVVD RVERADPDP GFKOYGOTE KVCLAHLFTY GKTLTFKEAD SKCSKOSIYK GVCSDENGS GKCHOGKCIP TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	ACTTGGAGAG CTC 41 DYDILSLSNI GKNESEYTAK DKRHLVYKSE QHENGTLGLLVV QIRILKSPQE QPFONGTLGL LVTTHELGEN TIESKAGEN CCKNVQDYETA FCEREQQUSE CCKNVQDYET QYESLSLEHP TIQEDPSITOS	51 QOHSVEREDL WODFFTGHVV VKSGERIYM AYVCSPEAMS FGAEHDPOLL GERSNEVCON OKKCOEAINNA CACNETINNA CACNETINNA EXCEPTIONS EXCEPTIONS	60 120 180 240 360 420 480 600 660
40 45 50 55	CHATTGGENG GGCACTAGA Seq ID NO: Protein Aci 1 MGOSLLFLTS GEDBRYLAR FRYCCTIAND: RGESSTINY RGESTINY RGESTTINY RGESTT	GOAGTOGTOG COTCOAGCOTS 555 Proteinession #: 1 11 11 WYPFYLAPRP TYPSALKRHYK IRDDDYLIRI NEBLLEPKOL LIBLIDENVDD ARDVEMLES SPVGKNBITL GOKYVMFIJLANDT FOLHYLANDT FOLHYLANDT SPEDLITANDT SPE	CTCATGCCTG GGTGACGAGG Requence F003174.2 21 FDDF0F0F0F0F0 FDF0F0F0F0F0 FDF0F0F0FF0 FF0F0AEFN1E FFF0F0AEFN1E FFF0A	TANTOCOMC TORGATCTSC 31 RLEKLDSLLS SONFKOVUVUD FÜHREVNDTK FÜKRENDEN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN GEKORGTUN HENDEN LONG HENDEN LONG BERNENNEN 832.1	ACTTGGAGAG CTC 41 DYDILSUSHI GRMSSETTAK DERMLYTKSE DERMLYTT DERMLYTKSE DERMLYTT DER	S1 QCHSVRIKEDL	60 120 180 240 300 360 420 480 600 660 720 780
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AGGAAAGCCC TGTACAATAG GATTTTTTGA CATGAATAGC AAATGTGAGA AACGAGTACA 2040 2100 COATCTAATT GAACGATTIT GGGATTTCAT TGACCAGCTG AGCATCAATA CTITTGGAAA CITITITAGEA GACAACATEG TIGGGTETGT CETGGTTTTC TECTTGATAT TITTGGATTEE 2220 TTTCAGCATT CTTGTCCATT GTGTGTAACG TCGAAATGCT GAGCAGCATG GATTCTGCAT 2280 15 COGTTCGCAT TATCAAACCC TTTCCTGCGC CCCAGACTCC AGGCCGCCTG CAGCCTGCCC 2340 CTGTGATCCC TTCGGCGCCA GCAGCTCCAA AACTGGACCA CCAGAGAATG GACACCATCC 2400 AGGAAGACCC CAGCACAGAC TCACATATGG ACGAGGATGG GTTTGAGAAG GACCCCTTCC 2460 CAAATAGCAG CACAGCTGCC AAGTCATTTG AGGATCTCAC GGACCATCOG GTCACCAGAA 2620 GTGANAAGGC TGCCTCCTTT ANACTGCNGC GTCNGAATCG TGTTGACAGC ANAGANACNG 2580 20 AGEGCTAATT TAGETCECAG CECTECEGAC TEAGEGEGC AAAATATETT TATAGATETG 2640 ACCTACAATC AATCACAGCT TATATTTTGT GAAGACTGGG AAGTGACTTA GCAGATGCTG 2700 CHARTCHART ANICACHOCI ININITIOI GRANGETON ANIONCIA GENERACIO TGANAAGGTA AGGTGAAGGT GAATCTAGCT TATTTTGAGG CTTTCAGGTT TTAGTTTTTA ABATATCTTT TGACCTOTGG TGCARAAGCA GAAAATACAG CTGGATTGGG TTATGAGTAT 2880 25 TTACGTTTTT GTAAATTAAT CTTTTATATT GATAACAGGC ACTGACTAGG GAAATGATCA 2940 GTTTTTTTT ATACACTGTA ATGAACCGCT GAATATGAAG CATTTGGCAT TTATTTGTGA 3000 GAAAAGTGGA ATAGTITTIT TITTITTITT TITTITTITGC CITCAACTAA AAACAAAGGA GATABATTTA CTATACATTG TATCTAAATT GTGGGTCTAT TTCTAGTTAT TACCCAGAGT 3120 TTTTATGTAG CAGGGAAAAT ATATATCTAA ATTTAGAAAT CATTTGGGTT AATATGGCTC 210/ 30 3240 TTCATAATTC TAAGACTAAT GCTCAGAACC TAACCACTAC CTTACAGTGA GGGCTATACA TOGTAGCCAG TTGAATTTAT GGAATCTACC AACTGTTTAG GGCCCTGATT IGCTGGGCAG
TTTTTCTGTA TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCTT 3300 AGAMANTICA CTATTGGCTG GGAGTGGTGG CTCATGCCTG TARTCCCAGC ACTTGGAGAG 3421 GCTGAGGTTG CGCCACTACA CTCCAGCCTG GGTGACAGAG TGAGATCTGC CTC 35

Seq ID NO: 557 Protein sequence Protein Accession #: NP 068604.1

31 41 51 40 MRQSLLFLTS VVPFVLAPRP PDDPGFGPHQ RLEXLDSLLS DYDILSLSNI QQHSVRKRDL QUISTRUETLL TESALKRIPK LYLTSSTERF SQNFKUVVVD GKNESEYTVK WQDFFTGHVV GEPDSRVLAH IRDDVIIRI NTDGAEYNIE PLWRFVNDTK DKRMLVYKSE DIKMVSRLQS 180 PKVCGYLKVD NEELLPKGLV DREPPEBLVH RVKRRADPDP MKNTCKLLVV ADHRFYRYMG 45 ROBESTITNY LIELIDRYDD IYRNISHDNA GFKGYGIQIE QIRILKSPQE VKPGEKHYNM 300 AKSYPMEEKD AWDVKMLLEQ PSFDIASEAS KVCLAHLFTY QDFDMGTLGL AYVGSPRANS 360 AKSYPNEKU ANDARILEG FSFILZSKA KVCHAFFI (KTILTKEAD LVTTHELIGHN FOARHDPOIL AECAPNEDOG GKYNYPIAV SODHENNKMP SNCSKQSIYK TIESKAGECF GERSNKVCGN 480 SRVDEGEECD PGINYLANDT CONSDCTLKE GVQCSDRNSP CCKNCQFETA QKKCQEAINA 540 50 TOKSVSYCTG NSSECPPPON AEDDTVCLDL GKCKDGKCIP FCEREGGLES CACHETDISC KVCCRDLSGR CVPYVDAEQK MLFLRKGKPC TVGPCDMGK CEKRVQDVIE RFMDFIDQLS 600 660 INTEGRELAD NIVGSVLVPS LIPWIPFSIL VHCV

55 Seq ID NO: 558 DNA sequence Nucleic Acid Accession #: NM_004994.1 Coding sequence: 20..2143

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AACCACGACGACGACGC CCACGGCTCC CCCGACGGTC TGCCCCACCG GACCCCCAC 1380 TGTCCACCCC TCAGAGCGCC CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGGCCCCAC 1500 85 AGGICCCCCC ACTGCTGGCC CTTCTACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA 1560 TOCCTOCAAC OTGAACATCT TOGACGCCAT CGCGGAGATT GGGAACCAGC TGTATTTGTT 1620 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCCGGCCGC AGGGCCCCTT 1680

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	a						
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30	GGTTACTCAT GACGCCAAGG GATCTGGACT	CCTGGGCTCA GAGCAGGACG GCAGGCTGGC	GGTAAGAGGG GAGCCATGGA TGCTGCTGCT	CCCGAGCTCG CCCCGCCAGG GCTGCTTCGC	GAGGCGGCAC AAAGCAGGTG GGAGGAGCGC	ACCCAGGGG CCCAGGCCAT AGGCCCTGGA	
30	GGTTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGC	CCTGGGCTCA GAGCAGGACG GCAGGCTGGC TGCGTGCAGA	GGTAAGAGGG GAGCCATGGA TGCTGCTGCT AAGCAGATGA	CCCGAGCTCG CCCCGCCAGG GCTGCTTCGC CGGATGCTCC	GAGGCGGCAC AAAGCAGGTG GGAGGAGCGC CCGAACAAGA	ACCCAGGGG CCCAGGCCAT AGGCCCTGGA TGAAGACAGT	120 180 240
	GGTTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGC GAAGTGCGCG	CCTGGGCTCA GAGCAGGACG GCAGGCTGGC TGCGTGCAGA CCGGGCGTGG	GGTAAGAGGG GAGCCATGGA TGCTGCTGCT AAGCAGATGA ACGTCTGCAC	CCCGAGCTCG CCCCGCCAGG GCTGCTTCGC CGGATGCTCC CGAGGCCGTG	GAGGCGGCAC AAAGCAGGTG GGAGGAGCGC CCGAACAAGA GGGGCGGTGG	ACCCAGGGG CCCAGGCCAT AGGCCCTGGA TGAAGACAGT AGACCATCCA	120 180 240 300
30 35	GGTTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGC GAAGTGCGCG	CCTGGGCTCA GAGCAGGACG GCAGGCTGGC TGCGTGCAGA CCGGGCGTGG TCGCTGGCAG	GGTAAGAGGG GAGCCATGGA TGCTGCTGCT AAGCAGATGA ACGTCTGCAC TGCSGGGTTG	CCCGAGCTCG CCCCGCCAGG GCTGCTTCGC CGATGCTCC CGAGGCCGTG CGGTTCGGGA	GAGGCGGCAC AAAGCAGGTG GGAGGAGCGC CCGAACAAGA GGGGCGGTGG CTCCCCGGCA	ACCCAGGGG CCCAGGCCAT AGGCCCTGGA TGAAGACAGT AGACCATCCA AGAATGACCG	120 180 240
	GGTTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGC GAAGTGGGCG CGGACAATTC CGGCCTGGAT CTGCAACGCC	CCTGGGCTCA GAGCAGGACG GCAGGCTGGC TGCGTGCAGA CCGGGCGTG TCGCTGGCAG CTTCACGGGC	GOTAAGAGGG GAGCCATGGA TGCTGCTGCT AAGCAGATGA ACGTCTGCA TGCSGGGTTG TTCTGGCGTT TCAGCTCGCG	COCGAGETCG COCGCCAGG GCTGCTTCGC CGGATGCTCC CGATGCTCG CGGTTCGGGA CATCCAGCTG GGCGCTCGAC	GAGGCGGCAC AAAGCAGGTG GGAGGAGCGC CCGAACAAGA GGGCGGTGG CTCCCCGGCA CAGCAATGCG CCGGCAGGTA	ACCCAGGGG CCCAGGCCAT AGGCCCTGGA TGAAGACAGT AGAACCATCCA AGAATGACCG CTCAGGATCG ATGAGAGTGC	120 180 240 300 360
	GGTTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGC GAAGTGCGCC CCGACAATTC CCGCCTGGAT CTGCAACGCC	CCTGGGCTCA GAGCAGGACG GCAGGCTGGC TGCGTGCAGA CCGGGCGTGG TCGCTGGCAG CTTCACGGGC AAGCTCAACC	GGTAAGAGGG GAGCATGGA TGCTGCTGCT AAGCAGATGA ACGTCTGCAC TGCSGGGTTG TTCTGGCGTT TCACCTCGCG AGTGCTACAG	CCCGAGCTCG CCCGCCAGG GCTGCTTCGC CGGATGCTCC CGAGGCCGTG CGGTTCGGGA CATCCAGCTG GGCGCTCGAC CTGTCGGC	GAGGGGGAG AAAGCAGGTG GGAGGAGGGG CCGAACAAGA GGGGCGGTGG CTCCCCGGCA CAGCAATGCG CCGGCAGGTA CTGAGCCAGGG	ACCCAGGGGG COCAGGCCAT AGGCCCTGGA TGAAGACAGT AGACCATCCA AGAATGACCG CTCAGGATCG ATGAGATGC AGGCTGCCA	120 180 240 300 360 420 480 540
35	GGTTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGC GAAGTGGGGG COGACAATTC CGGCCTGGAT CTGCAACGCC ATACCCGCC GGGTACATCG	CCTGGGCTCA GAGCAGGACG GCAGGCTGGC TGCGTGCAGA CCGGGCGTGG TCGCTGGCAG CTTCACGGGC AACGCCAACC AACGCCGGTCG	GGTAAGAGGG GAGCATGGA TGCTGCTGCT AAGCAGATGA ACGTCTGCAC TGCSGGGTTG TTCTGGGGTT TCTGGCTTACAG AGTGCTACAG TGAGCTGCTA	CCCGAGCTCG CCCGCCAGG GCTGCTTCGC CGGATGCTCC CGAGGCCGTG CGGTTCGGGA CATCCAGCTG GGCGCTCGAC CTGTGTGGGC CAACGCCAGC	GAGGGGGCAC AAAGCAGGTG GGAGGAGGGG CCGAACAAGA GGGGCGGTGG CTCCCCGGCA CAGCAATGCG CCGGCAGGTA CTGAGCCGGGG GATCATGTCT	ACCCAGGGGG COCAGGCCAT AGGCCCTGGA TGAAGACAGT AGACCATCCA AGAATGACCG CTCAGGATCG ATGAGAGTGC AGGCGTGCCA ACAAGGGCTG	120 180 240 300 360 420 480 540 600
	GGTTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGC GAAGTGGGCC CGGCCTGGAC CTGCAACGCC ATACCGCCC GGGTACATC CTTCGACGGC	CCTGGGCTCA GAGCAGGACG GCAGGCTGGC TGCGTGCAGA CCGGGCGTGG TCGCTGCAG CTTCACGGGC AACGCGGTGG CCGCGGTCG AACGTCACC AACGTCACCC	GGTAAGAGGG GAGCCATGGA TGCTGCTGCT AAGCAGATGA ACGTCTGCAC TGCSGGGTTG TCTGGGGTT TCACCTCGCG AGTGCTACAG TGAGGCTGCTA TGAGGGCAGC	COCCAGCTOS COCCAGCAGG COTOCTOGC COGATOCTCC COGAGCCOGTC COGATCCAGCTC GCCCTCGAC CTCTCTCGGC CAACGCCAGC TAATGTGACT	GAGOCGGCAC AAAGCAGGTG GGAGGAGCGC CCGAACAAGA GGGCCGGTGG CTCCCCGGCA CAGCAATOCG CCGGCAGGTA CTGAGCCGGG GATCATGTCT GTGTCCTTGC	ACCCAGGGG CCCAGGCCAT AGGCCCTGGA TGANGACAGT AGACCATCCA AGAATGACCG CTCAGGATCG ATGAGATGCA AGAGGGTGCCA ACAAGGCTG ACTGCCGGG	120 180 240 300 360 420 480 540 600
35	GGTTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGG GAAGTGCGG CGGACAATTC CGGCCTGGACT ATACCCGCC GGGTACATCG CTTCGACGGC CTGTGTCCAG	CCTGGGCTCA GAGCAGGACG GCAGGCTGGC TGCGTGCAGA CCTGGGCAG CTTCACGGGC AAGCTCAACC AACGCGTGG CCGCCGGTCG AACGTCACCT AACGTCACCT AACGTCACCT GATGAATTCT	GOTANGAGOG GASCCATGGA TGCTGCTGCT ANGCAGATGA ACGTCTGCAC TGCSGGGTTG TCACCTCGCG AGTGCTACAG TGAGCTGCAG GCACTCGGGA GCACTCGGGA GCACTCGGGA	COCCAGCTOS COCCAGO COCCAGO COTOCTTOSC COGATOCTCC COGAGOCOTO CATCCAGCTO GGCGCTCOAC CTGTGTGGGC CACCAGCT TAATGTGACT TOGAGTAACA	GAGOCGGCAC AAAGCAGGTG GGAGGAGCGC CCGAACAAGA AGGGCGGTGG CCGCAGCATCACGG CAGCATTACCT GTGTCCTTGC GGCCCAGGGT GCCCAGGGT	ACCCAGGGG CCCAGGCCAT AGGCCTGGA TGAAGACAGT TGAAGACAGT AGACATCCA AGAATGACCG CTCAGGATCG ATGAGAGTGC AGGCTGCCA ACAAGGCTG CTGTCCGGGG TCACGCTCAG	120 180 240 300 360 420 480 540 600
35	GGTTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGC GAAGTGGGG CGGACAATTC CGGCCTGGAT TTGCAACGCC GGTACATCG CTTCGACGCC CTGTGTCCAG TGGCTCCAT TGGCTCCTT	CCTGGGCTCA GAGCAGGAGG GCAGGCTGGC GCAGGCTGGCAG CCGGGCGTGG CTCACGGGC AACGCGGTCG AACGCGGTCG AACGCGGTCG GATGAATCT TGCAGGGGT GATGAATCT TGCAGGGGT TGCAGGGGT TGCAGGGGT	GOTAAGAGGG GAGCCATGGA TGCTGCTCT AAGCAGATGA ACGTCTGCAC TGCSGGGTTG TTCTGGCGT TCACCTCGGG AGTGCTACAG TGACGGCAGC GCACTCGGGA CCGCTGTAA TCGGGGTGCC	CCCGAGCTCG CCCGCCAGG GCTGCTTCGC CGAGGCCGTG CGGTTCGGGA CATCCAGCTG GGGCGTCGGC CAGCGCAGC CTGTCTGGGC CAGCGCAGC CTGTGTGAGCT TGGAGTAACA CTCTGACCTC CCCTCCAGAG	I GAGGCGGCAC AAAGCAGGTG GGAGGACGACACACACACACACACACACACACACACAC	ACCCAGOGG COCAGGCAT AGGCCTGGA TGAAGACAGT TGAAGACAGT AGACTGCA GTCAGGATCG ATGAGGTGCA ACAAGGCTGCA ACAAGGCTGCA CTGTCCGGGT TCACGCTCAG CCTACTCTGC TGGCCTCAAC	120 180 240 300 360 420 480 540 600 660 720 780 840
35 40	GETTACTORY GACGCZAGG GATCTGGACT GTGCTACAGC GAAGTGGGG CGGCACATTC CGGCCTGGAT CTGCACGGC CTGTGCCGG TGGCTGCCGG TGGCCTGTCCCGC CTGCACACCC CCCCGACCC CCCCGACCC CCCCGACCC CCCCCGACCC CCCCCGACCC CCCCCCACCC CCCCCCCC	CCTGGGGTCA GAGCAGGAGG GAGCAGGAGG GCAGGCTGGCA CCGGGCGTGGCAG CTTCACGGGC AACGCTCAACC AACGCGTGCAA CCGGCGGTCG AACGTCACCT GATGAATTCT TGCCAGGGGT CCACCCCTTG	GGTAAGAGGG GAGCCATGGA TGCTGCTCTCT AAGCAGATGA ACGTCTGCAC TCCSGGGTTG TCACCTCGCG AGTGCTACAC GGCACTCGCAC CCGCTGTAA TCCGGCTGTAA TCCGGCTGCC	COCCAGCTOS COCCAGCOMAG COCCACCAGG COSATOCTOC COSATOCTOC COSATOCTOC COSTOCCAGC COSTOCCAC COSTOCCAGC COSTOCCAC COSTOCCAGC COSTOCCAGC COSTOCCAGC COSTOCCAGC COSTOCCAGC COSTOCCAC COSTOCCAGC COSTOCCAC COS	I GAGCCGCAC AAAGCAGGTG GGAGGAGGGGGGGGGGGG	ACCAGOGG COCAGOCAT AGGCCTOGA TGAAGACAOT AGACCATCA AGACTATCA GAATTACCG CTCAGGATGC ACAGGGTGCA ACAAGGCTGCA CTACCTCAG CTACCTCAG CTACTCTC TGGCCTCAG CCAAACCCAT	120 180 240 300 360 420 480 540 600 660 720 780 840 900
35	GETTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGG GAAGTGGGG CGGACAAATTC CGGCCTGGAT CTTCGACGGC CTTCGACGGC CTTCGACGGC CTTCGACGGC CCGTCCTCCAG TGGCCCAGATCCCC CCCCGAATC	CCTGGGCTCA GAGCAGGAGG GCAGGCTGGC GCAGGCTGGCA GCAGGCTGCAA CCTTCAACGGG CCGCGGGTG AACGTCAAC AACGCAAC AACGCAAC AACGCAAC AACGCAAC AACGCATCA AACGCACC AACACCCTTG ACACTCTAA	GGTAAGAGGG GAGCCATGGA TGCTGCTGCTA AAGCAGATGA ACGTCTGCAC TGCSGGGTTG TTCTGGGGTT TCACCTGGGGA TGAGCTGCTA TGAGCTGCTA TGAGGCAGC GCACTCGGGA CCCGCGTGAA TCCGGCTGCC CCTCGGGGAGCA	CCCGAGCTCG CCCGAGCTCG CCCGCCAGG CCGACCCCTGGCCCGG CGGACCCCTGGCCCGGCCC	I GAGGCGGCAC AAAGCAGGTG GGAGGCAGGCAC CGGACACAGA CCGGCAGGCA CTGGCAGGCA CTGCCAGGCAGGCA CTGCCAGGCAGCA CTGCCAGCAGCA CTGCACAGACA CACACAGACA CCACGACTA CCACGACTA CCACGACTA CCACGACTA CACACACA CACAGACTA ACATCACCA ACATCACCA CACAGGCCT	ACCCAGOGG CCCAGOGGA AGGCCTGGA AGGCCATCA AGACCATCCA AGAACTACCA ACTAGGATTGC ACTAGGATTGC ACTAGGATTGCA ACTAGGCTCAG CCTACTOGGG TCAGCCTCAG CCTACTCTCAC CCAAACCCAT CCGGGGTCAAC CCCAAACCCAT	120 180 240 300 360 420 480 540 660 720 780 840 900 960
35 40	GETTACTCAT GACGCCAAGG GATCTGGACT GTGCTACAGG GAAGTGGGG CGGACAATTC CGGCCTGGAT CTGCAAGGCC ATACCGCCC CTTCGACGGC CTTCGACGGC CTTCGACTCGC CCTCGAATCG CCTCGAATCG CCTCGAATCG CCTCGAATCG CCTCGAATCG CCCAGGCCCA GAGGCCAAGGCCCA	CCTGGGCTCA GAGCAGGAGG GAGCAGGAGG GCAGGCTGGC TCGCTGGCAG CCGGCGTGGCAG AACGCGTGGCA AACGCGTGGCA AACGCGTGGCA AACGCCTCAC AACGCTCACC TCCACGGGTC AACTCACCCTTG ACCACTCTA ACCACTCTAA	GGTAAGAGGG GAGCCATGGA TGCTGCTGCT AAGCAGATGA ACGTCTGCAC TCTGGGGTT TCACCTCGGG AGTGCTACAG GGACTGCACA GGACTGCACA TGAGCTGCTA TGAGCTGCTA TGAGCTGCTA TGAGCTGCAC CCCGGGGCCC CCCGGGGCCC CCCGGGACAG	COCCAGETOS COCCAGETOS COCCAGETOS COSATOSTOS COCCO COS COS COCCAG COS COCCAG COS COCCAG	I GAGGCGGCAC AAAGCAGGTG GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAACAAGAGAC	ACCAGOGGA ACCAGOGGA COCAGOCAT AGGCCTOGA AGGCATCCA AGACCATCCA AGAATTACCG ATGAGATGC ATGAGATGC ATGAGATGC ATGAGATGC ACTAGGGTTCCA ACAAGGGTTCCA ACAAGGGTTCCA ACAAGGCTTCA CTACCCTCAC CTACTCTCTC CCGCTCAAC CCAAACCCAT CCAGAGCGTA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
35 40	GOTTACTCAT GACGCCAAGG GATCTGGACT GAGGTCACAGG GAAGTTCGCC GGACAATTC GGGCTGGAAT TTGCAAGGC ATACCCCCC GGGTACATCG CTTGGACGG CTGTGTCCAAG TGGCTGGAAT CCCTGGAATC CCCTGGAATC GCCAGGCCCA GACACCTGGAAT AGGCCAGG TCCTGCAAAA ATTGGCAGCC	COTGGGCTCA GAGCAGGACG GAGGCTGGC GAGGCTGGC TGCGTGGAGA COGGGCTGG TCCACGGGC AAGGTCAACC AAGGCGTGG AAGGTCAACC GATGAATCT TGCCAGGGG CCACCCCTTG ACCACTCTA ACCAGTCAGA GGGGGGCCC TTGCAGGGG CCACCCTTTG ACCAGTCAGA GGGGGGCCC TTTGGTGG	GGTAAGAGGG GAGCCATGGA TGCTGCTCTCT AAGCAGATGA ACGTCTGCAC TGCSGGGTT TCACCTCGGG TGAGCTACAG GAGCTGCAC GAGCTGCAC GCACCTGGGA CCCCGGGACCA GCGGGACCA GCGCGCAC GCGCGCAC GCGCCCCAC GCGCCCCAC GCGCCCCAC GCGCCCCAC GCGCCCCCAC GCGCCCCCAC GCGCCCCCCAC GCGCCCCCCAC GCGCCCCCCCAC GCGCCCCCCCAC GCGCCCCCCCAC GCGCCCCCCCC	COCCAGCTOS COCCAGCTOS COCCAGCTOS COSATOSTO COSATOSTO COSATOSTO COSATOSTO COSATOSTO COSATOSTO COSATOSTO COSATOSTO COSATOSTO COSATOSTO COSATOSTO COSTOCO	I GAGGCGGCAC AAAGCAGGTG GGAGGAGGTAC CCGGACAATACACAGGAGGAGGTA CCACAGGATACAGGAGGAGTA ACATCACCACAGAGACATTGCGCACGACAATTTGTTTGGCTC CGGAGCAATT	ACCCACCGGG CCENGGCCRT AGGCCCTGGA AGACCATCCA AGACCATCCA AGACTACCA ATGAGATGC ACGGGTGCCA ACCACCACCA ACCACCACCACCACCACCACCACCA	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140
35 40 45	GETTACTCAT GACGCLAGG GATCTGGACT GTGCTACAGC GAAGTGCGGAC ATACCGCCG GGGTACATCG GTTCGAGGC GTTCGAGGC GTTGTCCAG TGGCTGGAATC CCCTCGAAATC CCCCTGGAATC CCCTGGAATC CCCTGGAATC CCCTGGAATC GCAGGCCAGGC	COTGGGCTCA GAGCAGGAGC GAGGCTGGC GAGGCTGGC GAGGCTGGC GAGGCTGGC GATCAACGCGGTCG AAGGTCAACC GATCAACC GATGAATTC GACGGGTGG ACCACTTCTA ACCACTTCTA ACCACTCATA ACCACTCAGA CTTGGTGGG CGGGGGCC CTTCTGTTGG GGGGGGCCC CTCTGTTTGG CTCACCTACT	GOTANGAGOG GAGCCATGGA TGCTGCTCCT AAGCAGGATGA ACGTCTGCAC TCCSGGGTTG TCTCGCAC AGTGCTACAC TGACCTCCTAC TGACCTCCTAC TGACGCAC CCCCCTTGCGCAC CCTCCGAGACA GCGCCGCCTCC CCTCGGAGACA GCGCCGCCTCCCCCCCCCC	COCCAGCTG COCCAGG COCC	I GAGGGGGAC AAAGCAGTA GGGGGAGGAGAC CTGCACGGCA GTGACCTTAC GGCCAGGGTA CCGAGACATA CCGAGCAGACACACACACACACACACACACACACACAC	ACCCACOGGG CCCAGGGCAT AGGCCTGGA AGGCCATCGA AGACCATCCA AGACCATCCA AGACCATCCA ACAAGGATGC ACAAGGCTCA ACAAGGCTCA CCTGCCAGGCTCA CCTGCCTCAGCCCAG CCAAACCAT CCCAGGGATGA CCACAGCAGCA CCACAGGCAGA CCACAGGCACAG ACACCACTGG CCCACAGG ACTCCTGTT	120 180 240 360 420 480 540 660 660 720 780 840 960 1020 1080 1140 1200
35 40	GGTTACTCAT GACGCLAAGG GATCTGGACT GAGGTCACAGG GAAGTTCGGC GGACAATTC GGCGTCACATC GGGTCACATC GTTGCACAGG CTTGGACGGC CTTGGACGGC CTCGACATC CCCTGGACC CACATCTGTC GCCAGGCCCA ATTGCCAGG TCCTGCAAAA ATTGCGCCAG AAATTCCCTC CCCACATC CCCACACC AAATTCCCCT CCCACACC AAATTCCCCT CCCACACC CCACACCCCACACC CCACACCCCACACC CCACACCCCACACC CCACACCCCACACC CCACACCCCACACCCCACACCCCCACACCCCCACACCCCC	COTGGGCTCA GAGCAGGCAG GAGGCAGGCAGGCAGGCAGGCAGGCA	GSTANGAGGG GAGCCATGGA TGCTTGCTGCT AGGCGGATGA ACGTCTGCAC TCCGGGGTTG TCACCTGGGG AGTGCTACAG GCACCTGGGA CCGCTGTAA TCCGGGGAGCCC CTCGGAGAGC AGGCGCAC CGGGAGGCCC TCCGAGAGCCCC TCCGAGAGCCCC TCCGAGAGCCCC TCCGAGAGCCCC TCCGAGAGCCCC	COCGAGCTGG COCGGCAGG GCTGCTTGGG CGGATGCTCGG CGGTTCGGGA CATCCAGCTG GGGCCTGGA CATCCAGCTG CAACGCCAGC TAATCTGACT TCGAGCTAACA CTCTGACCTC CCCTCCAGAG AGTGAGACCC GGGAGTACAA CACCAGGAC TAATAAAGGC TGGTTCCTA TGGGTACCCT TGGGTACCCT TGGGTACCCT TGGGTACCCT TGGGTACCCT TGGGTACCCT TGGGTACCCT TGGGTACCCT TGGTTTCCTA TGGGTACCCT TGGTTTCCTA TGGGTACCCT TGTTTTTCCA	I GAGGOGGCAC AAAGCAGGTG GGAGGAGGTG CTCCCCGGCA CAGCATCA CAGCAGGTA CTGAGCAGGTA CCCACGACAAGA CCCACGACAAGA CCCACGACAAGA CCCACGACAAGA CCCACGACAAGA CCCACGACTA CTGAGAGCAT TOTOTGGCTC TGTTOTCATC TGTTOTCATC ACATCCCACAACAAGA CCCACGACTAACAAGA CCCACGACTAACAAGA CCCACGACTACAACAACAACAACAACAACAACAACAACAACAACAA	ACCCAGGGG CCMGGCCAT AGGCCCTGGA AGACCATCGA AGAACTACCA AGAACTACCA ATGAGGATGC ATGAGGTGCA ACAAGGGTGCA ACAAGGCTGCA CTACCTCAC CCAAACCCAT CCAGGCGGG AGGGGAGGA CCAAACCCAT CCAGGCGGG ACTCCAGGGGAGGA ACTCCTGGA CTCCAGGGGAGGA ACTCCTGGA	120 180 240 300 360 420 540 660 720 780 960 960 1020 1140 1200
35 40 45	GETTACTCAT GAOGCCAAGG GATCTGGACT GTOCTACAGG GAAGTGGGCG GAAGTGGCGC ATACCCGCCC GGGTACATCC GGCTCGAATC CCCTCGAATC CCCTCGAATC CCCTCGAATC CCCCGAATC CCCCGAATC GCCAGGCCA GAAGCCCAG GAAGCCCAG GAAGCCAG GAACCCGCA CCCCCACACT CCCCCAAA	COTGGGCTCA GAGCAGGACG GAGCATGC GCAGCAGCAGCAGCAGCAGCAGCAGCAGCACCACCAGCAG	GOTANGAGOS GAGCATUSA TOCRECTOCT AAGCAGATOA ACGTCTGCAC TOCSGGGTT TTCRSGGGTT TTCACCTGCAC GCACTCGCAC GCACCCCC CCCCAGCCCC GCCAAGCCC GCCAAGCCC GCCAAGCCC GCCAAGCCC GCCAAGCCC GCCAAGCCC GCCAAGCCC GCCAAGCCC GCCAAGCCC GCCAAGCCC	COCCAGOCAGE COCCAGGE	I GAGGGGGCAC AAAGCAGGGGCGCGCACAACAAGA GGGGGGGG	ACCCAGGGG COCAGGGGG TGAAGACACTA AGGCCTGGA TGAAGACACCA AGAATGACCG TCAGGATGCA AGAGGTGCA AGAGGTGCA AGAGGGTGCA AGAGGGCA TCAGGCTCAG CCTACTCAG CCAAACCCAT TGGCCTCAAC CCAAACCCAT CCACAGGGATGA ACTCCACTAGG TCCACT	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1200 1200
35 40 45	GGTTACTCAT GAGGCCAAGG GATCTGGACT GTGCTACAGC GAAGTGGACT GTGCTACAGC GAAGTGGACT CTGCAAGGCC GGACATTGCA CTGCAAGGCC CTTCGAAGGCC CTTTGCAAGGC CTTGGACAGC CTTGGACAGC CTTGGACAGC CTTGGACAGC CTTGGACAGC CACATCTGC CACATCTGC CACATCTGC CACATCTGC CACATCTGCC CACATCTGCC CACATCTCC CCCACACC CACATCTCC CCCACACC CCCACGCC CTTCGCCACAC CCCCCCCC CTTCGCCACAC CTTCGCCACAC CTTCTCCCCCC CTTCTCCCCCC CTTCTCCCCCC CTTCTCCCCCC	COTEGGETCA GRACAGGAG GRACAGGAG GRACAGGAG GRACAGGAG TOCTGCAGG TOCTGCAGG TOCTGCAGG COTTCCAGGA TOCTGCAGG AAGGTCAACC AACGGCTGCAG AAGGTCAACC GATGAATTC TOCCAGGGGT CCACCCCTTC ACCAGTCAGA ACCACTCTA ACCAGTCAGA GGGGGGCCC CTTCTGTAGA GGGGGGCCC GTCTGTCGCAGGGGGGCCC GCTGCTCGGCGGGGGCCC GCTGCTTGGCGGGGCGCG GCGGGTTGGC GCGGGTTGGC GCGGGTTGGCGCGGCGGCGCGCGC	GTTANGAGOGG GRGCCATGGA TOCTGCTOCT TOCTGCTOCT ANGGCGATGGA TOCTGCAGCGGG TTCGGGGTT TTCTGGGGTT TTCTGGGGTACAG TTANGTGCTAT TANGGCGAC GGCACCGGGG CCCCGGGCGCCG CCCGGGGCCCC CCCGGAGCA GGCGCCGCGG GCCGTGTA TCTGGCCG CCGGGGCCCC CCCGGGGCCCC CCCGGGGCCCC CCCGGGGCCCC CCCGGGGCCCC CCCGGGGCCCC CCCGGGGCCCC GGCTTTGGAC GCCCAGCCCC GGCTTTGGAC	COCCAGGE COC	GROCOGCAC ANACIAGETTO GROCOGCAC ANACIAGETTO GROCOGCAC COGRACADA GROCOGCAC CARCATOCO COGOCACOTTA COGOCACOTTA COGOCACOTTA COGOCACOTTA COCACACAC ACATOCOC COCACACAC ACATOCOC COCACACAC ACATOCOC COCACACAC ACATOCOC COCACACAC COCACAC COCACACAC COCACAC	ACCAGGGGG COLAGGGGGA TGANGACAGT TGANGACAGT TGANGACAGT TGANGACAGT AGACATCAC AGAATTACCG ATCAGATTGC ACAGGGTCAG ACAAGGGTCAG CTGTCGGGGTCAG CTAGTCTCT TGGCCTCAG CCAAACCCAT CCCAAACCCAT CCCAGGGGTGA CACAGGGTGAG ACTACTTCTCT TGGCTCAG CTCCACTGG ACTTCCTGT TCTCCTGT TCTCCTGT TGATCCCAG ATTCTGGCCAG ATTCTGGCCAG	120 180 240 300 360 420 540 660 720 780 960 960 1020 1140 1200 1200
35 40 45 50	GRITACIONI RAGIOCAGE RACIOSAGE RACIO	COTOSGOTICA GNACAGGACG GNACAGGACG GNACAGGACG GNACAGGACG GNACAGGACG GNACAGGACG GNACAGGACG GNACAGCACG ANGATCAACC ANGATCAACC GNACAGCACC GATGAAATCC TGCCAGGGGT CCAACGGCT ACCAGTCAAC ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTCTA ACCAGTTCTA ACCAGTTCTA ACCAGTTCTA ACCAGTTCTA ACCAGTTCTA ACCAGTTA ACCAGTTTA ACCAGTTTA ACCAGTTA	GRTANARAGOS GAGCOCTOSCA TOCHOCTOSCA AGGCAGATOSCA TOCHOCTOSCA AGGCAGATOSCA TOCHOCTOSCA AGGCAGATOSCA TOCHOCTOSCA AGGCAGATOSCA TOCHOCTOSCA AGGCAGATOSCA TOCHOCTOSCA TOCHOCTOSCA TOCHOCTOSCA TOCHOCTOSCA COCCOCCOSCA TOCHOCTOSCA	COCCAGO TO COCCACO TO	ANACCACACA GROSOGCAC ANACCAGGTO GROSOGCAC GROSOGCAC GROSOGCAC GROSOCCAC GROS	ACCCADAGGG COLGAGGCATTA AGGCCCTIGAG TRANGALOHOT AGACCATTCA AGACCATTCA AGACCATTCA AGACCATTCA AGACGATTCA AGAGGGTIGCA CTIVITOSIGA CTIVITOSIGA CTIVITOSIGA CTIVITOSIGA CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT CCANACCCAT ACTIVITOSIGA ACTIVITOSIGA ACTIVITOSICA TUTTOSICAT CTIVITOSICA COCCA COCC	120 180 240 300 360 420 480 540 660 660 720 780 960 960 1020 1080 11200 1260 1320 1330 1340
35 40 45	GOTTACTORT GROSCOAGG GROTTACHC GROTT	CT099GTCA SACAGGAGG GAGGTGG GAGGTGGG GAGGTGGG GAGGTGGG GAGGTGGG GAGGTGGGA AGGTCAACC AAGGGAGGG GAGGAATCA GAGGGGGGG GAGGAATCA TGCAAGGG GATGAATCA GAGGGGTGG AAGGGTCAAC AAGGGATCA AAGGGATCA AAGGGATCA AAGGGATCAA CAGGTCAAC GATGAATCC TGCAAGGGGT GAGGAATCC GATGAATCC TGCAAGGGGT GAGGAATCC GATGAATCC	GRTANGAGGG GAGCCATGGA GAGCATGGA GAGCATGGA AGCAGATGA AGCAGATGA AGCAGATGA AGCAGATGA AGCAGATGA AGCAGATGA AGCAGATGA AGCAGATGA AGCAGATGA AGCAGCAG CCCCCCCCCC	COCCAGO TO COCCAGO TO THE COCCAGO TO THE COCCAGO TO THE COCCAGO TO THE COCCAGO TO THE COCCAGO TO THE COCCAGO TO THE COCCAGO TO THE COCCAGO TO THE COCCAGO TO THE COCCAGO THE C	GROGOGCAC ANAGCAGGTO GRAGGAGGCC COGACCAGCA COGACCAGCA COGGCCAGTA CTGAGCCGGG GATCATCTC GGCCAGGTA CCGACAGCA CCGACAGCA CCGACAGCA CCGACAGCA CCGACAGCA CCGACAGCA CCGACAGCA CCGACAGCA CCGACAGCA CCGACACCA CCGACAGCAGCA CCGACACCA CCGACAGCAGCA CCGACACCAGCA CCGACACCAGCA CCGACACCAGCA CCGACACCAGCA CCGACACCAGCA CCGACACCAGCA CCGACCACCACCA CCGACCACCACCA CCGACCACCACCACCA CCGACCACCACCACCACCACCA CCGACCACCACCACCACCACCACCACCACCACCACCACCA	ACCADOGGE COLOGOGCAT AGENCIA COLOGOGCAT AGENCIA COLOGOGCAT COLOGOG	120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1220 1320 1320 1340 1560
35 40 45 50	GETTACTOAT GROSCAAGG GRATCHOGAT GROSCAAGG GRATCHOGAT GROSCAAGG GRAGG GROSCAAGG GROSCAGG GROAG	CTTGGGGTCA GAGCAGGGGGGGGGGGGGGGGGGGGGGGG	GOTANARAGOS GASCATORA TACTOCTOCTO ARGCARACA AR	COCCAGO TO COCCACO TO	GROGOGICAC ANAGCAGGTO GROGOGICAC ANAGCAGGTO GROGOGICAC GROGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	ACCAGGGGG COLGGGCAT AGGCCTGGG TGAGGCTGGG TGAGGCGGG AGGCGGGG AGGCGGGG AGGCGGGG AGGCGGG AGGCGGG AGGCGGG CTAGGGCGG CTAGGGCGG CTAGGGCGG CCAGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCCAGGGGGGG CCCAGGGGGGGGGG	120 180 240 300 360 420 480 540 660 720 780 900 900 900 1020 1140 1200 1250 1320 1320 1320 1500 1500 1500
35 40 45 50	GETTACTOAT GROSCAAGG GRATCHOGAT GROSCAAGG GRATCHOGAT GROSCAAGG GRAGG GROSCAAGG GROSCAGG GROAG	CTGGGGTCA GACAGGAGG GACAGGAGG GAGGAGGAG GAGGAGGAG GAGGAGGAG GAGGAG	GOTANARAGOS GASCATORA TACTOCTOCTO ARGCARACA AR	COCCAGO TO COCCACO TO	GROGOGICAC ANAGCAGGTO GROGOGICAC ANAGCAGGTO GROGOGICAC GROGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	ACCAGGGGG COLGGGCAT AGGCCTGGG TGAGGCTGGG TGAGGCGGG AGGCGGGG AGGCGGGG AGGCGGGG AGGCGGG AGGCGGG AGGCGGG CTAGGGCGG CTAGGGCGG CTAGGGCGG CCAGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCAGGGGGG CCCAGGGGGGG CCCAGGGGGGGGGG	120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1220 1320 1320 1340 1560

60 Seq ID NO: 569 Protein sequence Protein Accession #: NP_055215

	1	11	21	31	41	51	
65	MUDARKTONO	AMINTAGHLL	LLLLRGGAGA	LECYSCVOKA	DDGCSPNKNK	TVKCAPGVDV	60
	CTEAVGAVET	IHGQFSLAVX	GCGSGLPGKN	DRGLDLHGLL	AFIQLQQCAQ	DRCNAKLNLT	120
	SRALDPAGNE	SAYPPNGVEC	YSCVGLSREA	COGTSPPVVS	CYNASDHVYK	GCFDGNVTLT	180
			RDGVTGPGPT				240
			APVRPTSTTK			DEEPRLTGGA	300
70	AGHODRSNSG	QYPAKGGPQQ	PHNKGCVAPT	AGLAALLLAV	AAGVLL		

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	1	11	21	31	41	51			
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		AGCTGACGAC					60		
		GCATCCTGGC					120		
80		CCTTCGGCCT					180		
		TCCTGGAGCA					240		
		GGGGCTCGGT					300		
		GCCTGCGCTC					360		
		GCAACCGCCA					420		
85		AGCAGGCCGG					480		
		AGGCCAGCCT					540		
	AGCACCTTCT	CGTGCATCAT	GCAGAAGTGG	GGAGGCAAGC	GCGAGGTCAT	GTACACGGCC	600		

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		TCGGCGATTC					660
	GATCCAGCCT	GCACCATCGA	GATGCTTCGA	GTCCTGGAGG	AGGATCCCCA	AGTAGGGGGA	720
		ATGTCCAGAT					780
	GTGCGGTACT	GGATGGCCTT	CAACGTGGAG	CGGGCCTGCC	AGTOCTACTT	TGGCTGTGTG	840
5	CAGTGTATTA	GTGGGCCCTT	GGGCATGTAC	CGCAACAGCC	TCCTCCAGCA	GTTCCTGGAG	900
	GACTGGTACC	ATCAGAAGTT	CCTAGGCAGC	AAGTGCAGCT	TCGGGGGATGA	CCGGCACCTC	960
	ACCAACCGAG	TCCTGAGCCT	TGGCTACCGA	ACTAAGTATA	CCGCGCGCTC	CAAGTGCCTC	1020
		CCACTAAGTA					1080
	TACTTOOGGG	AGTGGCTCTA	CARCTUTUTE	TOGTTOTATA	AGCACCACCT	CTGGATGACC	1140
10		TGGTCACGGG					1200
		GCCGCATCTG					1260
		CCACCTACGC					1320
		TCCTCTATAT					1380
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25		RRAGOALKLP					120
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	OTTROUTHOUGH	GGKREVMYTA	BAST CDCADA	TOUGHERMAN	DDI CONTRACTO	AL BAD BORGO	240
		YDSWISFLSS					300
30	PURE OUT OF	KCSFGDDRHL	AVERLINE WAR	muma novo:	OCTOOLNOUS.	THOOMBHONO	360
50		WEHKHELMMT					420
		RGNAEMIFMS					480
		LLGGLAYTAY					540
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		ATTTCCTTCG					120
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45		COGCAGACOG					240
40		GTGTTTGCCG					300
		AGATTGGCTG					360
		CATGTAATAG					
		TGAATCTTAA					420
50		TTCATAACAC					480
Dυ	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540

GYCHGOGGAG GAGTYTCHGA ANGGYGYTT MAGCAGCA GGATAGCTT YGCTGGGGA ANATGCANTA TGYCATCHG TGGATGGAG GATGCTTHG ANGGCABA ATTCCACT GHGATGCHA TCTACTGCT TGATGCGGAC CHATTYCHA GTTTGGGCA AGCAGTCHA GGANANGGA HGTTANGAGC TYTATCCATT TTUTTGHGG TGGGGACGA AGAANATTTG GATTCCHAG CGATTATGA TGGGGTCGA AGTGTTGTGT GTTTGGGGA GCAGCTGCT 600 660 55 TTAGATCCAT TCATACTGTT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC 840 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900 ACASTRACA TOTOTARAN CONSTRUCT STITTING ANTICATOR THITAMAGAT ACASTRACA TOTOTARAN CONSTRUCT STITTITIS AMSTROTAC ANTICARANA TOTOSTINIS TONIGOTORY GONOTACTIA CAMARCANT TOTOGRAGOA ACASTACAN 960 1020 TTCTCTAGAC AGGTGTTTTC CTCATACACT GGAAAGGAAG AGATTCATGA AGCAGTTTGT 60 AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTTACA 1140 TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCAGT TTTGTACCAG 1200 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTTGA CAGATGGCTA TCAAGACTTG GGTGCTATTC TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1260 1320 TGCACTAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380 65 ARTOCTGARC TIGATCTITT CCCTGARTA ATTGGARCTO ARGARATAT CARGGAGGAG GARGAGGGAR ARGACTTGA GARAGGGGCT ATTGTGART CTGGTRTAGAG CARTGTGARG ARCCARATCA GGARARAGGA ACCCCAGATT TCTRCACAM CARGTACAA TGGCATMGG 1440 1500 1560 ACGARATACA ATGARGCCAA GACTARCOGA TCCCCAACAA GAGGAAGTGA ATTCTCTGGA AAGGGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCAGTCAC TAAATTAGCC 1680 70 ACAGAAAAAG ATATTTCCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740 GAAGGTACTT CAGCCTCTTT ARATGATOGC TCTARARCTG TTCTTAGATC TCCACATATG 1800 SACTORITY OF CONCUST ANY PURSUE ACADEMICS TRACEGRATA TOROGRAPHO 1860 AGTITATIGA CCAGTITCAA GCITGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920 GCAACTTCTG CTATCCCATT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCCTCC 75 GAAAACCCAG AGACAATAAC ATATGATGTC CITATACCAG AATCTGCTAG AAATGCTTCC 2040 GAAGATTCAA CITCATCAGG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT 2100 GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTTGATG AATCTGAGAA GACAACCAAG TCCTTTTCTG CAGGCCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAAATGCCA 2220 2280 80 CATTATTCTA CCTTTGCCTA CTTCCCAACT GAGGTAACAC CTCATGCTTT TACCCCATCC 2340 2400 2460 2520 TOSGCCTTGC ATGCTACGCC TGTATTTCCC AGTGTCGATG TGTCATTTGA ATCCATCCTG 85 TOTTCCTATG ARGUIGACC TITGCTTCA TITTCCTCTG CITCCTCAG TAGTGARTG 2640
TITCCCCATC GATACAGT TITCCAART CITCACAGG GTGATTGCT ACTAGGAGG COTTCCATCG TITCCCAGA GTGATTGCT ACTAGGAGG COTTCCATCG TITCCTGCC GTGCCTGGG GTGATTGCT ACTAGGAGC 2760

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	TTTGGTAGTG	AATCIGGIGI	TCTTTATAGA	ACGCTTATGT	TTTCTCAAGT	TOWACCACCC	2000
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCITCTIA	TGCCTTGTCT	2940
_	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCTGCAAT	ACCTGTGCAT TATACCAATA	3000
5	CATTOTOTOC	OTOTA ACTTA	TORGGGTTCC	TTATTTAGCG	GOYYTAGOCA	TATACCAATA	3060
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	CCIMAGICIT	CGITARIAAC	CCCAACIGCA	TCATIACTOC	MOCCIACICA	IGCCCICICI	3460
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGIGAAT	TTCTTTTACC	TGACACAGAT ATATACAACA	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACCT	GTTTCTGTAG	CTGAATTTAC	ATATACAACA	3240
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10	1010101110	***********	manage a most of	Amoomma CC	CHECKSON	CACAGTCATG CICIGITICC	3360
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	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGOGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
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	CATCATCACA	TENCTOLAGE	TOTAGAAAA	A A CHITTET CAG	TTCAACCTAC	ACATACTORC	3540
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15	TCTCAAGCAT	CIGGIGACAC	TTUGCTTAAA	CCTGTGCTTA	GIGCAMACIC	MGMGCCMGCM	3600
15	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ACATACTOTO AGAGCCAGCA ATTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAC	TGAAGTATTG	CTACAACCTT	CCITTCAGGC	TTCTGATGTT GGTTGAAACC TTCTGCTTCA	3720
	GACACCTTYGC	TTABABACTOT	TOTTOCAGOT	GEGGGGGAGTG	ATTCAATATT	GGTTGAAACC	3780
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	CCCMMGTTG	ATMAMATTAG	TICIACHAIG	TIGURECICA	TIGINICANA	TICIOCTICA	3040
~~	AGTGAAAACA	TGCTGCACTC	TACATCIGIA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT ATATGAACCA	3900
20	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCCTATG	CAAGTGAGAA	ATATGAACCA	3960
	OTHER DETT A	BENCHMANN	TTCCCACCAA	OTGOTACCTT.	CTTTTCTACAC	TAATGATGAG AAGGCATGTA	4020
	GIIIIGIIAA	ANNOLUMNO	22CCCACCAA	01001/10011	00000333300	3.1.00001m0m3	4000
	TIGITOLAAA	ORRCGAATTT	GGAGATTAAC	CAGGCCCATC	CCCCAAAAGG	MAGGCATGIA	4000
	TTTGCTACAC	CIGITITATC	AATTGATGAA	CCATTAAATA	CACTAATAAA	TAAGCTTATA	4140
	CATTOCGATG	ASSTTTTAGE.	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	TAAGCTTATA ATTTGCTGGT TATAGGAAAT	4200
25	AMMOOD A CINC	mmacromore and a	mh Ch Tmmomh	TOTAL CTOATO	ATTOTOTOTO	TATAGGARAT	4260
23	ATTCOMCAG	TIGCTICION	INCALITION	TCIMCIGNIC	ATTCTGTTCC	TATACOMAL.	4320
	GGGCATGTTG	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GITCIGIAAC	CTCAACAAAG TGATGCCGGT	4320
	TTGCTGTTTC	CTTCTAAGGC	AACTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
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	1170100010	1001001001	CAMPONDA	moma momera m	COMONDOCEN	TRONG NAMED	4500
30	MUMUGTAGIG	ATGGCTTATC	CHITCHIANG	TOTALGICAL	GCICKICCIA	INGMONNICA	4500
30	CAGGAAAAGG	TAATGAATGA	TTCAGACACC	CACGAAAACA	GTCTTATGGA	TCAGAATAAT	4560
	CCARTCTCAT	ACTUACTATO	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGTATCC	4620
	TONO A CAGERO	BARCTCGTAT	COLCACADAGE	CCTCCTAAAT	CACCATCAGC	ABATOGGCTA	4680
	-CHUNCHUIC	MMCTGGTAT	oonchonno.	CCIOOINUUII	CHICARICHOC		4740
	TCCCAAAAGC	ACAATGATGG	MARAGAGGAA	AATGACATTC	AGACTGGTAG	TGATGATGAC TAGAGAATCA TCAGAATAAT AAGTGTATCC AAATGGGCTA TGCTCTGCTT AAGTGGATCA CAGTTTTGCA AATTGCA	4740
	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTTCTGACAA	GTGATGAAGA	AAGTGGATCA	4800
35	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTTGCA	4860
	CACA CERANO	BRADAGAMOC	TONTOCONTO	CTOCCLOCAG	GTCACTCAGA	AATAACTCCT GTTCCACGTT	4920
	GACACIANIO	MOUNDATION	10011000H1C	CIGOCAGCAG	CIGNCICNON	74174107007	4980
	GGATTCCCAC	AGTCCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAGT	GTTCCACGTT	4980
	TCAGAGGCAG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
	ADADOODAGA	AGLAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TGAGGGGTTG TTTTATCTGT TGCACACTTT	5100
40	ORA: CCORON	MONAGOCHO:		magagaga a a m	COMMOCRANC	maan an anno	5160
40	CTAGTGGTTC	TTGTGGGTAT	TUTCATUTAC	TOGMOGNAMI	GCTTCCAGAC	TOCHCACTIT	2100
	TACTTAGAGG	ACAGTACATC	COCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA TGCAGATTTA CCAGGAAGTG	5220
	ATTTCAGATG	ATGTCGGAGC	AATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	5280
	CATCCAACTA	CONTRACTOR OF THE CONTRACTOR O	TODAGATTE	GACACACTGA	AMCAGUTTUA	CCAGGAAGTG	5340
	CHIGCHNOIN	GIGGGIIIAC	1000000111	ONONCHOION	0000011110	1010011010	5444
4.5	CAGAGCIGIA	CTGTTGACTT	AUGTATTACA	GURGAURGUT	CONTINUENCE	NGACAACAAG	5400
45	CACAAGAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
	CTTTCCTCAAA	AGGATGGGAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	AGACAACAAG GCTAGCACAG TGATGGCTAC	5520
	AACACACCAA	DACCTTATAT	TOCTOCCCAN	GGCCCCACTGA	DATOCACAGO	TGATGGTAC TGAAGATTTC CCTCGTGGAG GTACGGGAAC	5580
	AACAGACCOOL	MAGCITATAL	IGCIGCCCOA	GGCCCACTGA	MICCACAGO	10000001111	5640
	TOGAGAATGA	TATGGGAA CA	TARTUTUGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGMG	5640
	AAAGGAAGGA	GAAAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	5700
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	CIAMODONCA	CHANANTAN	MONOGOCICC	CHONDRIGONY	GNECCHOIGG	ACGIGIOGIC	5880
	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
	CACTGCAGTG	CTYGGAGTTGG	ABGRACAGGC	ACATATATTG	TOCTAGACAG	TATGTTGCAG	6000
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22	CAGATTCAAC	ACGAAGGAAC	TUTCAACATA	TTTGGCTTCT	TAMANCACAT	CCGTTCACAA	6060
	AGAAATTATT	TGGTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTCATGATAC	ACTGGTTGAG	6120
	OCCUTACTTA	GTARAGARAC	TGAGGTGCTG	GACAGTCATA	TTCATGCCTA	TOTTGTOGTC TATGTTGCAG CCGTTCACAA ACTGGTTGAG TGTTAATGCA GCTCCTGAGC CAGGGAAAAG ATCCCTGAGT	6180
	OTTOO TO A TOO	OTTOO NOCE A CO	MOOCHARACA	BAGCTACAGA	AACA ATTCCA	CONCOUNTRACE	6240
	CICCIONIIC	CIGGNCCHOC	nouchnnich	Moctionov	rescription.		6300
	CAGTCAAATA	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGGAAAAG	6300
60	AATOGAACTT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TIGGCATITC	ATCCCTGAGT	6360
	GODGGGGGGCD.	CAGACTACAT	CANTGOCTOC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
	GGNGNAGGGA	CHONCINCAL	EGRECOCCIOC	LOCKECT LOC	ADDECEDOOS	GAGCAATGAA GATGATATGG	6480
	TTCALCALLA	CCCASCACCC	TOTOGITORE	ACCUT CUMOO	MITICIOONO	OUTOVIUTO	0400
	GACCATAATG	CCCAACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
_	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATTGTG	AGAGCTTTAA	GGTCACTCTT	6600
65	ATTCCCTCARC	ABCACABATO.	TOTATOTAAT	GAGGRAAAAC	TTATAATTCA	GGTCACTCTT GGACTTTATC	6660
00	mms of 1 ocurs	Charachers	mma moma one	OTTO CONCENSION	PODDECE COC	TCCTAAATGG	6720
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	CCAAATCCAG	ATAGCCCCAT	TAGTAAAACT	TTTGAACTTA	TANGTGTTAT	AAAAGAAGAA GACGGCAGGA	6780
	GCTGCCAATA	GOGATGGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
	* COMPANY	CECTONOL LO	COTTA MOCINO	CAACTACAAA	ANCARA TEC	COTOGATOTT	6900
70	ACTITICISTS	CICIOACANC	CCTIATGUAC	CHUCTWOULU	MONANTEC	CGTGGATGTT CATTGAGCAG AGAGAATCCA	6960
70	TACCAGGTAG	CCAAGATGAT	CAATCTGATG	AGGCCAGGAG	TCTTTGCTGA	CATTGAGCAG	6960
	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAATCCA	7020
	Character	TOTAL ACTOR	*************	COCCACTOR	ATVTCAGCAG	TOTTTTTOTAL	7140
	GNGTCTTTAG	* * TANCACAG	WW0000100	GOODHC CAC	ATCTOMOCHT.	- CALLICCIC	7140
	TTCCTAAAAT	TAGGCAGGAA	AATCAGTCTA	GITCIGITAT	CTGTTGATTT	CCUATCACCT	7200
75	GACAGTAACT	TTCATGACAT	AGGATTCTGC	CGCCAAATTT	ATATCATTAA	TGTTTTCCTC CCCATCACCT CAATGTGTGC	7260
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		*************	TOOTS DOOR	mmomoma mmo	Ammuna ACAC	AAAAmmoraa	7380
	TATTTCTAAG	ANTGGAATTG	TOGENTITIT	TICIGTATIG	ATTT PARCAG	nnnna FTCAA	/380
	TTTATAGAGG	TTAGGAATTC	CAAACTACAG	AAAATGTTTG	TTTTTAGTGT	CAAATTTTTA	7440
80	ARREADANCE.	CTCTTYCCATA	TCATATTCAN	CATTTTACAA	CTGCAGTATT	CACCTAAACT	7560
		CICTICCATA	LOMINITICAA	CULTITUCAN	CTGCWGTV11	Ch a amount	7500
80	AAAIAAAAA			GCCCTAGTGT	CTCCATGGAC	CHUNITTATA	7620
80	AGAAATAATC	TGTTACTTAT					
80	AAATAAAACA AGAAATAATC TTTATAATTG	TGTTACTTAT	TATTTTACTA	CTGAGTCAAG	TITTCTAGTT	CIGIGIAATT	7680
80	AGAAATAATC TTTATAATTG	TGTTACTTAT TAGATTTTTA ATGACGTAGT	TATTTTACTA	GTCTTACT**	ACCAGTTTT	TGACATTGTA	7680
80	AGAAATAATC TTTATAATTG GTTTAGTTTA	TGTTACTTAT TAGATTTTTA ATGACGTAGT	TATTTTACTA TCATTAGCTG	CTGAGTCAAG GTCTTACTCT	ACCAGTTTTC	TGACATTGTA	7740
	GTTTAGTTTA GTTTAGTTTA TTGTGTTACC	ATGACGTAGT TAAGTCATTA	TCATTAGCTG ACTTTGTTTC	GTCTTACTCT AGCATGTAAT	ACCAGTTTTC TTTAACTTTT	TGACATTGTA GTGGAAAATA	7680
85	GTTTAGTTTA TTGTGTTACC GABATACCTT	TAGATTTTA ATGACGTAGT TAAGTCATTA	TATTITACIA TCATTAGCIG ACTITGITIC GAACTITITA	GTCTTACTCT AGCATGTAAT TGAGAATAAC			7680 7740 7800
	GTTTAGTTTA TTGTGTTACC GABATACCTT	TAGATTTTA ATGACGTAGT TAAGTCATTA	TATTITACIA TCATTAGCIG ACTITGITIC GAACTITITA	GTCTTACTCT AGCATGTAAT TGAGAATAAC			7680 7740 7800
	GTTTAGTTTA TTGTGTTACC GAAATACCTT AATGGTTTTT	TAGATTTTA ATGACGTAGT TAAGTCATTA CATTTTGAAA ATCCAAGGAA	TCATTTACTA TCATTAGCTG ACTTTGTTTC GAAGTTTTTA TTGCAAAAAT	GTCTTACTCT AGCATGTAAT TGAGAATAAC		TGACATTGTA GTGGAAAATA ACATTGTTCA AAAAAAAAA	7680 7740 7800
	GTTTAGTTTA TTGTGTTACC GAAATACCTT AATGGTTTTT	TAGATTTTA ATGACGTAGT TAAGTCATTA	TCATTTACTA TCATTAGCTG ACTTTGTTTC GAAGTTTTTA TTGCAAAAAT	GTCTTACTCT AGCATGTAAT TGAGAATAAC			7680 7740 7800
	GTTTAGTTTA TTGTGTTACC GAAATACCTT AATGGTTTTT	TAGATTTTA ATGACGTAGT TAAGTCATTA CATTTTGAAA ATCCAAGGAA	TCATTTACTA TCATTAGCTG ACTTTGTTTC GAAGTTTTTA TTGCAAAAAT	GTCTTACTCT AGCATGTAAT TGAGAATAAC			7680 7740 7800

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5	1	11	21	31	41	51	
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	MRILKRPLAC	IOLLCVCRLD	WANGYYROOR	KLVERIGWSY	TGALINQKNWG	KKYPTCNSPK	60
			KFOGWDKTSL				120
	PKASKITTHW	GKCNMSSDGS	EHSLEGOKPP	LENGIYCFDA	DRFSSFEEAV	KGKGKLRALS	180
10	ILPEVGTEEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPMSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFK	DIVSISESOL	AVFCEVLTMO	Q9GYVMLNDY	LONNFREQQY	KPSRQVFSSY	300
	TGKEEIHEAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLITOGYOD	LGAILMNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPRLDLPPE	420
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15	RSPTRGSEPS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540
	GSKTVLRSPH	MILSGTARSL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPPIS	600
			VLI PESARNA				660
			IRVDESEKTT				720
	TEVTPHAFTP	SSRQQDLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVFPL	VTPLLLDNQI	780
20	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSE	LPRHLHTVSQ	840
	ILPOVISATE	SDKVPLHASL	PVAGGDLLLE	PSLAQYSDVL	STTHAASETL	EFGSESGVLY	900
	KTLMFSQVEP	PSSDAMMHAR	SSGPEPSYAL	SONEGSOHIF	TVSYSSAIPV	HDSVGVTYQG	960
			ASLLQPTHAL				1020
	PVSVAEFTYT	TSVFGDDNKA	LSKSEIIYGN	ETELQIPSEN	EMVYPSESTV	MPNNYDNVNK	1080
25	LNASLQETSV	SISSTKGMFP	GSLAHTTTKV	FDHEISQVPE	NNFSVQPTHT	VSQASGDTSL	1140
	KPVLSANSEP	ASSDPASSEM	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	VDTLLKTVLP	1200
	AVPSDPILVE	TPKVDKISST	MLHLIVSNSA	SSENMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
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30	PHRDGSVTST	KLLFPSKATS	ELSHSAKSDA	GLVGGGEDGD	TDDDGDDDDD	DRGSDGLSIH	1440
	KCMSCSSYRE	SQEKVIONDSD	THENS LINDON	NPISYSLSEN	SEEDNRVTSV	SSDSQTGMDR	1500
	SPGKSPSANG	LSQKHNDGKE	ENDIQTGSAL	LPLSPESKAW	AVLTSDEESG	SGQGTSDSLN	1560
	ENETSTDFSF	ADTNEKDADG	ILAAGDSEIT	PGFPQSPTSS	VTSENSEVFE	VSEAEASNSS	1620
0.5	HESRIGLAEG	LESEKKAVIP	LVIVSALTFI	CPAAFAGIFI	YWRKCFQTAH	FYLEDSTSPR	1680
35	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCTVDLGI	1740
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			EVIVMITHLY				1860
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40	AKRHAVGPVV	VHCSAGVGRT	GTYIVLDSML	OGIOHECLAN	IFGFLKHIRS	QRNYLVQTEE	1980
40	QYVFIHDTLV	EAILSKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIQQSDY	2040
	SAALKQCNRE	KNRTSSIIPV	ERSRVGISSL	SGEGTDYINA	SYIMGYYQSN	EFI ITQHPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDGQNMAED	EFVYWPNKDE	PINCESFKVT	LMAEEHKCLS	2160
	NEEKLIIQDF	ILEATQDDYV	LEVRHFQCPK	WPNPDSPISK	TPELISVIKE	EAANRDGPMI	2220
40	VHDEHGGVTA	GTFCALTTLM	HQLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVIL	2280
45	SLVSTRQEEN	PSTSLDSNGA	ALPDGNIAES	LESLV			
		574 DNA sec					
			n #: Bos sec	ruence			
50	Coding sequ	ence: 148-	4518				
50							
	1	11	21	31	41	51	
	1	1	1		!	1	
	CACACATACG	CACGCACGAT	CTCACTTOGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TOAGAAGCAG	AGGAG COGCA	120
55			TCTGGAAATG				180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
			CCCAAAACAA				360
c0	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
60	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACOGT	480
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65	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
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			TCCCTGCACA				900
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70	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
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	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200

TOGGARAGE CHIGARICST THATGATACE AUGSTINGAR AGTINGARS TO CAGTIOGATE GAGAGGACCA AACCAAGCAT GAATTITGA CAGATGCAT TOGAACCTA TOGAACCTATC TCAATAATT GCTACCCAAT ATGAGTATG TCTTCAGAT AGTAGCCATA

TGCACTAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT

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AAGGGTGATG TICOCAATAC ATCITTAAAT TCCACTICCC AACCAGTCAC TAAATTAGCC

ACAGAAAAAG ATATTTCCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG

ACMBRAJAM PARTITUCE I BACTETICHO ACTORROTO ANDROCO TOCCACTOTI 14 AGRICOLOGO (TOMANOS) 14 AGRICOLOGO (TOMANOS) (TOMANOS) (TOTANAS (TOTANOS) (TOMANOS (TOMANOS) (TOMANOS (TOMA)))))))))

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		AGACTAATTA					2220
	TCCTTTTCTG	CAGGCCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
_		CCTTTGCCTA					2340
5	TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
	GTATACAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTCAGCCCT	GACTITITATC	2520
	TGTCTAGTGG	TTCTTGTGGG	TATTCTCATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
	TTTTACTTAG	AGGACAGTAC	ATCCCCTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
10	CCAATTTCAG	ATGATGTCGG	AGCAATTCCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	A DOCA CARGO	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
	CAGCTTGCTG	AAAAGGATGG	CARACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
15	TACABCAGAC	CAAAAGCTTA	TATTGCTGCC	CANGGCCCAC	TGARATCCAC	AGCTGAAGAT	3000
	TTCTTGGAGAG	TGATATGGGA	ACATABTGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAAATG	TGATCAGTAC	TOGCCTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	A A COMPONIO	TCACTCAGAA	CACTOTOCAA	CTGCTTGCCT	ATTATACTOR	GAGGAATTTT	3180
	AMCITICION	ACACAAAAAT	AAAAAAGGGC	TOTOGRADAG	GARGACCCAG	TGGACGTGTG	3240
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20	OTCACACACT	TTGTGAGAAA	GCCAGCCTAT	GCCAAGGGCC	ATGCAGTGGG	GCCTGTTGTC	3360
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	CASCASALIC	ATTTGGTACA	AACTGAGGAG	CRATATOTOT	TCATTCATCA	TACACTOSTT	3540
25	CHANGMANII	TTAGTAAAGA	AACIGAGGAG	CTCCACACTC	ATATTOMO	CTATISTEADT	3600
23	COLORGOCATAC	TTCCTGGACC	AACIGAGGIG	ACA A ACCTAC	ACREACANT	CCAGCTCCTG	3660
	LCCCTCACTCA	ATATACAGCA	CACHOOCHINA CACHOOCHINA	TOTOCIACOC	TARROCARTO	CARCAGGGAA	3720
	MUCCHUICHA	CTTCTTCTAT	GAGIGACIAI	CLINCAGOCC	TAMBIOCINI: 0	mmca.mcccomc	3780
	AAGAATCGAA	GCACAGACTA	CATCCCTGTG	GAAAGAT CAA	GOOT LOCKY	CCACACCAR	3840
30	AGTOGAGAAG	TTACCCAGCA	CATCANTIGCC	CLERCATOR	ACCAMMONO	CACCAMCAMA	3900
30	GAATTCATCA	TTACCCAGCA	COCTCTCCTT	CALACCATCA	MOGNITICIO	GOOGLONIA	3960
	TGGGACCATA	ATGCCCAACT ACTGGCCAAA	GGTGGTTATG	ATTCCTGATG	GCCAAAAACAT	GGCAGAAGAT	4020
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		AAGAACACAA					4140
35	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CITGAAGTGA	GGCACTITCA	GTGTCCTAAA	4200
33	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTITIGAAC	TTATAAGIGT	TATAAAAGAA	4260
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	GTTTACCAGG	TAGCCAAGAT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	
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40	CCATCCACCT	CTCTGGACAG	TAATGGTGCA	GCATTGCCTG	ATGGAAATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAACA	CAGAAAGGGG	TGGGGGGACT	CACATCTGAG	CATTGTTTTC	4560
	CTCTTCCTAA	AATTAGGCAG	GAAAATCAGT	CTAGTTCTGT	TATCTGTTGA	TTTCCCATCA	4620
	CCTGACAGTA	ACTITICATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGTG	4680
4.5		CAAGACTTGT					4740
45	CAGTATTTCT	AAGAATGGAA	TTGTGGTATT	TTTTTCTGTA	TTGATTTTAA	CAGAAAATTT	4800
	CANTITATAG	AGGTTAGGAA	TTCCAAACTA	CAGAAAATGT	TTGTTTTTAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TGTAAATAAA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTCACCTAA	4980
	AGTAGAAATA	ATCTGTTACT	TATTGTAAAT	ACTGCCCTAG	TOTOTOCATO	GACCAAATTT	5040
50	ATATTTATAA	TIGTAGATIT	TTATATTTTA	CTACTGAGTC	AAGTTTTCTA	GTTCTGTGTA	5100
	ATTGTTTAGT	TTAATGACGT	AGTTCATTAG	CTGGTCTTAC	TCTACCAGTT	TTCTGACATT	5160
	GTATTGTGTT	ACCTAAGTCA	TTAACTTTGT	TTCAGCATGT	AATTTTAACT	TTTGTGGAAA	5220
	ATAGAAATAC	CTTCATTTTG	AAAGAAGTTT	TTATGAGAAT	AACACCTTAC	CAAACATTGT	5280
	TCAAATGGTT	TTTATCCAAG	GAATTGCAAA	AATAAATATA	AATATTGCCA	TTAAAAAAAA	5340
55	AAAAAAAAA	AAAAAAAAA	AAAAAA				

Seq ID NO: S75 Protein sequence: Protein Accession #: Eos sequence

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		LDFKAI IDGV					240
	TOTVONIVEK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSSY	300
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70	LIGTEELIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540
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		SEMPET ITYD					660
		ESFLOTHYTE					720
75	TEVTPHAFTP	SSROODLVST	VNVVYSQTTQ	PVYNAEASNS	SHESRIGLAE	GLESEKKAVI	780
	PLVIVSALTF	ICLVVLVGIL	IYWRKCFQTA	HFYLEDSTSP	RVISTPPTPI	FPISDDVGAI	840
	PIKHFPKHVA	DLHASSGFTE	EFETLKEFYQ	EVOSCTVDLG	ITADSSNHPD	MKHKNRYINI	900
	VAYDHSRVKL	AQLAEKDGKL	TDYINANYVD	GYNRPKAYIA	AQGPLKSTAE	DEWRMINSHN	960
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	VLDSHIHAYV	NALLIPGPAG	KTKLEKOFQL	LSQSNIQQSD	YSAALKQCNR	EKNRTSSIIP	1200
	VERSEVGISS	LSGEGTDYIN	ASYIMGYYOS	MEPI ITOHPL	LHTIKDFWRM	IWDHNAQLVV	1260
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	MHOLEKENSV	DVYQVAKMIN	LMRPGVFADI	EQYOFLYKVI	LSLVSTRQEE	MPSTSLDSNG	1440
	AALPDGNIAE						

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	1	!	L	<u> </u>	<u></u>	AACAAACAAA	60
	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GUAGGATTAA	AGGAGCCGCA	100
10	CAAAAAAAAC	ATTTCCTTCG	Crececeree	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120 180
10	CGGCGAGGGG	CCGCAGACCG	TCIGGAAATG	CGAATCCTAA	AGOGTTTOUT	CGCTTGCATT	240
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20	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
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	AATGGCTCAT	TGACATCTCC	TOOCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
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25	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAAG	1020
25	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
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	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260
30	GGTGCTATTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	
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	GAAGAGGGAA	AAGA CATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
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25	ACGAAATACA	ATGAAGCCAA TTCCCAATAC	GACTAACCGA	TOCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
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	AACTTGTCGG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
40	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
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	GGCAAAACAA	AGCTAGAGAA	ACAATTCCAG	CTCCTGAGCC	AGTCAAATAT	ACAGCAGAGT	3660
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	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	ACCATAATGC	CCAACTGGTG	3900
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	GGTATTTTT	TUTGTATTGA	TITTAACAGA	AAATTTCAAT	1 1 ATAGAGGT	INGGAATT'CC	4800

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AGUSTICIO GAMATAMA THATAMAN ORGANIZA ATMANDA CUTTOCHAN 496
GATATICAN CAMPANA THATAMAN ORGANIZA ATMANDA CUTTOCHAN 496
GATATICAN CHARLAGA FORMANI CALTAMAN BANATAM THATAMATI MARTITUTA 596
ATTAMAN CHARLAGA TETRAHOT THATAMAN THATAMATI MARTITUTA 516
CITAMITAM CHARLAGA TETRAHOT THATAMAN THATAMAN SALATITUTA 516
CITAMITAM CANCINANT THATAMATI THATAMAN AMATTAMAN 516
AGUSTATA THATAMATI CHARLAGA CANTOSTOA ATMATTITA CHARLAGAN 526
THOLDHAM AMATTAMAN CHARLAGAN CANTOSTOA ATMATTITA CHARLAGAN 5260
THOLDHAM AMATMAN AMATMAN THATAMAN THATAMAN 516
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Seq ID NO: 577 Protein sequence: Protein Accession #: BOS sequence

WO 02/086443

15 41 MRILKRPLAC IQLLCVCRLD WANGYYROOR KLVBEIGWSY TGALNOKNWG KKYPTCNSPK OSPINIDEDL TOWNVLKKL REGGMENTSL ENTFIRMTGK TVEINLTHOY RYSGYSEMY
PKASKITPHW GKCNMSSDGS EHSLEGQKFF LEMGIYCFDA DRYSSFERAV KGKGKLRALS 120 20 ILPEVOTEEN LOPKAIIDGV ESVSRFGKQA ALDPFILINL LPMSTDKYYI YNGSLTSPPC TDTVDMIVFK DTVSIESGOL AVCENTING OSSYMMADY LQNNFREGOY KFSRCVFSSY TCKEEIKEN CSSEPENVQA DPENYTSLLV TWERFWYUT TMIKKFAVLY QQLOGOQTK 240 300 HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPB LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480 25 RSPTRGSEPS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND GSKTVLRSPH MNLSGTASSL NTVSITEYEE ESLLTSPKLD TGARDSGGSS PATSAIFFIS 540 600 ENISOGYIPS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI 660 TAOPDVGSGR ESPLOTNYTE IRVDESEKTT KSPSAGPVMS OGPSVTDLEM PHYSTFAYFP 720 TEVTPHAFTP SSROODLVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP 30 LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPFTPIF PISDDVGAIP 840 IKHFPKHVAD LHASSGFTEE FEEVQSCTVD LGITADSSNH PUNKHKNRYI NIVAYDHSRV KLAQLAEDG KLYDIHANY VDGYNRPKAY IAAÇGPLKST AEDWWNHUE HRVEVIVMIT NUVEKGREKC DQYMFADGSE SYGNEVYTOK SVQVLAYYTV RHFTLRNYKI KKGSOKGRPS 900 960 1020 NUMERISMEN ORTHWANDS STORFUTTK STUDIATITY SHPTLERTK KRONDORFS (
GOVETOHET) ORTHWAND STORFUTTK ALTAREMY OFVERSAMS (GOTTITULA
(GOVETOHET) ORTHWAN ALTAREMY OFVERSAMS (GOTTITULA
TYRALITOP ARTHERNO (LLOGRICO SYVERALMON SHRONDRSSI IPVERSAM)
ANDERYWEN NUMERICA (GOTTION SHRONDRSSI IPVERSAMS
GOTTION SHRONDRSSI ORTHWAND SHRONDRSSI IPVERSAMS
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41

45 Seq ID NO: 578 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 501-4514

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	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
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		GAATCTTAAG					420
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		TGAAGCCAAG					1620
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		TATTTCCTTG					1740
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		GACTGCAGAA					1860
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		TATCCCATTC					1980
		GACAATAACA					2040
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5	TAGTGGTTCT	TGTGGGTATT	CTCATCTACT	GGAGGAAATG	CTTCCAGACT	GCACACTTTT	2580
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	TTTCAGATGA	TGTCGGAGCA	ATTCCAATAA	AGCACTTTCC	AAAGCATGTT	GCAGATTTAC	2700
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		ACTIGIAATI					4740
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		TCCAAGGAAT		AA FATAAATA	LIGUUNTTAA	AAAAAAAAAA	2240
	AMMUNAAAA	AAAAAAAAA	nan				
	0 TD NO.	550 D					
	pad TD MO:	579 Protein	1 sedneuce:				

55 Seq ID NO: 579 Protein sequence: Protein Accession #: EOS sequence

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	MVPKASKITF	HWGKCNMSSD	GSEHSLEGOK	PPLEMQIYCP	DADRESSEE	AVKGKGKLRA	60
60		ENLDFKAIID					120
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	SYTCKEEIHE	AVCSSEPENV	OADPENYTSL	LVTWERPRVV	YDTMIEKPAV	LYQQLDGEDQ	240
	TKHEFLTDGY	QDLGAILNNL	LPNMSYVLOI	VAICTNGLYG	KYSDQLIVDM	PTONPELDLF	300
	PELIGTEEII	KEEEEGKDIE	EGAIVNPGRD	SATNOIRKKE	PQISTTTHYN	RIGTKYNEAK	360
65	THRSPTRGSE	PSGKGDVPNT	SLNSTSOPVT	KLATEKDISL	TSQTVTELPP	HTVEGTSASL	420
	NDGSKTVLRS	PHINILSGTAE	SLNTVSITEY	EEESLLTSPK	LDTGAEDSSG	SSPATSAIPF	480
	ISENISOGYI	PSSENPETIT	YDVLIPESAR	NASEDSTSSG	SEESLKDPSM	EGNVWFPSST	540
	DITAOPDVGS	GRESPLOTNY	TEIRVDESEK	TTKSPSAGPV	MSQGPSVTDL	EMPHYSTFAY	600
	FPTEVTPHAF	TPSSROODLV	STVNVVYSQT	TOPVYNEASN	SSHESRIGLA	EGLESEKKAV	660
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	IPIKHPPKHV	ADLHASSGFT	BEFETLKERY	OEVOSCTVDL	GITADSSNHP	DNKHKNRYIN	780
	IVAYDHSRVK	LAGLAEKDGK	LTDYINANYV	DGYNRPKAYI	AAOGPLKSTA	EDFWRMIWEH	840
	NVEVIVMITN	LVEKGRRKCD	OYWPADGSEE	YGNFLVTOKS	WOVLAYYTVR	NFTLRNTKIK	900
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75	RTGTYIVLDS	MLOQIOHEGT	VNIFGFLKHI	RSORNYLVQT	RECYVFIHDT	LVEAILSKET	1020
	RVLDSHTHAY	VNALLIPGPA	GKTKLEKOFO	LLSOSNIOOS	DYSAALKOON	REKNETSSII	1080
	PVERSRVGIS	SLSGEGTDYI	NASYIMGYYO	SNEPILTOHP	LINTIKDEWR	MIWDHNAQLV	1140
	VMIPDGCNMA	EDEFVYWPNK	DEPINCESFK	VTLMABBEKC	LSNEEKLI 10	DFILEATQDD	1200
	YVLEVRHFOC	PKWPNPDSPI	SKTFELISVI	KEEAANRDGP	MIVHDEHGGV	TAGTFCALTT	1260
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Seq ID NO: 580 DNA sequence Nucleic Acid Accession #: BOS sequence Coding sequence: 148-4632

85

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20	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140 1200
	CACTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTIG	1260
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35	GCAACTTCTG	CTATCCCATT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCCTCC	1980
33	GAAAACCCAG GAAGATTCAA	AGACAATAAC	ATATGATGTC TTCAGAAGAA	TCACTALACCAG	ARTCTOCTAG	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTTGATG	AATCTGAGAA	GACAACCAAG	2220
40			GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
40	CATTATTCTA	CCTTTGCCTA	CTTCCACGGTC	A A COMPORTAT	CTCATGCTTT	PACCOCATOO	2400
	GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC		2520
45	CTAGTGGTTC	TIGIGGGTAT	TCTCATCTAC		GCTTCCAGAC		2580 2640
40	TACTTAGAGG	ACAGTACATC	AATTCCAATA	ABACCACTUTE	CARAGCATGT	TGCAGATTTA	2700
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	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCACCC		2820
50			TATCGTTGCC ACTGACTGAT			TGATGGCACAG	2880 2940
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	TYGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	3060
	AAAGGAAGGA	GAAAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	3120 3180
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55	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	3300
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	CTCCTCATTC	CTGGACCAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GGGTCTCACT	3660
	CTGTCACCCA	GGCTGGAGTG	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCCTCTCCCT	3720 3780
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	GAAGGCACAG	ACTACATCAA	TGCCTCCTAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	3960 4020
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	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTCAGTGTCC	TAAATGGCCA	4260 4320
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80	CTARARTTAG	GCAGGAAAAT	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCC	ATCACCTGAC	4740
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	TAGTTTAATG						5280
	TGTTACCTAA						5340
_		TTTGAAAGAA					5400
5	GGTTTTTATC	CARGGAATTG	CAAAAATAAA	TATAAATATT	GCCATTAAAA	AAAAAAAAA	5460
	AAAAAAAAA	алааааааа	A				

Seq ID NO: 581 Protein sequence:

10	Protein Ac	cession #: /	sus sequence	•			
	1	11	21	31	41	51	
	ī	Ī	Ī	1	1	1	
	MRILKRPLAC	IOLLCVCRLD	WANGYYROOR	KLVEBIGWSY	TGALNOKIWG	KKYPTCNSPK	60
	OSPINIDEDL	TOVNUNLKKL	KPOGWDKTSL	ENTFIRMTGK	TVEINLINDY	RVSGGVSEMV	120
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	TGKEEIHEAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
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	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540
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		ESFLOTHYTE					720
25	TEVTPHAFTP	SSRQQDLVST	VNVVYSQTTQ	PVYNEASHSS	HESRIGLARG	LESEKKAVIP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFOTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHPPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCTVDLGI	TADSSNHPDN	KHKNRYIMIV	900
	AYDHSRVKLA	OLAEKDGKLT	DYIMANYVDG	YNRPKAYIAA	QGPLKSTAED	FWRMIWEHNV	960
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30	SOKGRPSGRV	VTQYHYTOWP	DMGVPEYSLP	VLTFVRKAAY	AKRHAVGPVV	VHCSAGVGRT	1080
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	LDSHIHAYVN	ALLIPGPACK	TKLEKQFQGL	TLSPRLECRG	TISAHCNLPL	PGLTDPPTSA	1200
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		AANRDGPMIV					1440
	RPGVFADIEO	YOFLYKVILS	LVGTRQEENP	STSLDSNGAA	LPDGNIAESL	ESLV	

40 Seq ID MO: 582 DNA sequence Nucleic Acid Accession #: NM_002851.1 Coding sequence: 148..7092

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	CAAAAAAAAA	COGCAGACOG	CICCCCCCCC	CICICONCIC	TONOMMOCAG	AGGMGCCGCA	180
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	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCITACA	420
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55	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
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60	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
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	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
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70	GARGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAAATCA	GGAAAAAGGA	ACCCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
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	PERSONAL	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
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	100001110	AGACTAATTA	CACTCACATA	COTTOTTOTTO	ANTOTOMORA	CACAACCAAG	2220
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	areas areas	CCTTTGCCTA	CHICACHO	CACCURACAC	CUCATOTTT	TACCCCCATCC	2340
85	CALLALICIA	AGGATTTGGT	CTTCCCAACT	AACCHOOTAT	P CECCCAGAC	PACCCUPACCO	2400
00	TOURGACARC	GTGAGA CACC	TOURCOUTC	MOCTACACTA	CTOSCHORE	TOCTCTACTC	2460
	GIMINGAATG	TGCTTGACAA	TOTACOT	1001HUNGIA	GIGARGICII	DACTACTOR	2520
	ACCCCTTTGT	TOCTTOACON	TCHOWTCCTC	ANCHEIRCCC	C. C. LOCI IC		2320

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	TOSGCCTTGC	ATGCTACGCC	TGTATTTCCC	AGTGTCGATG	TGTCATTTGA	ATCCATCCTG	2580
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	ACTGAACTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
15	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
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	TCTCAAGCAT	CTGGTGACAC	TICGCTTAAA	CCTGTGCTTA	GIGCAAACTC	AGAGCCAGCA	3600
••	TOCTOTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
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	ACCOUNTABLE	TEGETGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
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35	ATCTCATACT	CACTATCTGA	GAATTCTGAA	GAAGATAATA	GAGTCACAAG	TGTATCCTCA	4620
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85	AATAATCTGT	TACTTATTGT	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	7620
	ATLATTOTAG	ATTITUTE	TTTACTACTG	AGTCAAGTTT	TCTAGTTCTG	TGTAATTGTT	7680 7740
	TAGTITAATG	AUSTAGTTCA	TIMGCIGGIC	TIMOTOTAGO	MOTITICION	Childratio	40

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Seq ID NO: 583 Protein sequence

Protein Accession #: NP_002842.1 31 41 10 MRILKRFLAC IQLLCVCRLD WANGYYROOR KLVEBIGWSY TGALNOKNING KKYPTCNSPK OSPINIDEDL TOVNVNLKKL KFOGWDKTSL ENTFIHNTGK TVBINLTNDY RVSGGVSEMV 120 FKASKITFHM GKCMMSSDGS BHSLEGOKPP LEMQIYCFDA DRFSSFBBAV KGKGKLRALS ILFEVCTBEN LDFXAIIDGV BSVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 100 240 15 IDTVDMIVFK DTVSISESQL AVFCEVLING OSGYVMIAMDY LQNNFREQQY KRSRQVFSSY TGKESHIEAN CSSPENNYAD DESYYTSLLV TWERFRVYVN THEKFAVLY QULGEDOTK HEFLINGTQD LGAILMNLLP NMSYVLQIVA ICTMGLYGKK SDQLIVDMYT NMFBLDLFFE 300 420 LIGTEBIIKE EEEGKDIEEG AIVNDGROSA INQIRKKEPQ ISTITHYNRI GTKYNEALDEREN RSPIRGSEFS GKGDVPNTSL NSTSOPVIKL AIRKDISLIS QTVIELPHIT VEGTSASIND 480 640 20 GSKTVLRSPH MALSGTAESL NIVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600 ENTROPY FR SEMPETITYD VLIPESARNA SEDSTSSESE ESLKDPSMEG NVWFPSSTDI 660 TAMPOVGSGR ESFLOTNYTE IRVDESEKTT KSFSAGPVMS OGPSVTDLEM PHYSTFAYFP TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNGETPLQ PSYSSEVFPL VTPLLLDNQI 780 INTTPAASSS DSALHATPVF PSVDVSFESI LSSYDGAPLL PFSSASFSSE LFRHLHTVSQ 840 25 ILPOVISATE SUKVPLHASL PVAGGDLLLE PSLACYSDVL STIHAASETL EFGSESGVLY 900 KTLMFSOVEP PSEDAMNHAR SSGPEPSYAL SDMEGSQHIF TVSYSSAIPV HDSVGVTYQG 960 SLFSQPSHIP IPKSSLITPT ASLLQPTHAL SCDCEWSGAS SDEEFLLPDT DGLTALNISS 1020 PVSVAEFTYT TSVFGDCNKA LSKSEIIYGN ETBLQIPSFN BWYYPSESTV MPMMYCHVNK 1080 LNASLQETSV SISSTROMFP GSLAHTTIKV FOHBISQVPE NNFSVQFTHT VSQASGDTSL KPVLSANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP 1140 30 1200 AVPSDPILVE TPKVDKISST MLHLIVSNSA SEEMMLHSTS VPVFDVSPTS EMGASLQGL TISYASEKYE PVLLKSESSH QVVPSLYSKD ELPQTANLEI NQAHPPKGRH VFATPVLSID 1260 1320 EPLNTLINKL IHSDEILTST KSSVTGKVFA GIPTVASDTF VSTDHSVPIG NGHVAITAVS 1380 PHRDGSVTST KLLFPSKATS ELSHSAKSDA GLVGGGEDGD TDDDQDDDDD RDSDGLSIHK 1440 35 CMSCSSYRBS QEKUMNIDSDT HENSLMDQNN PISYSLSENS EEDNRVTSVS SDSQTGMDRS 1500 POKSPSANGL SOKHNDOKEE NDIQTOSALL PLSPESKAWA VLTSDEESGS GOGTSDSLNE 1560 NETSTOPSFA DTNEKDADGI LAAGDSEITP GFPOSPTSSV TSENSEVEHV SEAEASNSSH ESRIGLAEGL ESEKKAVIPL VIVSALTFIC LVVLVGILIY WRKCFQTAHF YLEDSTSPRV 1680 ISTPPTPIFP ISDDVGAIPI KHFPKHVADL HASSGPTEEF ETLKEFYQEV QSCTVDLGIT 1740 40 ADSSNIPPONK HKNRYINIVA YDHSRVKLAQ LABKDGKLTD YINANYVDGY NRPKAYIAAQ 1800 GPLKSTAEDF WRMIWEHNVE VIVMITHLVE KGRRKCDQYW PADGSEEYGN FLVTQKSVQV LAYYTVRNFT LRNTKIKKGS QKGRPSGRVV TQYHYTQWPD MGVPEYSLPV LTFVRKAAYA 1920 LAYTYURIFT LENTKIKKGG QKGRFSGRV TYNHTYGHFD MAPRISLPV LIYVKAAAX KERNAPPVVV USANGVGRT D'IYULDSMU, GUGETTYNI FORHKIRSQ RIYUYTEG YVFHBTIVB AILSKETSVI DERIHAYWA LLIPOPAGKT KLEKOPOLLS QGRIQOGDVS AALKQCRIEK HRTSSIIPVE RSRVGISSLS GBGTDYIHAS YIMGYYQSNE FIITQHPLH TIKDFWRHIN DERAQLVVNI PODGNMAEDE FYYWFRKDEP INCESFKVTL WAEBIKCLSN 1980 2040 2100 2160 EEKLIIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT FELISVIKEE AANROGPMIV HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM RPGVFADIEQ YQFLYKVILS 2280 LVSTRQEENP STSLDSNGAA LPDGNIAESL ESLV 50

Seq ID NO: 584 DNA sequence Nucleic Acid Accession #: NM_005688.1 Coding sequence: 126..4439

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COGGGCAGGT GGCTCATGCT CGGGAGCGTG GTTGAGCGGC TGGCGCGGTT GTCCTGGAGC AGGGGCGCAG GAATTCTGAT GTGAAACTAA CAGTCTGTGA GCCCTGGAAC CTCCGCTCAG 120 AGAAGATGAA GGATATCGAC ATAGGAAAAG AGTATATCAT COCCAGTCCT GGGTATAGAA 190 60 GTGTGAGGGA GAGAACCAGC ACTTCTGGGA CGCACAGAGA CCGTGAAGAT TCCAAGTTCA GGAGAACTCC ACCOTTGGAA TGCCAAGATG CCTTGGAAAC AGCAGCCCGA GCCGAGGGCC 240 300 TOTCTOTTGA TGCCTCCATG CATTCTCAGC TCAGAATCCT GGATGAGGAG CATCCCAAGG
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CCCSTSTGGC CCAAGAAG GGGGAGCTCT CAATGGAAGA CSTSTGGCT CTGTCCAAGC 480 65 540 ACGACTOTTO TOACGTGAAC TGCAGAGAC TAGAGAGACT GTGGCAAGAA GAGCTGAATG 600 AAGTTGGGCC AGACGCTGCT TCCCTGCGAA GGGTTGTGTG GATCTTCTGC CGCACCAGGC 660 TCATCCTGTC CATCGTGTGC CTGATGATCA CGCAGCTGGC TGGCTTCAGT GGACCAGCCT 720 TCATGGTGAA ACACCTCTTG GAGTATACCC AGGCAACAGA GTCTAACCTG CAGTACAGCT 780 70 TOTTOTTAGT GCTGGGCCTC CTCCTGACGG AAATOGTGCG GTCTTGGTCG CTTGCACTGA 840 CTTGGGCATT GAATTACCGA ACCGCTGTCC GCTTGCGGGG GGCCATCCTA ACCATGGCAT 900 TTARGRANT CCTTARGTTA ARGARANTA ARGAGNANTC CCTGGGTGAG CTCATCAACA
TTTGCTCCAA CGATGGGCAG AGARGTTTA AGGCAGCAGC CGTTGGCAGC CTGCTGGCTG 960 1020 GAGGACCOST TOTTGCCATC TTAGGCATGA TFTATAATST AATTATTCTG GGACCAACAG 1080 75 GCTTCCTGGG ATCAGCTGTT TTTATCCTCT TTTACCCAGC AATGATGTTT GCATCAGGGC TCACAGCATA TTTCAGGAGA AAATGCGTGG CCGCCACGGA TGAACGTGTC CAGAAGATGA 1140 1200 ATGARGUTET TACTTACATT ARATTETCA ARATGATGC CIGGGTCARA GCATTTTCCC AGAGTGTTCA AAAAATCCGC GAGGAGGAGC GTCGGATATT GGAAAAAGCC GGGTACTTCC 1320 AGGGTATCAC TGTGGGTGTG GCTCCCATTG TGGTGGTGAT TGCCAGOGTG GTGACCTTCT 1380 80 CTOTTCATAT GACCCTGGGC TTCGATCTGA CAGCAGCACA GGCTTTCACA GTGGTGACAG 1440 TOTTCHATTC CATGACTTTT GCTTTGAAAG TAACACCGTT TTCAGTAAAG TCCCTCTCAG 1500 ARGCCTCAGT GOCTGTTGAC AGATTTAAGA GTTTGTTTCT AATGGAAGAG GTTCACATGA 1560 TARRIGACIA ACCAGCORGE COTCACATOR AGRIFAGAGAT GARRANTIGOC ACCTEGGORT 1620 GGGACTCCTC CCACTCCAGT ATCCAGAACT CGCCCAAGCT GACCCCCAAA ATGAAAAAAG 1680 85 ACAMGAGGGC TICCAGGGGC AAGRAAGAGA AGGTGAGGCA GITGCAGGC CATGAGCATC 1740
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COGRAGAGGA AGAAGGCAAC ACACCCCC TGGGCCACCT GGGCTACAG AGGACACTGC 1860

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	AGCIGCIGGA	TGACODICCOM	AGCATOGCOC	TOTAL	CACGGGGGGGG	ATCATCCTTC	3480
	CIGIGCOGCI	CONCERNIC	ACCULATION OF THE PARTY OF THE	CCCCCCCCCC	CATCTCTTAT	GCTGTCCAGT	3540
	TAACGGGGCT	GUNGALICCC	ACCCURACE	TEGERATETGA	CACAGAAGCT	CGATTCACCT	3600
30	0327328383	GRECARTOR	TECATTABGA	CTCTGTCCTT	GGAAGCACCT	GCCAGAATTA	3660
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	CTCACCGCAG	TCGTCGCACA	GICTCICICI	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
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	CAAAAAATCTG	AAATGTGAA	TAAAATTATT	TIGGATTPTG	LWWWWWWW	VVVVVVVVVV	3820
	AAAAAAAAA	MARNUMAN					
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	1	11	21 	31	41 	51 	
			RERTSTSGTH				60
75			YHHGLSALKP				120
			SSDVNCRRLE				180
			VKHLLEYTQA				240
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80			VQKIREEERR				420
			NSMTFALKVT				480
			SSHSSIQNSP				540
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	NHIFNSAIRK	HLKSKTVLFV	THOLOYLVDC	DEVIFMERGO	ITERGTHEEL	MNLNGDYATI	780
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5	VPHSVYGVYI VSDSMKDNPH KFFDTTPTGR LVILFSVLHI LDDNQAPFFL GLFQFTVRLA RYRENLPLVL IGLADLRSKL	QAACGPLAFL MQYYASIYAL ILMRFSKIMD VSRVLIRELK FTCAMRULAV SETBARFTSV KKVSFTIKPK SIIPQEPVLF SVGERQLLCI	SMAVMLILKA EVDVRLPFQA RLDNITQSPF RLDLISIALI ERINHYIKTL EKIGIVGRTG SGTVRSNLDP	IRGVVPVKGT EMFIQNVILV LSHITSSIQG TTTGLMIVLM SLEAPARIKN SGKSSLGMAL PNOYTEDQIW	LRASSRLHDE FFCVGMIAGV LATIHAYNKG HOQIPPAYAG KAPSPDNPQE FRLVELSGGC DALERTHMKE	LFRRILRSPM FPWFL/AVGP QEFLHRYQEL LAISYAVQLT GEVTFENAEM IKIDGVRISD CIAQLPLKLE	900 960 1020 1080 1140 1200 1260 1320
10	MLTIAHRLHT	VLGSDRIMVL	AQGQVVEFDT	PSVLLSNDSS	REYAMPAAAE	NKVAVKG	
15		586 DNA se id Accession mence: 89	1 #: NM_001	327.1			
	1	11	21	31	41	51	
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	Seq ID NO: Nucleic Ac: Coding seq	588 DNA se id Accession uence: 52	ı ≸ı Eos se	quence			
45	1	11	21	31	41	51	
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	TCCGCTGCCT	CAACTGCAAT	GACAACACTG	ATGGCATTCA	CTGCGAGAAG	TGCAAGAATG	300 360
80	CTCTTAGTGC	TOGATGTGAC COGATGTCTG	AACTCTGGAC	GGTGCAGCTG	TARACCAGGT	GTGACAGGAG	420 480
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	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGCCTGTCCT	900
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	CAGCCAGTAA	CATGGAGCAA	CTGACAAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
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	TCCTGGATTC	AGTGTCTCGG	CTTCAGGGAG	TCAGTGATCA	GTCCTTTCNG	GTGGAAGAAG	2700 2760
	CARAGAGGAT	CAAACAAAAA	QCGGATTCAC	TCTCAACGCT	GGTANCCAGG	CATATOGATG	2820
	AGTTCAAGCG	TACACAAAAG AAGTGGGAGA	AATCTGGGAA	ACTUGAAAGA	AGARGEACHG	CAGCICITAC	2880
35	AGAATGGAAA	ACAAGAAGCA	GAGAAATCAG	ATCAGCIGCT	TTCCCGTGCC	GTTGAGAGCA	2940
33	AAAGCAGAGC	CCTCAGAGAG	CTGAGTATGG	*CONTROCORCY	CACAAAACCA	CARCCTCARG	3000
	TOCTTAAAAA	GAGACTOTCC	TTTORCCTOC	AGG I GGMCAN	A CATOCACT	CACAGAGAGA	3060
	ANGCUATGAA	AAGAGCCCTG	COGNICACE	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
	OCCURRENCE OF	CCTGGAAATC	TOCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACTTGG	3180
40	A DOCCE A TOT	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
-10	GTGAGATGAG	GGAAGTGGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACA CGAATA	3300
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	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAGCIT	TCCCGAGCCA	3480
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	PUCAUPUGGG	CCACCTCCAT	TTGCTGGAGA	CARGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	ACABOTTOGA	GARCATTAGG	GACAACCTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	ARGCTGCCAT	AAATATTTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCATG	TGAGTGGGTG	GGATGGGGAC	ATTTGAACAT	GTTTAATGGG	3780
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	ammandana.	ATTCAATCCT	1010001100	CACCASASAT	GATTOCOCATC	PATGTATTTT	4560
	ATTAGTCCTA	CTCAATCTCC	TOTAL PROPERTY.	CTCCACCCAT	ANTARGAGAS	TOTTOCTACT	4620
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	TARCACCACT	CCCLATTCCT	GGAGGAACCA	GAGGCACTTC	CACCTTGGCT	GGGAAGACTA	5100
	TGGTGCTGCC	TTGCTTCTGT	ATTTCCTTGG	ATTTTCCTGA	AMSTGTTTTT	AAATAAAGAA	5160
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75	Seq ID NO:	591 Prote	in sequence				

Seq ID NO: 591 Protein sequence Protein Accession #: NP_005553.1

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	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDPRSCK	PCPCHNGFSC	SVMPBTEEVV	480

85

PCT/US02/12476

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	CIHNTAGIYC	DQCKAGYFGD	PLAPMPADKC	RACNONPAGE	BPVGCRSDGT	CVCKPGFGGP	600
	NCBHGAFSCP	ACYNQVKIQM EGASRSLGLQ	DOFMOQUERM	EALISKAQGG	DGVVPDTELE	GRMQQAEQAL	660 720
5	RLITQMQLSL	AESEASLGNT	NIPASDHYVG	PNGFKSLAGE	ATRLAESHVE	SASHMEQLTR	780
	ETEDYSKOAL	SLVRKALHEG	VGSGSGSPDG	AVVQGLVEKL	EKTKSLACQL	TREATQABLE	840 900
		ONGKEGREKS					960
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25	GCCCCAGTGG	AGGATTTACT	CCTATGCCGG	CGACAACATC	GTGACCGCCC	AGGCCATGTA	360
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	TOGCTOGGCT	GCTGCTTCTC ACCTCTTACC	TCTGCCTTCT	GGGAGGTGCC	CTACTTTGCT	GTTCCTGTCC	780 840
	CARROLOTIC	CHCHCACA CA CA	CACCCARAGO	CACABARATCA	TOTTONABOR	TAGGGGGGGGG	900
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45	TTTCATTGGT	CTCTATCTCC	TGAATCTAAC	ACATTTCATA	GCCTACATTT	CATCACCAAA	1560 1620
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	AAAADDAAAA	алаллалала	AAA				
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MAINGLOGILE PILAFIGHIO ATVETALOON REVENUESE VTAQAMIRSOL MMSCVSQSTG GO GICCAVVSEL MIGRATURE ARAMVOILL GYLAFFANT GROCKECEEE DEVIGUENMY 120 COGLEPLAGE LAUVARANY GOULDE UNETWARKS FOQALFTONA AASLCLIGGA 180 LLCCSCEPRET TSYSTERRY KHRESUSEEN VETWARKS FOQALFTONA AASLCLIGGA 180

WO 02/086443

Seq ID NO: 594 DNA sequence Nucleic Acid Accession 8: NM_006180.1 Coding sequence: 352..2820

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Seq ID NO: 595 Protein sequence Protein Accession #: NP_006171.1

75 MSSWIRWEGF AMARLHGECH LVVGFWRAAF ACPTSCKCSA SRINGSDESP GIVAFPRLEP NSVIDENITE IFIANÇKILE IINEDDVEAY VGLKNLTIVD SGLKEVAHKA PLKNSNLQHI NFTRNKLTSL SRKHFRHLDL SELILVONPF TCSCDIMMIK TLQEAKSSPD TQDLYCLNES 120 SKNIPLANLO IPMCGLPSAN LAAPHLTVEE GKSITLSCSV AGDPVPNMYW DVGMLVSKHM 240 80 NETSHTOGSL RITHISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH 300 WCIPPTVKGN PKPALCWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT 360 LIAKNEYCKO EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420 DUTTINTOREH LEUVAUVUTA SUUGECLIAM LELLKLARHS KECMKGPASV ISNDDDSASP 480 LHHISNGSNT PSSSEGGPDA VIIGMTKIPV IEMPQYFGIT NSQLKPDTFV QHIKRHNIVL 85 KRELGEGAFG KVFLAECYNL CPEQDKILVA VKTLKDASDN ARKOFHRBAE LLTWLQHEHI 600 VKFYGVCVEG DPLIMVFEYM KHGDLNKFLR AHGPDAVLMA EGNPPTELTQ SQMLHIAQQI 660 AAGMVYLASO HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYYRVG GHTMLPIRNM 720

WO 02/086443 PPESIMYRKF TTESDYNSLG VYLWBIFTYG KQPWYQLSHN EVIECITQGR VLQRPRTCPQ 780 EVYELMIGCW QREPHYRNII KGIHTLLQNL AKASPYYLDI LG

Seq ID NO: 596 DNA sequence Nucleic Acid Accession #: AF410899 Coding sequence: 483..2999

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	TGCATACCGG	ACCCCATTC	GCATCTAACA	AGGAATCTGC	GCCCCAGAGA	GTCCCGGACG	180
	COGCCGGTCG	GTGCCCGGCG	CGCCGGGCCA	TGCAGCGACG	GCCGCCGCGG	AGCTCCGAGC	240
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25	TUAATTITAU	GATCCTGGTG	COGNOGRATI	TGICIAGGAA	CONTITIONS OF THE	ATOTOTOTO	960
23						CTGAATGAAA	1020
	ACACTOTOCA CONCONNON	MANAGET TATAL	CONGICCAG	ACACTCHOOA	TTOTACTO		1080
	AMOTOGOOGG	ACCURACCEC	ACTIGUEGE	PAGGARAGIC	TATCACATTA	TCCTGTAGTG	1140
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	TAGGCGAAGG	CTTGGTGGCA	AUDIGIGITICS	TAGCIGARIG	CINIANCUIC	CONCOCNACO	2280
	AGGACAAGAT	TGAGGCCGAG	GTGAMGACCC	LOCALOR	TCACCACATA	OCHCOCHIOG	2340
	ACTICCACCG	CGTGGAGGGC	CACCCCCCCCC	TOTAL	TORGOTACATO	ARGCATGGGG	2400
50	ACCOUNTS	GTTCCTCAGG	GUT CP COCCO	CTOATGCCCT	CONGREGATE	GAGGGCAACC	2460
50	OCCOCACCGA	ACTIGACICAGO	TOGCAGATGC	TGCATATAGC	CCAGCAGATC	GCCGCGGGCA	2520
	TOGTOTACCT	GGCGTCCCAG	CACTTCGTGC	ACCOCCATT	GGCCACCAGG	AACTGCCTGG	2580
	TOGGGGGAGAA	CTTGCTGGTG	AAAATCGGGG	ACTITIGGGAT	GTCCCGGGAC	GTGTACAGCA	2640
	CTGACTACTA	CAGGGTCGGT	GGCCACACAA	TGCTGCCCAT	TCGCTGGATG	CCTCCAGAGA	2700
55	GCATCATGTA	CAGGAAATTC	ACGACGGAAA	GCGACGTCTG	GAGCCTGGGG	GTCGTGTTGT	2760
	GGGAGATTTT	CACCTATGGC	AAACAGCCCT	COTACCACCT	GTCANACAAT	GAGGTGATAG	2820
	AGTGTATCAC	TCAGGGCCGA	GTCCTGCAGC	GACCCCGCAC	GTGCCCCCAG	GAGGTGTATG	2880
	AGCTGATGCT	GGGGTGCTGG	CAGCGAGAGC	CCCACATGAG	GAAGAACATC	AAGGGCATCC	2940
	ATACCCTCCT	TCAGAACTTG	GCCAAGGCAT	CTCCGGTCTA	CCTGGACATT	CTAGGCTAGG	3000
60	GCCCTTTTCC	CCAGACCGAT	CCTTCCCAAC	GTACTCCTCA	GACGGGCTGA	GAGGATGAAC	3060
	ATCTTTTAAC	TGCCGCTGGA	GGCCACCAAG	CTGCTCTCCT	TCACTCTGAC	AGTATTAACA	3120
	TCAAAGACTC	CGAGAAGCTC	TCGAGGGAAG	CAGTGTGTAC	TTCTTCATCC	ATAGACACAG	3180
	TATTGACTTC	TTTTTTGGCAT	TATCTCTTTC	TCTCTTTCCA	TCTCCCTTGG	TIGITCCTIT	3240
65	TICTTITTT	AAATTTTCTT	TTTCTTCTTT	TTTTTCGTCT	TCCCTGCTTC	ACGATTCTTA	3300
05	CCCTTTCTTT	TGAATCAATC	TOGGETTETGE	ATTACIATIA	MCTCTGCATA	DACKARGGCC	3360
	TTAACAAACG	TAATTTGTTA	TATCAGCAGA	CACTCCAGTT	TGCCCACCAC	MACTANCIONI MACTANCIONI	3480
	GCCTTGTTGT	ATTCCTGCCT	TTGATGTGGA	TOMONOMO	T DOCUMENT	THI TICKCII	3540
	AAACTTTGTC	ACTICIOCIO	TACAGATATC	GAGAGITICI	COCTOTOTO	AAAAAAAAAAA	
70	TTATTATTAT	TACTUTTCTT	COCCURRATION	AMOGGGGGAGAMA	ANANCCAGAG	AGAAAGAAGA	3660
70	TOTATTATTATCA	ACCOCATATA	GGGAGGAACA	ABGACBACCA	CTGGGATCAG	CTGGTGTCAG	3720
	TOCCTACTTA	GGAAATACTC	AGCAACTGTT	ACCTGGGAAG	AATGTATTCG	GCACCTTCCC	3780
	CTGAGGACCT	TTCTGAGGAG	TARABAGACT	ACTGGCCTCT	GTGCCATGGA	TGATTCTTTT	3840
	CCCATCACCA	GARATGATAG	COTGCAGTAG	AGAGCAAAGA	TOGCTTCCGT	GAGACACAAG	3900
75	ATGGCGCATA	GIGIGCICGG	ACACAGTTTT	GTCTTCGTAG	GTTGTGATGA	TAGCACTGGT	3960
	TTGTTTCTCA	AGCGCTATCC	ACAGAACCTT	TGTCAACTTC	AGTTGAAAAG	AGGTGGATTC	4020
	ATGTCCAGAG	CTCATTTCGG	GGTCAGGTGG	GAAAGCC			
	Sea ID NO:	597 Prote	in sequence				

Seq ID NO: 597 Protein sequence Protein Accession #: AAL67965.1

80

	1	11	21	31	41	51	
	1	1	1	1	1	1	
	MSSWIRWHGP						60
85	NSVDPENITE	IFIANOKRLE	IINEDDVEAY	VGLRNLTIVD	SGLKFVAHKA	FLKNSNLQHI	120
	NFTRNKLTSL	SRKHFRHLDL	SELILVGNPF	TCSCDIMWIK	TLQEAKSSPD	TODLYCLNES	180
	SKNIPLANLQ	IPNCGLPSAN	LAAPNLTVEE	GKSITLSCSV	AGDPVPNMYW	DVGNLVSKHM	240

	WO 02/						
	WCIPFTVKGM LIAKNEYGKD	RITNISSDDS PKPALQWFYN EKQISAHFMG	GAILNESKYI WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	PTHMNNGDYT	300 360 420
5	VGPASVISND	LSVYAVVVIA DDSASPLHHI	SMGSNTPSSS	EGGPDAVIIG	MIKIPVIENP	QYFGITMSQL	480 540
	FHREARLIATN	RHNIVLKREL LQHEHIVKFY	GVCVEGDPLI	MVFBYMKHGD	LNKFLRAHGP	DAVLMARGNP	600 660 720
10	DYYRVGGHTM	HIAQQIAAGM LPIRWMPPES PRTCPQEVYE	IMYRKETTES	DVWSLGVVLW	EIFTYGKOPW	YQLSNNEVIE	780
10	Seq ID NO:			HMKKNIKGII	THIQHERMAS	PATEDING	
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	AAAACCTTGA	GGTGATTCAT	CTTCCAGGCT		CAAGTCTCTC		60
20	CTCTGGGTCC	TTAATGGCAG	CAGCCGCCGC	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	120 180
	GGATGAAAAG	ACTITITETTE	ACTATGACTG	ACCACGGTGG TGGCAACAAG	ACAGTCACAC	CTGTCAGTCC	240 300
	CCTGGGGAAG	ARACTARATG ATACTTACAG	TCACAACGGC	CTGGAAAGCA	CAGAACCCAG	TACTGAGAGA	360 420
25	CCAACCCCTC	ACCCTGCAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480 540
	AATGTGGACA	ACCOUNTED	CTGGAGCCAG	AAAGATGAAA	GANANGTGGG	AGAATGACAA	600
30	CTTCTTGATG	GGCATGGACA	GCACCCTGGA	GCCAAGTGCA	GGAGCACCAC	TCGCCATGTC	720
30	CATCCTCCCC	ACCCAACTCA TGCTTCATCC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	780 840
	AAGCTGATAC CCAGCTGCCC	CAAAAGGCTC	CTGTGAGCAC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	900 960
35	TGGACCCAAT	AGCTCATTCA ATTATGCAAT	CTGCCTTGAT	TCCTTTTGCC TGCTACCTGA	AACAATTTTA	CCAGCAGTTA	1020
5.5	TTCTGGCTGA	CTAAACAAGA GAATGATGAT	TATATCATTT	TCTTTCTTCT	CTTTTTGTTT	GGAAAATCAA	1140
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40	TTTAAATAAA	ATTTATATTA GAGTTCTATT	TOCCAAAAAA	AAAAAAAAA	AA	TGTACTGATA	1320
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	Protein Ac	cession #1 1	BAB61048.1				
45	1	11 	21	31 I	41	51 	
45 50	1 MAAAAATKIL FLHYDCGNKT LQARMSCBQK		21 GMSRAGRADP LNVTTAWKAQ FSFDGQIFLL	HSLCYDITVI NPVLREVVDI FDSEKRNWTT	PKFRPGPRNC LTEQLEDIQL VHPGARKNKE	AVQGQVDEKT ENYTPKEPLT KNENDKVVAM	60 120 180 240
	1 	11 - LCLPLELLES VTPVSPLGKK AEGHSSGSWQ IGWLEDFLMG	21 GMSRAGRADP LNVTTAWKAQ FSFDGQIFLL MDSTLEPSAG	HSLCYDITVI NPVLREVVDI FDSEKRNWTT APLAMSSGTT	PKFRPGPRNC LTEQLEDIQL VHPGARKNKE	AVQGQVDEKT ENYTPKEPLT KNENDKVVAM	120 180
	1 	11 LCLPLLLLLS VTPVSPLGKK AEGHSSGSWQ IGWLEDFLMG	21 GMSRAGRADP LNVTTAWKAQ FSFDGQIFLL MDSTLEPSAG equence	HSLCYDITVI NPVLREVVDI FDSEKRNWTT APLAMSSGTT	PKFRPGPRNC LTEQLEDIQL VHPGARKNKE	AVQGQVDEKT ENYTPKEPLI KNENDKVVAM LCCLLIILPC	120 180
50	1 MARARATKIL FLHYDCONENT LOARMSCHOOL SPHYFSMCDC FILEGI Seq ID NO: Nucleic Ac: Coding sequ	11	21 GMSRAGRADP LNVTTAWEAG PSFEOGIFUL MDSTLEPSAG equence 1 #: NM_001 182 21	HSLCYDITVI MPVLREVUDI FDSEKRNWTT APLAMSSGTT 898.1	PKFRFGPRWC LTEQLEDIQL VHPGARKWKB QLRATATTLI	AVQGQVDEKT AVQGQVDEKT ENYTPKE PLT ICHENDKVVAM LCCLLIILPC	120 180 240
50	1 MARARATKIL MARARATKIL LOARMSCEQK SPHYPSMGDC PILPGI Seq ID NO: Nucleic Ac: Coding sequ	11	21 GMSEAGRADP LNVTTANKAQ FSFEOGIFLL MDSTLEPSAG 4: NM_001 82 GCAGCTCCMG	HSLCYDITVI MYVLREVUDI FDSEKRMYTT APLANSSGTT 898.1 31 CTTTGTGCTC TGGCCACCCT	PKFRPGPRHC LTEQUEDIQL VHPGARKHKE QLRATATTLI 41 TGCCTCTGAG	AVQOQYDEKT AVQOQYDEKT AVQOQYDEKT ENYTPKEPLT KHENDKVVAM LCCLLIILPC	120 180 240 240
50	1 MARARATKIL FLHYDCONKT LQARMSCEQK SPHYFSMGDC FILPGI Seq ID NO: Nucleic According sequity and sequit	11 LCLPLLLLS VTPYSPLGKK AEGHSSGSWQ IGWLEDFLMG 600 DNA seid Accession acnee: 57 11 CTCCTCCTCT GAGGATAGG GAGGATAGG GGGGGCCCTT	21 GMSRAGRADP LNVTTANKAQ FSEDQIFLL MDSTLEPSAG equence 1 #: NM_001 82 21 GCAGCTCCAG GCAGCTCCAG ATANTCCGGC ATANTCCGGCA	HSLCYDITVI MYVLREVUDI FDSERRINTT APLANSSGTT 1898.1 31	PKFRPGPRNC LTEQLEDIQL VHPGARINKE QLRATATTLI 41 ITGCTCTGAG AGCTGTGGCC TAACAGGCC	AVGGQVDERT AVGGQVDERT AVGGQVDERT AVGGQVDERT KNEMDKVVMM LCCLLIILPC 51 GAGACCATGG CTCGGACTGGA CTCGAATGATG ACCAAAGATG	120 180 240 240
50 55 60	1 MARARATKILL FLHYDCONKT LQARMSCEQK SHYFSMGDC FILPGI Seq ID NO: Nucleic According sequitarian sequit	11 LCLPLLLLS VTPYSPLOKK AEGHSSGSWQ IGWLEDFIMG 600 DNA seid Accession acnec: 57 11 CTCCTCCTC GAGGATAGG GGGGGCCTT ACGTCCGCTG GGGTGCCCTG GGGTGCCCTG ACGTCCCCTG GGAGTAGGAG GGTGCCCTG	21 GMSEAGRADP LNVTTANKAQ FSEDQIFLL MDSTLEPSAG equence 1 #: NM_001 82 21 GCAGCTCCAG GCAGCTCCAG CATTACCCGG CACTTCGCCA CGGGTACTAA	 HSLCYDITVI NFVLREVUDI FDSERRMTT APLAMSSGTT 898.1 31 	PKFRFGPRHC LTEQLRDIQL VHPGARNHKE QLRATATTLI 41 1 TGCCTCTGAG AGCTGTGGCC TAACAAGGCC ACAAGGCCACAGGCCTTC CAAGTCCCAG	AVGGQVDERT AVGGQVDERT AVGGQVDERT ENTPREPLT RIENDERVVM LCCLLIILPC 51 GAGGACCATOG CTCGACTGGA CTCAATGATG GGGGGGTGGA CCCAACTTGG CCCAACTTGG	120 180 240 240 60 120 180 240 300 360
50	1 MAARAATKIL FLHYDCONKT LOAKMSCEOK SFHYFSMEDC FILEGI Seq ID NO: Nucleic Accoding sequitarian sequita	11 LCLPLLLLS VTPVSPLOKK AEGHISSGSWQ IGWLEDFLMG 600 DNA sid Accession acnce: 57 11 CTOCTCTCCT GAGTACCCTG GGAGGATAGG GGGGGATAGG GGGGGATAGG GGGGGATAGG GGGGGATAGG GGGGGATAGG GGGGGATAGG GGAGGATAGG GGGGGATAGG GGAGGATAGG	21 GMSRAGRADP LNVTTANKAQ FSEDQIFLL MDSTLEPSAG quence 1 #: NM_001 182 21 GCAGCI CCAG CTGCTCCTGC ATANTCGCG CACTITGCCA CTGGTATAGCA CTGGTATAGCA CTGGTATAGCA CTGGTATAGCA CTGGTATAGCA CTGGCCCCA CTGGTATAGCA CTGGCCCCA CTGGCCCCA CTGGCCCCA CTGGCCCCA CTGGCCCCA CTGGCCCCA CTGGCCCCA CTGGCCCCA	HSLCYDITVI NPVLREVUDI FDSERRWITT APLANSSGTT 898.1 31 CTTTGTGCTC TGGCCACCCT TGGGCACCTT TCAGGAGTAT TCAGGAGGACA CCATATGTAGCACCA TCAGAGGAGCA CCATATGTAGCACAGGAGCA TCAGAGAGGACA TCAGAGAGAGACA TCAGAGAGAGACA TCAGAGAGAGA	PKFRPGPRNC LTEQLRDIQL VHPGARKNKE QLRATATTLI 41 TGCCTCTGAG AGCTGTGGGC TAACGCAGAC TAACAAGGCC ACAGACCCTT CAAGTCCCAG	S1 GAGACCATOG CTCAAAGATG GGGGGGGGAGCATTGC CTCAAAGATG CCCAAACTTGC CTCTCAATGATC ACCAAACATGC CTCTCAATGATC ACCAAACATGC CTCAATGATC ACCAAACATTGC CTCAATGATC ACCAAACATTGC CTCAATGATC ACCAAACATTGC CTCAATGATCAACTTGC CTCAATGATCAACTTGC CTCAATGATCAACTTGC CTCAATGATCAACTTGC CTCAATGATCAACTTGC CTCAATGATCAACTTGC CTCAATGATCAACTTGC CTCAATGATCAACTTGC CTCAATGATCAACTTGC CTCAATGATCAACTTCAATGATCAACTTCAATGATCAACTTCAATGATCAACTTCAATGATCAA	120 180 240 240 120 180 240 300 360 420 480
50 55 60	MARARATKIL FLHYDOGNKT LQARMSCECK SPHYPSMGDC PILPGI Seq ID NO: Nucleic Ac: Coding sequ 1 GGCTCTCACC CCCAGTATCT GCCCCAACA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA A	11	21 GREAGRADP LRVTTANKAQ FSFOOTFLL MOSTLEPSAG CIPLL MOSTLEPSAG CIPLC CAG CAG CAG CAG CAG CAG CAG CAG CAG CA	HSLCYDITVI NPVLEEVUDI FDSEKRMVIT APLANSSGIT APLANSSGIT 898.1	PKFRPGPRIC LTEGLROTOL VHPGARKHKE QLRATATTLI 41 TGCCCCTGAG AGCTGTGGGC TAAGSCAGAC TAAGAGGCC CAAGAGCCC ACAGACCGTT CAAGTCCCAG ACCAGCCCT TCCCAAGCCCT TCCCAAGCCCT TCCCAAGCCCT TCCCAAGCCCT TCCCAAGCCCCT TCCCAACCCCCC	AVQQVDERT ENYTPREPLT ENYTPREPLT ENEMBRYVAN LCCLLITLEC 51 GAGACCATOG CTOGCTGGA CTCAATGATG ACCAAAGATG GGGGGGTGA CCCAACTTGG CTCTTCTCAGGA CAAGAATGCT TGTMTGGTC	120 180 240 240 120 180 240 300 360 420 480 540
50 55 60	1	11	21 GREAGRADP LAVITAMKAQ FEBROOTELL MDSTLEPSAG SQUENCE A #: NN_001 H2 21 GOMETICAN GOMETICAN CAGCAGAAC ARACAGAMGT TOGGCCGCG CAGCAGAC ARACAGAACT TOGGCCGCGT TOGGCCGCCT CAGCAGACCAGACCAGACCAGACCAGACCAG	HSLCYDITVI NPVLREVUDI POSERRIMIT APLANSSGTT APLANSSGTT S98.1 CTTTGTGCTC TGGCCACCTT GAGCCACCTT AGCCAGCACCACCACCACCACCACCACCACCACCACCACC	PKFRFGPRNC LTEQLEDIQUE LTEQLEDIQUE LTEQLEDIQUE VHPOARSUKE QLEATATTLI 41 TGCCTCTGAG AGCTGTGAG AGCAGCCGT TAACAAGGCC ACAGCCGTT CAAGTCGCT TCCAAGTCGTCT TCCCACCCCC CCCATTGTGCC CCCATTGTGCC CCCATTGTGCC CCCATTGTGCC CCCATTGTGCC	AVOGOVDERT ENTYPEE PLT KNENDKTVAM LCCLLITLPC 51 GAGACCATGG CTCGGCCTGGA CTCAATGATG GGGGGGTGA CCCAACTTG CCCAACTTG CTTTTCGAGC TGTAGTGCT TGTAGTGCT TGTAGTGCT TGCGCCAAGA	120 180 240 240 120 180 240 300 360 420 480
50 55 60 65 70	1	11	21 GMSEAGRADP LANTIANKAQ FSPEOQUELL MOSTLEPSAG SUMMERCE A 1 1 MM_001 182 21 GCAGCTCCAG CASCTACTAC CASCTACACAC CASCCTACTACTAC CASCCTACTACTAC CASCCTACTACTAC CASCCTACTACTACTACTACTACTACTACTACTACTACTACTA	HSLCYDITVI NPVLREVUDI POSERRIMIT APLANSSGTT APLANSSGTT S98.1 CTTTGTGCTC TGGCCACCTT GAGCCACCTT AGCCAGCACCACCACCACCACCACCACCACCACCACCACC	PKFRFGPRNC LTEQLEDIQUE LTEQLEDIQUE LTEQLEDIQUE VHPOARSUKE QLEATATTLI 41 TGCCTCTGAG AGCTGTGAG AGCAGCCGT TAACAAGGCC ACAGCCGTT CAAGTCGCT TCCAAGTCGTCT TCCCACCCCC CCCATTGTGCC CCCATTGTGCC CCCATTGTGCC CCCATTGTGCC CCCATTGTGCC	AVOGOVDERT ENTYPEE PLT KNENDKTVAM LCCLLITLPC 51 GAGACCATGG CTCGGCCTGGA CTCAATGATG GGGGGGTGA CCCAACTTG CCCAACTTG CTTTTCGAGC TGTAGTGCT TGTAGTGCT TGTAGTGCT TGCGCCAAGA	120 180 240 240 120 180 240 300 360 420 480 540 660
50 55 60 65	1	11	21 SASEAGRADE LAVITANKAQ FEBOLOGY LAVITANKAQ FEBOLOGY LAVITANKAQ FEBOLOGY LAVITANKAQ FEBOLOGY LAVITANKAQ FEBOLOGY LAVITANKAQ FEBOLOGY LAVITANKAQ FEBOLOGY LAVITANKAQ CANTACONA CANTACONA ALCARANGOT TOGOACCAGA COCACCITIC GOCCTOGOTAC LILI SEQUENCE COLOCITIC GOCCTOGOTAC LILI SEQUENCE COLOCITIC GOCCTOGOTAC LILI SEQUENCE COLOCITIC GOCCTOGOTAC LILI SEQUENCE COLOCITIC GOCCTOGOTAC LILI SEQUENCE COLOCITIC GOCCTOGOTAC LILI SEQUENCE COLOCITIC GOCCTOGOTAC LILI SEQUENCE COLOCITIC COLO	HSLCYDITVI NPVLREVUDI POSERRIMIT APLANSSGTT APLANSSGTT S98.1 CTTTGTGCTC TGGCCACCTT GAGCCACCTT AGCCAGCACCACCACCACCACCACCACCACCACCACCACC	PKFRFGPRNC LTEQLEDIQUE LTEQLEDIQUE LTEQLEDIQUE VHPOARSUKE QLEATATTLI 41 TGCCTCTGAG AGCTGTGAG AGCAGCCGT TAACAAGGCC ACAGCCGTT CAAGTCGCT TCCAAGTCGTCT TCCCACCCCC CCCATTGTGCC CCCATTGTGCC CCCATTGTGCC CCCATTGTGCC CCCATTGTGCC	AVOGOVDERT ENTYPEE PLT KNENDKTVAM LCCLLITLPC 51 GAGACCATGG CTCGGCCTGGA CTCAATGATG GGGGGGTGA CCCAACTTG CCCAACTTG CTTTTCGAGC TGTAGTGCT TGTAGTGCT TGTAGTGCT TGCGCCAAGA	120 180 240 240 120 180 240 300 360 420 480 540 660
50 55 60 65 70	1 MARARTKIL MARARTKIL MARARTKIL MARAKEE FILIPOOINT LOARNIGER SEQI ID NOI NUCLBIC ACCORDING MUCLBIC ACCORDING COCIONAGOA ANTOGOTACA ACTACTACAG A	11 C.P. ALL ALL ALL ALL ALL ALL ALL ALL ALL AL	21 UNERAGRADE LENTTANKAD FSENGOIFLL UNSTLEPSAG SQUENCE 1 %: NM_001 ECCTTOCAC CONTECTOCA	BUCYDITVI NPVLEEVUDI FESSERWENT 898.1 STEECHENT 1 CTTTGTGCCC GTGGCACCT GTGGCACCACT GTGGCACCACCACCACCACCACCACCACCACCACCACCACCA	PREPROPRIED LTEQUEDIOL VIREORISMES QUEATATTLI 41 TOCCTCTOAG ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGAGA ACCACCAGAGAGAG	AVOGOVDERT SHYTTKEELT SOURSENEVYMA LCCULTIBEC 51 GAGACCATOG CTOGCCTGGA TCTTTCGGCAGA GCCCTGGACTTCTTTTTTCGCTC TCTTTCGCCAACA TCTTCGCCAACA TCTTCGCCAACA TCTTCGCCAACA TCTTTCGCCCAACA TCTTTCGCCCAACA TCTTTCGCCCAACA TCTTTCGCCCAACA	120 180 240 240 120 180 240 300 360 420 480 540 660
50 55 60 65 70 75 80	MAAAATKILI MAAAATKILI MAAAATKILI LAAMMGEBK PILFYOGONI Mucleic Accoding sequ GGCTCTCACC CCCARTACT GCCCAACAA ACTACTACTA ACACCATCAC TCTACCACAC ACTACTACAC ACACCACAC ACACCACAC ACACCACACAC ACACCAC	11 CLPELILLS CLPELILLS CLPELILLS CLPELILLS CONCERNING 600 DEA sid Accession 600 DEA sid Accession 600 DEA sid Accession 600 DEA sid Accession 600 DEA sid Accession 600 DEA sid Accession 600 DEA sid Accession 600 DEA sid Accession 601 Protection 601	21 GNSAGRADP GNSAGRADP GNSAGRADP FSFOQIFLL NOTINENS SQUENCE 1 %: NN_001 GCAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTAGCAG GTAGC	BSLCYDITVI NFYLERUVDI FROSERREWTI APELNISSUTT APELNISSUTT APELNISSUTT APELNISSUTT TO APELNISSUTT APELNISSUTT APELNISSUTT TO APELNISSUTT TO APELNISSUTT TO APELNISSUTT APELNI	PREPROPRIED LTEQUEDIOL VIREORISMES QUEATATTLI 41 TOCCTCTOAG ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGAGA ACCACCAGAGAGAG	AVOGOVDERT SHYTTKEELT SOURSENEVYMA LCCULTIBEC 51 GAGACCATOG CTOGCCTGGA TCTTTCGGCAGA GCCCTGGACTTCTTTTTTCGCTC TCTTTCGCCAACA TCTTCGCCAACA TCTTCGCCAACA TCTTCGCCAACA TCTTTCGCCCAACA TCTTTCGCCCAACA TCTTTCGCCCAACA TCTTTCGCCCAACA	120 180 240 120 120 180 240 360 420 420 660 720
50 55 60 65 70 75	MAAAATKILI MAAAATKILI MAAAATKILI LAAMMGEBK PILFYOGONI Mucleic Accoding sequ GGCTCTCACC CCCARTACT GCCCAACAA ACTACTACTA ACACCATCAC TCTACCACAC ACTACTACAC ACACCACAC ACACCACAC ACACCACACAC ACACCAC	11 C. PEALLLS C. PEALLLS C. PEALLLS C. PEALLLS C. PEALLS	21 GNSAGRADP GNSAGRADP GNSAGRADP FSFOQIFLL NOTINENS SQUENCE 1 %: NN_001 GCAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTCCAG GTAGCTAGCAG GTAGC	BSLCYDITVI NFYLERUVDI FROSERREWTI APELNISSUTT APELNISSUTT APELNISSUTT APELNISSUTT TO APELNISSUTT APELNISSUTT APELNISSUTT TO APELNISSUTT TO APELNISSUTT TO APELNISSUTT APELNI	PREPROPRIED LTEQUEDIOL VIREORISMES QUEATATTLI 41 TOCCTCTOAG ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGA ACCACCAGAGA ACCACCAGAGAGAG	AVOGOVDERT SHYTTKEELT SOURSENEVYMA LCCULTIBEC 51 GAGACCATOG CTOGCCTGGA TCTTTCGGCAGA GCCCTGGACTTCTTTTTTCGCTC TCTTTCGCCAACA TCTTCGCCAACA TCTTCGCCAACA TCTTCGCCAACA TCTTTCGCCCAACA TCTTTCGCCCAACA TCTTTCGCCCAACA TCTTTCGCCCAACA	120 180 240 120 120 180 240 360 420 420 660 720

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	CATGGAGTTG	TGAAAGAATA	GCTGCAAAGC	ACCTAACACA	TAGTAAGGTT	CCCAGTGCAG	120
		TGGGTTGAGT					180
5	GGGTGGCAGG	CCGGTCCCCC	ACAAAAGATA	ACTUATUTE	TAATTTGCAA	GCTGCCTCAA	240
)		GGGGAACAGC	TCAACAATGG	GTCCCACTGC	CTCCTGGTGT	TGATAGAGAT	360
	TOOCCTORCO	CCCACCCTGG	CCCCCCCCCC	TCTGCTGAGC	ACCOMMODITA	ACCOUNT	420
	gggcTCCqCG	CCCCCCAGCC	CTGCCCCCCG	CGAAGGCCCC	CCGCCTGTCC	TEGCOTCCCC	480
	CGCCGGCCAC	CTGCCGGGGG	GACGCACGGC	CCGCTGGTGC	AGTGGAAGAG	CCCGGCGGCC	540
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	CGGGGGCCGC	GCGGCGCGGG	CTGGGGGCCC	GGGCAGCCGC	GCTCCGGCAG	CGGGGGGGGGG	660
		CTGCGCTCGC					720
	CGACGAGCTG	GTGCGTTTCC	GCTTCTGCAG	CGGCTCCTGC	CCCCGCGCGCGC	GCTCTCCACA	780
15	CGACCTCAGC	CTGGCCAGCC	TACTGGGCGC	COOGCCCCTG	CGACCGCCCC	COGGCTCCCG	900
13	GCCCGTCAGC	TGGAGAACCG	TOTAL COCCAC	GCGCTACGAA	GCGGTCTCCT	CCCTCCCCCTC	960
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	CCTCCCCCT	AGTOCCACTA	accreace accreace	TCAGCCAGGG	ACGARGGCCT	CARROTTORG	1080
		CGGTGGGTGA					1140
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	OGAGCCCTTC	GGACCCACTT	CTCACAGACT	CTGGCACTGG	CCAGGCCTCG	AACCTGGGAC	1260
	CCCTCCTCTG	ATGAACACTA	CAGTGGCTGA	GGCATCAGCC	CCCGCCCAGG	CCCTGTAGGG	1320
	ACAGCATTTG	AAGGACACAT	ATTGCAGTTG	CTTGGTTGAA	AGTGCCTGTG	CTGGAACTGG	1380
25	CCTGTACTCA	CTCATGGGAG	CIGGCCCC				
23	Seq ID NO:	603 Prote	in sequence				
	Protein Ac	cession #: 1	P_003967.1				
30	1	11	21	31	41	51	
טכ	1	!	1	!	1	1	60
	MELGLGGLST	LSHCPWPRRQ ARWCSGRARR	PALWPTLAAL	ALLSSVAEAS	LGSAPRSPAP	REGPPPVLAS	120
	PAGRUPGGRI	PVRALGLGHR	ODDIVEDDEC	OUCCODING	UDIGLACIAC	ACAT.PDDDCC	180
	BENSUBULDE	TRYEAUSEMD	VNSTWRTVDR	LEATACGCLG	INDUCATIONS	ALONI LINE TO LOO	=00
35	REVOUECORE	IKIDAVOLID	7.101 II.C. 12.C	DUNINCOCEDO			
-	Seq ID NO:	604 DNA s	equence				
	Nucleic Ac	ld Accession	n #: NM 0570	91.1			
	Coding seq	uence: 783.	.1445				
40	1	11	21	31	41	51	
	Ī	1	Ī	Ì	1	1	
	ACTGGCCGCT	GAGAGAAGAA	TCGGGTGGAG	CAGAGAGCAG	CTGCTGCAGG	GCAGACAGCC	60
		ATCTGCACGT					120
15		CCCTCACTCA					180
+3	CGCGTGTCTA	CAAACTCAAC	TCCCGGTTTC	COTGCCTCTC	CACCGCTCGA	GTTCTCTACT	240 300
	CTCCATATCC	GAGGGGCCCC		TACCCCCCTC			360
				CONTROLOGICA	ACGCTGGGGC	MANAGET GOOG	420
				GONICIGGIO	ACCC1GGGGC	GCCCGGCCCC	
	CGGGGCAGGG	cracaccac					
50	CACCGGACGG	CTGCGGCGGC	GGGCAGGAGG	AGGECTGAGGG	GCCCCCAGCC	CTCGCTGCCA	480
50	CACCGGACGG	CTGCGGCGGC	CGCCAGCAGC	AGGTCCCTCG	GGCCCCAGCC	CTCGCTGCCA	
50	CACCGGACGG CAGACAAGGC CCCGGGCCTG TAAAAGAGGC	CTGCGGCGGC CCGGGGGCTC GAGCCCCACA ACTGCCAGGT	CCCCAGCAGC CCCGAGGGTG GTACAGTCCT	AGGTCCCTCG CAGACTGCCT GGGCATGCGC	GCCCCCAGCC GCCAAGGCCA TGTTTGAGCT	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA	480 540
50	CACCGGACGG CAGACAAGGC CCCGGGCCTG TAAAAGAGGC	CTGCGGCGGC CCGGGGGCTC GAGCCCCACA ACTGCCAGGT	CCCCAGCAGC CCCGAGGGTG GTACAGTCCT	AGGTCCCTCG CAGACTGCCT GGGCATGCGC	GCCCCCAGCC GCCAAGGCCA TGTTTGAGCT	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA	480 540 600
	CACCGGACGG CAGACAAGGC CCCGGGCCTG TAAAAGAGGC GCCCAGCACT TCAACAGGAG	CTGCGGCGGC CCGGGGGCTC GAGCCCCACA ACTGCCAGGT GGTCCCCGGA GGTGGGGGAA	CGCCAGCAGC CCCGAGGGTG GTACAGTCCT AAGGTGCCTA CAGCTCAACA	AGGTCCCTCG CAGACTGGCT GGGCATGCGC GAAGAACAAG ATGGCTGATG	GCCCCAGCC GCCAAGGCCA TGTTTGAGCT GTGCAGGACC GGCGCTCCTG	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA CCGTGCTGCC GTGTTGATAG	480 540 600 660 720 780
	CACCGGACGG CAGACAAGGC CCCGGGCCTG TAAAAGAGGC GCCCAGCACT TCAACAGGAG AGATGGAACT	CTGCGGCGGC CCGGGGGCTC GAGCCCCACA ACTGCCAGGT GGTCCCCGGA GGTGGGGGAA TGGACTTGGA	CGCCAGCAGC CCCGAGGGTG GTACAGTCCT AAGGTGCCTA CAGCTCAACA GGCCTCTCCA	AGGTCCCTCG CAGACTGCCT GGGCATGCGC GAAGAACAAG ATGGCTGATG CGCTGTCCCA	GGCCCAGCC GCCAAGGCCA TGTTTGAGCT GTGCAGGACC GGCGCTCCTG CTGCCCCTGG	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA CCGTGCTGCC GTGTTGATAG CCTAGGCGGC	480 540 600 660 720 780 840
	CACCGGACGG CAGACAAGGC CCCGGGCCTG TAAAAGAGGC GCCCAGCACT TCAACAGGAG AGATGGAACT AGCCTGCCCT	CTGCGGCGGC CCGGGGGCTC GAGCCCCACA ACTGCCAGGT GGTCCCCGGA GGTGGGGGAA TGGACTTGGA GTGGCCCACC	COCCAGCAGC CCCGAGGGTG GTACAGTCCT AAGGTGCCTA CAGCTCAACA GGCCTCTCCA CTGGCCGCTC	AGGTCCCTCG CAGACTGGCT GGGCATGCGC GAAGAACAAG ATGGCTGATG CGCTGTCCCA TGGCTCTGCT	GGCCCAGCC GCCAAGGCCA TGTTTGAGCT GTGCAGGACC GGCGCTCCTG CTGCCCCTGG GAGCAGCGTC	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA CCGTGCTGCC GTGTTGATAG CCTAGGCGGC GCAGAGGCCT	480 540 600 660 720 780 840 900
	CACCGGACGG CAGACAAGGC CCCGGGCCTG TAAAAGAGGC GCCCAGCACT TCAACAGGAC AGATGGAACT AGCCTGCCCT CCCTGGGCTC	CTGCGGCGGC CCGGGGGCTC GAGCCCACA ACTGCCAGGT GGTCCCCGGA GGTGGGGGA TGGACTTGGA GTGGCCCACC GGGGCCCGCC	COCCAGCAGE CCCGAGGGTG GTACAGTCCT AAGGTGCCTA CAGCTCAACA GGCCTCTCCA CTGGCCGCTC AGCCCTGCCC	AGGTCCCTCG CAGACTGGCT GGGCATGCGC GAAGAACAAG ATGGCTGATG CGCTGTCCCA TGGCTCTGCT CCCGCGAAGG	GGCCCCAGCC GCCAAGGCCA TGTTTGAGCT GTGCAGGACC GGCGCTCCTG CTGCCCCTGG GAGCAGCGTC CCCCCCGCCT	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA CCGTGCTGCC GTGTTGATAG CCTAGCGGC GCAGAGGCCT GTCCTGGCGT	480 540 600 720 780 840 900 960
	CACCGGACGG CAGACAAGGC CACGGGCCTG TAAACAGGGC GCCAGCACT TCAACAGGAG AGATGGAACT AGCTGCCCT CCCTGGCCTC CCCTGGCCTC	CTGCGGCGGC CCGGGGGCTC GAGCCCACA ACTGCCAGGT GGTCCCGGGA GGTGGGGGAA TGGACTTGGA GTGGCCCACC CGCGCCCGCC	CGCCAGCAGC CCGAGGGTG GTACAGTCCT AAGGTGCCTA CAGCTCAACA GGCCTCTCCA CTGGCCGCTC AGCCCTGCCC GGGGACGCA	AGGTCCCTCG CAGACTGCCT GGGCATGCGC GAAGAACAAG ATGGCTGATG CGCTGTCCCA TGGCTCTGCT CCCCCGGAAGG CGGCCCGCTG	GGCCCAGCC GCCAAGGCCA TGTTTGAGCT GTGCAGGACC GGCGCTCCTG CTGCCCTGG GAGCAGCGTC CCCCCGGCCT GTGCAGTGGA	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA CCGTGCTGCC GTGTTGATAC CCTAGGCGG GCAGAGGCCT GTCTGGCGT AGAGCCCGGC	480 540 600 660 720 780 840 900 960 1020
55	CACCIGACGG CAGACAAGGC CCCGGGCACT TAAAAGAGGC GCCCAGCACT TCAACAGGA AGATGGAACT AGCCTGCCCT CCCTGGGCTC CCCTGGGCTG GGCCGCGGGGGGGG	CTGCGGCGGC CCGGGGGCTC GAGCCCACA ACTGCCAGGT GGTCCCGGA GGTGGGGGAA TGGACTTGGA GTGGCCCACC CGACCTGCCG GCACCTGCCG GCACCTGCCG GCAGCCTTCT	CGCCAGCAGC CCCGAGGGTG GTACAGTCCTA AAGGTGCCTA CAGCTCAACA GGCCTCTCCA CTGGCCGGTC AGCCCTGCCC GGGGGACGCA CGGGGACGCA	AGGTCCCTCG CAGACTGGCT GGGCATGCGC GAAGAACAAG ATGGCTGATG CGCTGTGCT CCCGCGAAGG CGGCCCGCTG CCCGCCGCTG CCCGCCGCCGCCCCCCCC	GGCCCAGCC GCCAAGGCCA TGTTTGAGCT GTGCAGGACC GGCGCTCCTG CTGCCCCTGG GAGCAGCGTC CCCCCGGCTC GTGCAGTGGA TGCACCCCA	CTCGCTGCCA CACTTTTGGC TCCGGGAGA CCGTGCTGCC GTGTTGATAG CCTAGGCGG GCAGAGGCCT GTCCTGGCGT AGAGCCCGGC TCTGCTCTC	480 540 600 660 720 780 840 900 960 1020 1080
55	CACCGGACGG CAGACAAGGC CACGGCCTG TAAAAGAGGC GCCCAGCACT TCAACAGGAG AGATGCCCT CCCTGGCCCG CCCCGCCGG GCCCCGCCGG GCCCCCGCCGC	CTGCGGCGGC CCGGGGGCTC GAGCCCCACA ACTGCCAGGT GGTCCCCGGA TGGACTTGGA GTGGCCCACC CGCGCCCCGC CCACCTGCCG CCACCTTCT CCCGGCGCGCC	CGCCAGCAGC CCGAGGGTG GTACAGTCCT AAGGTGCTAACA CAGCTCAACA GGCCTCTCCA CTGGCCGCTC AGCCCTGCCC GGGGACGCA CGGCCGCGCC	AGGTCCCTCG CAGACTGGCT GGGCATGCCG GAAGAACAAG ATGGCTGATG CGCTGTCCA TGGCTCTGCT CCCGGGAAGG CGGCCCGCTG CCCGGGCGCCG GCCCGGCCG	GGCCCAGCC GCCAAGGCCA TGTTTGAGCA GTGCAGGACC GGCGCTCCTG CTGCCCCTGG GAGCAGCGTC GTGCAGTGGA TGCACCCCA CCGCGCTCGA	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA CCGTGCTGCC GTGTTGATAG CCTAGGCGGC GCAGAGGCCT GTCCTGGCGT AGAGCCCGG TCTGCTCTCC GCAGCGGGGG	480 540 600 720 780 840 900 960 1020 1080
55	CACCIGACGG CAGACAAGGC CAGAGGCATG TAAAAGAGGC GCCAGCACT TCACAGGAG AGATGGAACT AGCCTGCCCT CCCTGGGCTC CCCCGCCGGG GGCGCCCC CCCGCGCGG	CTGCGGCGGC CCGGGGGCTCGGG ACTGCCGGG ACTGCCGGG ACTGCCGGG ACTGCCGGG CGGCCCGC CCACCTGCCGG GCAGCCTCC CCGCGGCGCCCCC CCACCTGCCGC	CGCCAGCAGC CCCGAGGGTG GTACAGTCCT AAGCTGCCTACA GGCCTCTCCA ACGCCTCCCC AGCCTGCCC GGGGACGCA CGCCTGCCC GGGGACGCA CGGCCTGGGC TCGCCCGGGCCCCGGCCTGGGC TCGCCCGGGCTGGGC TCGCCCGGGCTGGGC	AGGTCCTCG CAGACTGGCT GGGCATGCGC GAAGAACAAG ATGGCTGATG CGCTGTCCC TCCCGGGAAGG CGGCCCGCTG CCCGGGCAG GCCCGGGCAG TGCCGGGCAG TGCCGGGCAG	GGCCCAGCC GCCAAGGCC TGTAGAGACC GTGCAGGACC GGCCTCCTG GAGCAGCGTC CCCCCGGCCT GTGCAGTGGA TGCACCCCA TGCACCCCA CCGCGCCTCGGC CCGCGCCCGCCC GTGCACCCCA CCGCGCCCGCCCC CCGCGCCCGCCCCCCCC	CTCGCTGCCA CACTTITGGC TCGGGGGAGA CCGTGCTGCC GTGTTGATAG CCTAGGCGG GCAGAGGCCT GTCCTGGCGT AGAGCCCGGC TCTGCTCTTC GCAGCGGGGG CTGGGCACC	480 540 660 720 780 840 900 960 1020 1080 1140
55	CACCIGACOG CAGACAAGG CACCIGGACOTG TAAAAGAGG TAAAAGAGA TCACAGGAAG TCACAGGAAG AGATGGAACT CCCCGCCOG GCCCGCCGG GCCCGCCGG CCCGCCGGGGGG CCCGGCGG	CTGCGGCGGC CCGGGGGCTC CAGGCCACA ACTGCCAGG GGTGCGGGAA TGGACTTGGA GTGGCCACC GCGCCCGC CCACCTGCCG GCACCTTCT CCGGGGGGGG CCGCCTGCCG GCACCTTCT CCGGGGGGGG CCGCCTGCCG GCTGGTGCG GCTGGTGCG GCTGGTGCG	CGCCAGCAGC CCCGAGGGTG GTACAGTCCT AAGGTGCCTA CAGCTCAACA CTGGCCGCTC AGCCTTGCC GGGGGAGGAC CGGGCTGGGC CGGGCTGGGC TCGCAGCTGGTC TCGCAGCTGGTC TCGCAGCTGGTC TTCCGCTTCT	AGGTCCTCG CAGACTGGCT GGGCATGCGC GAAGAACAAG ATGGCTGATG CGCTGTCTCCT CCCGGGAAGG CGGCCCGCTC CCCGGGCGCG CCCGGCGGCGCGCGC	GGCCCAGCC GCCAAGGCCA TUTTTGAGCT GTGCAGGACC GGGGCTCCTG GAGCAGCGTC CCCCCCGGCT GTGCAGTGGA TGCACCCCA CGGGCTCGG CGGGCTCGG CTGCGGCCGGC	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA CCGTGCTGCC GTGTTGATAG CCTAGGCGGC GCAGAGGCCC GCAGAGGCCC GCAGGGGGG GCTGGCTCTCCGCGCGC GCGGGGGGGGGG	480 540 600 720 780 840 900 960 1020 1080
55	CACOGACOG CAGACAAGGC CCOGGCCTG TAAAAGAGGC GCCCAGCACT TCAACAGAAG AGATGGAACT CCCTGGGCTC CCCTGGGCTC CCCGCGGCGGG GGCGCCGCGGGGGGGG	CTGCGGCGGC CCGGGGGCTC GAGCCCCACA ACTGCCAGGT GGTGGGGGAA TGGACTTGGA GTGGCCGGC GCACCTTGCG GCACCTTGCG CCGCGGGGGGGA CCGCCTGCGGCGGCGGCGGCGGCGGCGGGGGGGGGG	CGCCAGCAGC CCCAAGGGTG GTACAATCCT AAGGTGCCTA CAGCTCACACA CTGGCCGCTCCC AGCCCTGCCC GGGGAGCGCA CGGGCTGGGGGTC AGCCTGCCC AGCCCTGCCC AGCCCTGCCC AGCCTGCCC AGCCTGCGCACTAGG TCCCACTAGG TCCCACTAGG AGCCTACTAGA AGCCTACTAGA	AGGTCCTCG CAGACTGCCT GAGAACAAG ATGCTGATG CGCTGTCCCA TGGCTCTCTCT CCCGCGAAGG CGCCCCCTG CCCCGCGCAG TGCCCGCCGCC GCCCGCCCC GCCCGCCAG TGCCGCCCCCC GCCGGCAG TGCCGGCCGCC GCAGGGCCGCCC GCAGGGGCC GCAGGGGCC	GGCCCAGCC GCCAAGCCCA TUTTTGAGT TUTTTGAGT TUTTTGAGT GTGCAGGACC GGGCTCCTG CTGCCCCTGG GAGCAGCAT TGCACCCCA CCGCGCTCGG CGGGCTCGG CGGCTCGG CGGCTCGGC CTGCGGCCCCC CTGCACCGCCCCCCCCCC	CTCGCTGCCA CACTTTTGGC TCGGGGGAGA CCGTGCTGCC GTGTTGATAG CCTAGGCGGC GCAGAGGCCT GTCCTGGCGT TCTGGCGGC GCAGCGGGGCCAC GCGCGGCCCC CCCCCGGGCTCC CCCCCGGGGCC	480 540 660 720 780 840 900 1020 1080 1140 1200
55	CACGGACGG CAGGACGG CAGGACAGG CAGGACAGC CAGGACAC CAGGACAC CAGGACAC CAGGACAC CAGGACAC CAGGACAC CAGGACAC CAGGACAC CAGGACAC CAGGACAC CAGGACAC CAGGACGC CAGGAGGACC CAGGAGGACC CAGGAGGACC CAGGAGACC CAGGAGACC CAGGAGACC CAGCAC CAGGACC CAGCAC CACAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CAGCAC CACAC CACAC CACAC CACAC CA	CTGCGGCGGC CCGGGGGGCTC CAGCCCACA ACTGCCAGT GGTCCCCGGA CGTGGGGGAA TGGACTTGGA GTGGCCCGGC CCACCTGCGG GCAGCCTTCT CCGGGGGGG CCGCTGCGC CCGCTGCGC CAGCCTGCGC CAGCCTGCGC CAGCCTGCGC CAGCCTGCGC CAGCCTGCGC CAGCCTGGCC	GGCCAGCAGC GCCAGCAGG GTACAGTCCT ANGGTGCTAACA GGCTCTCCA CTGGCGCTC GGGGACGCA CGGCCTGCCC GGGGACGCA CTGGCCC CGGCTGGGG TCGCACTGGG TTCCCATTCT AGCCTACTGG TGTGCGAC ACCTGGGGAC ACCTGGGGAC ACCTGGGAC ACCTGGGAC ACCTGCAC ACCTGCAC ACCTCCAC ACCTGCAC ACCTCCAC ACCTCAC AC	AGGTCCTCG AGGATCCCTCG CAGACTGCCT GGGCATCGCC GAGAACANG CGCTGTCCCA TGGCTCTCCT TGGCTCTCCCT CCCCGGAAGG CGCCCGCTG CCCCGGCAGG CCCCGGCCG CCCCGGCCG CCCCGGCCGCCCCCCCC	GGCCAGCE GGCAGGCC GCCAGGCC GGCGCCCGC GGCGCCCGCC GGCGCCCGCC	CTGCTGCA CACTTTTGGC TCGGGGGAGA CCTIGCTGC GTGTTGCTGC GCAGAGGCCT GTCTTGGGT AGAGCCGGC TCTGCTCTTC GCAGCGGGGCACC GCGGGCCTC CCCCGGGGT TCCTTCATGG GGCTGCTGA	480 540 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440
55	CACOGACOS CAGACAS CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CAGACAC CACAC CACACAC CACA	CTGGGGGGGCCCCGGGGGCCCACAACTGCAGGAGAACTGCAGAACTTGGAACTTGGAACTTGGAACTTGGACCACCCGGGCGCGGGGGGGG	GGCCAGCAGC GCCAGCAGC GTACAGTCCT AAGGTGCCTA CAGCTCACAC GGCCTCTCCA GGCCTCCCC GGGGACGCA CGGCCTGCCC GGGGTGGGG TCGCAGCTGGCC TTTGCAGCTACT TCGCAGCTTCT TCGCTTCT TCGCTTCT TCGCTTCT TCGCTTCT TCGCTTCT TCGCTTGCCGAC ACCGTGGAC ACCGTGGAC	AGGTCCTCG CAGACTGCT GGGCATGCGC GAGAACAAG ATGGCTGATG CGCGTCTCCT CCCCGGAAGG CGCCGGCGC GCCGGCGCG GCCGGCGCG GCACGGCTG GGCCGGCAG TGCCGGCAGGCAG TGCCGGCAGGCAG TGCCGGCTC TGGCCCGCTT TGGCCCTCCGGC	GGCCCAGCC GGCAGGCCAGCCAGCCAGCCAGCCCAGGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCAGCCCAGCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCAG	CTCGCTGCA CACTTTTGGC TCGGGGGAGA CCGTGCTGCTGC GTGTTGATAG CCTAGGGGG GCAGAGGCCT GCAGCGGGGGGCACC GCGGGCTCTC CCCCCGGGGT TCCTTCATAG GGCTGCCTGC TCCTTCATAG GGCTCCTC	480 540 660 720 780 840 900 1020 1140 1200 1320 1320 1340 1500
55	CACGGACGG CAGGGCTG TARARAGAGGG GCCAGGACAT TCARCAGGAG AGATGGACCT CCCGGGCCGC CCCGGGGGGGGGG	CTGGGGGGG CCGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGCCAGCAGC GCCAGCAGC GTACAGTCCT ANGGTGCTAACA GGCCTCTCCA CTGGCCGCTC GGGGAGCGCA OGCCTGCCC GGGGACCGA TCCCAGCTGG TTCCCGCTTCT AGCCTTGCACTA AGCCTTGCC CGGGCTGGGC CGGGCTGGGC CGGGCTGGGC CGGGCTGGGC CGGCTGGGC CGGCTTGCACTGG ACCGGC ACTGGCC ACTGGCC ACTGGCC ACTGGCCACTGG ACCGGCGCC ACTGGCCACTGGA ACCGCGCACCACTGCACCACCACCACCACCACCACCACCACCACCACCACCAC	AGGTCCTCG AGGATCCCTCG CAGACTGCT GGGCATCGCC GAGAACANA ATGGCTGATG GGCTGTCCCA CCCCGGAAGG CCCCGGGCA GCCCGGGCA GCCCGGGCA GCCCGGGCC GCCCGGGCC GCCCGGGCC GCCCGGGCC GCCCGGGCC GCCCGGGCC GCCCGGGCC GCCCGGGCC GCCCGGGCC GCCCGGGCC GCCCGGGCC GCCCCGGGCC GCCCCGGGCC GCCCCGGCC GCCCCGGGCC GCCCCGGCC GCCCCGGCC GCCCCGGCC GCCCCGGCC GCCCCGGCC GCCCCCGGCC GCCCCCGGCC GCCCCCGGCC GCCCCCGGCC GCCCCCGGCC GCCCCCGCC GCCCCCGGCC GCCCCCGGCC GCCCCCGCC GCCCCCGCC GCCCCCGCC GCCCCCC	GGCCCAGCE GCCAAGGCA TGTTTGAGCT GTGCAGGAC GGGCCTCCT GTGCCCTGG GAGCAGCAT CCCCCCCGCT GTGCAGTGA CCGCCGCT GTGCAGTGA CCGCGCGC CTGCAGTGA CCGCGCGC CCGCGCT CGGCGCGC CCGCGCT CGCGCGCG	CTGCTGCA CACTTTTGGC TCGGGGAGA CCGTGCTGC GTGTTGATAG CTAGGCGGG GCAGAGGCT TCTGCTGCT GCAGCGGGG CTGGGCACC CCCGGGGT TCCTTCCTC CCCCGGGGT TCCTTGCTG GCTGCTGCTG GCTGCTGCTG	480 540 660 720 780 840 900 960 1020 1140 1260 1320 1380 1440 1500
55	CACOGACOS CAGACA	CTGGGGGGGCCCGAGGGCCCAGAGGCCCAGGGGGGAGAGCCCGGCCAGGGGGG	GGCAGAGAG CCCAAGAGGTG GTACAGTCCT AAGGTGCTA CAGCTCTCAACA GGCCTCTCCA GGCCTGCCC GGGGGGAGGCA GGGCTGGGG CGGGCTGGGG TGGCAGTTGCACA TTGCAGTTGT TGCAGCTGGAC ACCTGTGAC ACCTGTGAC ACCTGTGAC ACCTGTGAC ACCTGGAC ACCTGTGAC ACCTGTGAC ACCTGTGAC ACCTGTGAC ACCTGTGAC ACCTGTGAC ACCTGTGAC ACCTGTGAC ACCTGTGAC	AGGT COCTICS CAGACTGGGT GGGCATGGGC GAGAACAAG ATGGCTGATG CGCATGTGCT CCCGCGAAGG CGGCCGGCGG GCCCGGGGGG GCCCGGGGGG CCAGGGGGC CCAGGGGGC CCAGGGGGC CCAGGCCTA GGCCTCAGC CTGGGCCTAGGC CTGGGCCTAGGC CTAGGCCTTA GGCCTCAGCC CTAGTCCGG	GGCCCAGCE TGTTTGAGCT GGCATAGCACT GGGCCTCCTG GGCCCTCCTG GGCCCCCCCCCC	CTGCTGCCA CACTITISGC TCGGGGGGAGA CCGTGCTGCC TCGTGTGCC GCAGAGGCCT GTCTTGGGGT TCTTGGGGT TCTTGGGGT TCTTGCGGT TCTTGCGGT TCGGGGCAC GCGGGCTCT CCCCCGGGCT TCCTTCATGG GGCTGCCTG GCTGCCTGC GGGCTCTC GCGGGGT TCCTTCATAGG GGCTGCTC GCTCATAGG	480 540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500
i5 i0	CACCGACCGG CAGGACTG TAAAAGAGC GCCCAGCACT TCAACAGGAG AGATGGAACT AGCCTGCCCT CCCCGGCGGG GCCGGCGGGGGG GCCGGCGGGGGG GCCGGCCGCGCGGGGGG	CTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGCAGAGAG CCGCAGAGGGGGGGAGAGAGGGGGGAGCAGAGGGGGAGCGAGGGGGAGCGAGGGGAGCGAGGGGAGCAGAGGGAGCAGAGGGAGCAGAGGAG	AGTICCITICS CAGACTGCT GGCATCCG GAGAACANA ATGCTGATG GCGTGATG GCGTGATG GCCGCGGGG GCCGGGGG GCCGGGGG GCCAGGGCT GCCGGGGCT GCCGGGGCT GCCGGGGCT GCCGGGGCT GCCGGGGCT GCCGGGGCT GCCGGGGCT GCCCGGGGCT GCCCGGGGCT GCCCGGGCT GCCCGGGCT GCCCCGGGCT GCCCCGGGCT GCCCCGGGCT GCCCCGGGCT TGGACCCTAG	GGCCCAGCE GCCAGGCC GCCAGGCC GGCGCCCGGC GGGCCCCGG GGGCCCCGGC GGCCCCGGCC GGCCCCGCC GGCCCCGCC GGCCCCGCC GGCCCCGCC CGCCCCCC	CTGCTGCCA CACTITISGE TCGGGGGGGGG GTGTTGATAG GCAGAGGCCT GTCTTGGCGG GTCTTGGCGG GCAGCGGGGGGCACC GCGCGGGGGGCACC CCCCGGGGCT CTCCTCTCTGCGT TCCTTCTCTGCT GCGCACC GCGCACACCAG GGACACTGA GGACACTGA GGACACTGA GGACACTGA GGACACTGA GGACACTGA GGACACTGA GGACACTGA GGACACTGA GGACACTGA GGACACTGA GGACACTGA	480 540 600 720 780 840 900 1020 1140 1200 1320 1380 1440 1500 1560 1680
i5 i0	CACCGGACCGG CCCGGCCTG TAAAAGAGCCCCCCCCCC	CTGGGGGGCC CGGGGGCCCGGGGGGCCGGCGGGGGGGGG	GGCAGAGAG CCCAAGAGG GTACAGTCCT AAGGTGCTA AAGGTGCTA CAGCCTCCCA GGCCTCCCA GGCCTGCCC GGGGCTCCCC CGGGCTGCGC TCGCAGCTGCCC TCGCACCTCCC TCGCACCTGCCC TCGCACCTGCCC TCGCACCTGCCC TCGCACCTGCCC TCGCACCTGCCC TCGCACCTGCCC TCGCACCTGCCC TCGCACCTGCCC TCGCACCTCC TCGCACCTCCC TCGCACCTCC TCGCACCTCCC TCGCACCTCCC TCGCACCTCCCC TCGCACCTCCCCCC TCGCACCTCCCCCC TCGCACCTCCCCCC TCGCACCTCCCCCCC TCGCACCTCCCCCCC TCCCCCCCCCC	AGGTCCTICS CAGACTGGCT GGGCATGCGC GAGACTAGGC GAGACACAG ATGGCTGATG CGCCGCTGATG CCCCGGAAGG GGCCCGCTGCC CCCCGGCAGG CCCCGGGCCGCC CCCCGGCCGCC CCCCGGCCGCC CCCCGGCCGCC	GGCCCAGGC GCCAGGC TUTTTGAGCT GGCGCTCCTG GGCGCTCCTG CTGCCCCTGG GMGCAGCGTCCA TGCACCCCAC TGCACCCCAC CCGCCTCTGGC CTGCCCCACCC CCGCCTCGGC CTGCGACCA CCGCCTCGGC CCACCCCACC	CTGCTGCCA CACTITISGC TCGGGGGGAGA CCGTGCTGCC GCGTGTGTGATAG CCTAGGGGGC GCTGCTGCGTG GCACCGGG TCTGCTGTG GCACCGGGCTCC CCCCGGGGCT TCCTTCATGG TCCTCTCATGG GGCTGCCTG GCGCCTGG GCTGCCTGGGGGT TCCTTCATGG GCTGCCTGAAGG GCGACACTGA GAGACCTCAG GAGACCTCAC GAGACCTCAC GCGCACCTGAAAGC GCACACTGA GAGACCTCAC GCTGAAAGC GAGACCTCAC GCTGAAACCTG GAGACACTGA	480 540 600 720 780 840 900 960 1020 1140 1240 1340 1560 1560 1680 1740
i5 i0	CACCGACCGG CAGACGGG CCOGGCCTG TARARAGAGG GCCCAGCACT TCSACAGGAG AGATGGAACT AGCCTGCCCT CCCCGGCGGG GGCGGGGGGG GCCGGCCG	CTGGGGGGG CTGGGGGGCTC GAGCCCCAGA ACTGCCAGAT GGTCCCGGA GTGGGCCCGC GGGCCCGG GCACCCTTCC CCGGCGGG GCACCCTTCC CCGCGGGGGG GCACCCTTCC CAGCCTGGC CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACAGGCCC CTACCGGTGGA CAGAGCCCTC CTCGGAGAA CAGAGCCCTC CTCGGACAA CAGAGCCCTC CTCGGACAA CAGAGCCCTC CTCGGACAA	GGCAGCAGE CCOAAGGGTG GTACAOTCCT AAAGTCCTAACA GGCCTCTCCA AGCCTGCCC GGGGAGCGCA GGCCTGCCC GGGGAGCGCA CGGCCTGCCC TCCCACACACA CGCCTACCC CGGCCTGCGC TCCCACTAC AGCCCTACCC AGCCCTACCC AGCCCTACCC AGCCCTACCC AGCCCACCAC AGCCCACCAC AGCCCACCAC AGCCCACCAC AGCCCACCAC AGCCACCAC AGCCCACCAC AGCCCACCAC AGCCCACCAC AGCCCACCAC AGCCCACCAC AGCCACCAC AGCCCACAC AGCCCACCAC AGCCCACCAC AGCCCACCAC AGCCCACAC AGCCCACCACCAC AGCCACCAC AGCCCACAC AGCCCACCAC AGCCCACCAC AGCCCACCACCAC AGCCCACCAC AG	AGGT COCNOS CAGACTAGACT GGCCATGCCC GGCCATGCCC GGCCATGCCC GGCCGCCC GCCCGCCCC GCCCGCCCC GCCCGCCCC GCCCGCCCC GCCCGCCCC GCCCGCCCC GCCCGCCCC GCCCGCCCC GCCCGCCCC GCCCGCCCC GCCCGCCCC GCCCCCC	GGCCCAGGC GCCAGGC TOTTFGAGCT TOTGCAGGACC GGGCTCCTG GMGCAGCGTCCTG GMGCAGCGTCCGG GTGCCAGGCT GTGCAGTGGA TGCACCCCGGC GTGCAGTGGA GGGCTCGGG GCGCTCGGG CCTGGGACCG CCTGGGACCG CCAGGCTGGA ACAGGCTGGA ACAGGCAGA ACAGGTGAA ACAGGTGAA ACAGGTGAA ACAGGTGAAG AAGGCACGGC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCAGCC CTGGCCACGC CTGGCCACGCC CTGGCCACGC CTGGCCACGC CTGGCCACGC CTGGCCACGC CTGGCCACGC CTGGCCACGC CTGGCCACGC CTGGCCACGC CTGGCCACGC CTGCCCACC CTGGCCACGC CTGCCCACC CTGGCCACGC CTGCCCACC CTGCCCACC CTGCCCC CTGCCCC CTGCCCC CTGCCCC CTGCCCC CTGCCCC CTGCCCC CTGCCCC CTGCCCC CTGCCCC CTGCCCC CTCCC CTCCC CTCCC CTCCC CTCCC CTCCC CTCCC CTCCC CTCCC CTCCC CTCCC CTCCC CTC CTCC CTC	CTGCTGCCA CACTITISGE TCGGGGGGGG TCGGGGGGGGGGGGGGGGGGGGGGGG	480 540 600 720 780 840 900 1020 1080 1140 1260 1320 1380 1560 1560 1620 1740 1800
i5 i0	CACCGGACCGG CACGGACCGG CACGGACCTG TCAACAGGGA AGATTGGACCCCCCCCCC	CHIGGIGGIG COGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGI	GGCCAGCAGC GCCCAGCAGC GTACAOTCCT ANGGTGCCTA CAGCTCACAC GGGCTCACA GGCCTCCC GGGGGAGCCA GGCCCTGCCC GGGGACCAC GGGCCAGCAG ACCATGGGC TTGCCACTACTA ACCCTTCTACAC ACCCTTGCACA ACCCTTGCACA ACCCTTGCACA ACCCTTGCACA ACCCTTGCACA ACCCTTCCACA ACCTTCCACA ACCTTCCACA ACTTCCACA ACTTCCACA ACCACACTGACA ACCACACTGACAC ACTTCCACA ACTTCCACA ACTACACACTGAC ACCACACTGACAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACTACACA ACTACACTACAC ACTACACTAC ACTACACTACAC ACTACACTACAC ACTACACTACAC ACTACACTACAC ACTACACTAC ACTACAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACAC ACTACACTAC ACTACAC ACTACACTAC ACTACAC ACTACACTAC ACTACACTAC ACTACAC ACTACACTA	AGGTCCCTCG GAGGATCCCC GAGGATCCCC GAGGATCCCC GAAGAACAAG ATGGCTGATC GGCTCTCCT TGGCTCCCCCCCCC CCCCCCCCCC	GGCCCAGGC GCCAGGC TOTTFGAGCT TOTGCAGGACC GGGCTCCTG GMGCAGCGTCCTG GMGCAGCGTCCGG GTGCCAGGCT GTGCAGTGGA TGCACCCCGGC GTGCAGTGGA GGGCTCGGG GCGCTCGGG CCTGGGACCG CCTGGGACCG CCAGGCTGGA ACAGGCTGGA ACAGGCAGA ACAGGTGAA ACAGGTGAA ACAGGTGAA ACAGGTGAAG AAGGCACGGC CTGGCCAGCGC CTGGCCAGCGC AAGGCACGGC	CTGCTGCCA CACTITISGE TCGGGGGGGG TCGGGGGGGGGGGGGGGGGGGGGGGG	480 540 600 720 780 840 900 1020 1200 1200 1320 1340 1500 1560 1680 1740
55 50 55	CACCGGACCGG CACGGACCGG CACGGACCTG TCAACAGGGA AGATTGGACCCCCCCCCC	CTGGGGGGG CTGGGGGGCTC GAGCCCCAGA ACTGCCAGAT GGTCCCGGA GTGGGCCCGC GGGCCCGG GCACCCTTCC CCGGCGGG GCACCCTTCC CCGCGGGGGG GCACCCTTCC CAGCCTGGC CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACCTGGAGA CACAGGCCC CTACCGGTGGA CAGAGCCCTC CTCGGAGAA CAGAGCCCTC CTCGGACAA CAGAGCCCTC CTCGGACAA CAGAGCCCTC CTCGGACAA	GGCCAGCAGC GCCCAGCAGC GTACAOTCCT ANGGTGCCTA CAGCTCACAC GGGCTCACA GGCCTCCC GGGGGAGCCA GGCCCTGCCC GGGGACCAC GGGCCAGCAG ACCATGGGC TTGCCACTACTA ACCCTTCTACAC ACCCTTGCACA ACCCTTGCACA ACCCTTGCACA ACCCTTGCACA ACCCTTGCACA ACCCTTCCACA ACCTTCCACA ACCTTCCACA ACTTCCACA ACTTCCACA ACCACACTGACA ACCACACTGACAC ACTTCCACA ACTTCCACA ACTACACACTGAC ACCACACTGACAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACACTAC ACTACACTACACA ACTACACTACAC ACTACACTAC ACTACACTACAC ACTACACTACAC ACTACACTACAC ACTACACTACAC ACTACACTAC ACTACAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACACTAC ACTACAC ACTACACTAC ACTACAC ACTACACTAC ACTACAC ACTACACTAC ACTACACTAC ACTACAC ACTACACTA	AGGTCCCTCG GAGGATCCCC GAGGATCCCC GAGGATCCCC GAAGAACAAG ATGGCTGATC GGCTCTCCT TGGCTCCCCCCCCC CCCCCCCCCC	GGCCCAGGC GCCAGGC TOTTFGAGCT TOTGCAGGACC GGGCTCCTG GMGCAGCGTCCTG GMGCAGCGTCCGG GTGCCAGGCT GTGCAGTGGA TGCACCCCGGC GTGCAGTGGA GGGCTCGGG GCGCTCGGG CCTGGGACCG CCTGGGACCG CCAGGCTGGA ACAGGCTGGA ACAGGCAGA ACAGGTGAA ACAGGTGAA ACAGGTGAA ACAGGTGAAG AAGGCACGGC CTGGCCAGCGC CTGGCCAGCGC AAGGCACGGC	CTGCTGCCA CACTITISGE TCGGGGGGGG TCGGGGGGGGGGGGGGGGGGGGGGGG	480 540 600 720 780 840 900 1020 1080 1140 1260 1320 1380 1560 1560 1620 1740 1800
555 60 55	CACCGGGCGGG THANAGAGGGC CCCGGGCGGGGGGGGGGGGGGGGGGGGGGG	CHIGGIGGIGG CHOGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGI	COCCAGEAGE COCCAGEAGE GENERAL ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA COGGAC	AGGTCCCTCG GAGGATCCCC GAGGATCCCC GAGGATCCCC GAAGAACAAG ATGGCTGATC GGCTCTCCT TGGCTCCCCCCCCC CCCCCCCCCC	GGCCCAGGC GCCAGGC TOTTFGAGCT TOTGCAGGACC GGGCTCCTG GMGCAGCGTCCTG GMGCAGCGTCCGG GTGCCAGGCT GTGCAGTGGA TGCACCCCGGC GTGCAGTGGA GGGCTCGGG GCGCTCGGG CCTGGGACCG CCTGGGACCG CCAGGCTGGA ACAGGCTGGA ACAGGCAGA ACAGGTGAA ACAGGTGAA ACAGGTGAA ACAGGTGAAG AAGGCACGGC CTGGCCAGCGC CTGGCCAGCGC AAGGCACGGC	CTGCTGCCA CACTITISGE TCGGGGGGGG TCGGGGGGGGGGGGGGGGGGGGGGGG	480 540 600 720 780 840 900 1020 1080 1140 1260 1320 1380 1560 1560 1620 1740 1800
555 555 560 555 770	CACCGGGCGGG THANAGAGGGC CCCGGGCGGGGGGGGGGGGGGGGGGGGGGG	CHIGGGGGGCGCCGCCGCGCGGGGGGGGGGGGGGGGGGG	COCCAGEAGE COCCAGEAGE GENERAL ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA COGGAC	AGGTCCCTCG GAGGATCCCC GAGGATCCCC GAGGATCCCC GAAGAACAAG ATGGCTGATC GGCTCTCCT TGGCTCCCCCCCCC CCCCCCCCCC	GGCCCAGGC GCCAGGC TOTTFGAGCT TOTGCAGGACC GGGCTCCTG GMGCAGCGTCCTG GMGCAGCGTCCGG GTGCCAGGCT GTGCAGTGGA TGCACCCCGGC GTGCAGTGGA GGGCTCGGG GCGCTCGGG CCTGGGACCG CCTGGGACCG CCAGGCTGGA ACAGGCTGGA ACAGGCAGA ACAGGTGAA ACAGGTGAA ACAGGTGAA ACAGGTGAAG AAGGCACGGC CTGGCCAGCGC CTGGCCAGCGC AAGGCACGGC	CTGCTGCCA CACTITISGE TCGGGGGGGG TCGGGGGGGGGGGGGGGGGGGGGGGG	480 540 600 720 780 840 900 1020 1080 1140 1260 1320 1380 1560 1560 1620 1740 1800
555 60 55	CACCGGGCGGG THANAGAGGGC CCCGGGCGGGGGGGGGGGGGGGGGGGGGGG	CHIGGIGGIGG CHOGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGI	COCCAGEAGE COCCAGEAGE GENERAL ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA ANGEROCTA COGGAC	AGGTCCCTCG GAGGATCCCC GAGGATCCCC GAGGATCCCC GAAGAACAAG ATGGCTGATC GGCTCTCCT TGGCTCCCCCCCCC CCCCCCCCCC	GGCCCAGGC GCCAGGC TOTTFGAGCT TOTGCAGGACC GGGCTCCTG GMGCAGCGTCCTG GMGCAGCGTCCGG GTGCCAGGCT GTGCAGTGGA TGCACCCCGGC GTGCAGTGGA GGGCTCGGG GCGCTCGGG CCTGGGACCG CCTGGGACCG CCAGGCTGGA ACAGGCTGGA ACAGGCAGA ACAGGTGAA ACAGGTGAA ACAGGTGAA ACAGGTGAAG AAGGCACGGC CTGGCCAGCGC CTGGCCAGCGC AAGGCACGGC	CTGCTGCCA CACTITISGE TCGGGGGGGG TCGGGGGGGGGGGGGGGGGGGGGGGG	480 540 600 720 780 840 900 1020 1080 1140 1260 1320 1380 1560 1560 1620 1740 1800
555 60 655 70	CACCOSACCOS CARACA, ASSEC COSSISCITO TARANAGISIOS TERRACAGIS TERRACAGIS TER	CHOCOGOGO CONSTRUCTION OF THE CONTROL OF THE CONTRO	COCCAGCAGE COCCAGGAGE GRACATECT ANGETECTA ANGETECTA ANGETECTA COGCETANCA GOGCETANCA ANGETECTA TOCCACTA ANGETECTACTA ANGETECTACTAC GOGCAC ANTACACAC GOGGAC ANTACACAC GOGGAC ANTACACAC GOGGAC ANTACACAC GOGGAC ANTACACAC GOGGAC COTTO TOCCAC TOC	AGGTCCCTOG AGGTCCCTOG AGGACTGGCT AGGACTGGCT AGGACTGCCT AGGACTGCCT AGGACTGCCC AGGACTGCCC AGGACTGCCC AGGACTGCCC AGGACTGCCC AGGACTGCCC AGGACTGCCC AGGACCGCT AGCCCTCCGCC AGGCCCT AGCCCTCCGCC AGCCCC AGCCC AGCCCC AGCCC AGCCCC AGCCCC AGCCC	GGCCCAGGC GCCAAGGCCA TOTTGAGCT TOTTGAGCT TOTTGAGCT TOTGAGCAGCA GGCCTCCTG TOTGAGCCAG GAGCAGCAGCA CTGCCCCTG CTGCCCCCG CTGCCCCCG CTGCCCCCG CTGCCCCCG CTGCCCCCG CTGCCACCA CAAAGGCAG CAAAGGCAGA ACAGCCAGC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCACCA CAAAGGCAGA ACAGCCAGA ACAGCCCCCC TGCCCCCCCC	CTOGCTIGON CACTITIOGO CACTITIOGO CACTITIOGO CONSCIENCE	480 540 600 600 600 720 780 840 900 1020 1140 1260 1380 1560 1560 1620 1680 1740 1860
555 60 65 70	CACCOSACCOST CONTROLLA ADAMAGASICA CACCAGO CAC	CHOCOGOGOGO CONGRIGATO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO ANTOCAGO COA COA COA COA COA COA COA COA COA CO	COCCAGCAGE COCCAGCAGE GRACATCC ANGETCANCA GRACAACA GRACAACA GRACAACA GRACACACA GRACACACA GRACACACACACACACACACACACACACACACACACACAC	AGGTCCCTCG AGGACTGCCT GGGCATCGCC GGGCATCGCC GGGCATGCCC GGCCGCGCCGC	GGCCCAGGC GCCAAGGCCA TUTTTAJGCT GTGCCAGGC GGCCTCCTG GTGCCCTGG GGCCCCAGC GGCCCCAGC GGCCCCAGC CGGGCTCGG CTGGCGCCG CGGGCTGGG CTGGCGCCA CTGGCGCCG CTGGCGCCG CTGGCGCCG CTGGCGCCG CTGGCGCCG CTGGCGCCG CTGGCGCCG CTGGCGCCG CTGGCGCCG	CTOGCTIGODA CACTITIOGO CACTITIOGO COGNICATO COGNICATO COCONICATO C	480 540 600 600 600 720 780 840 900 1020 1140 1220 1320 1320 1560 1560 1620 1680 1740 1860
555 60 55	CACCOSPACIOS TARANAGASIC CAGAGA, ASCA TARANAGASIC TARA	CHOCOGOGO COORDINATION OF THE COORDINATION OF	COCCAGCAGE COCCAGCAGE GNACATICT ANGETECTA ANGETECTA CNGCTECAGE ANGETECTA ANG	AGGTCCCTOG AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACTAGOT AGGACCTTAGOT AGGACCTTA	GGCCCAGACC GCCAGACC GCCAGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCGCC GTGCACCAC GGGCCTCGCC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACA	CTOGCTGOCA CACTITTOGGO TOGGOGDAGA CACTITTOGGO TOGGOGDAGA CCCGOGGOGGO TOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGG	480 540 600 660 720 780 840 900 900 9102 1140 1260 1380 1680 1680 1680 1860
555 60 65 70	CACCOSALCOS CARGALASCA CACCACACA CACCACACA CACCACACACA CACCAC	CYGGGGGGG CYGGGGGGG CYGGGGGGG GAGCCCACA ACTGCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAG CAGCAGCT CCCAGCAG GCAGCTTCC CCCAGCAG GCAGCTTCC CCCAGCAG GCAGCTTCC CCCAGCAG CCCACCC CCCTCCAGA GCAGCTCC CCCTCCAGA CCCACCC CCCTCCAGA CCCACCC CCCTCCAGA CCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCCACCC CCCCCACCC CCCCCACCC CCCCCC	COCCAGCAGE COCCAGCAGE COCCAGCAGE ANGOTOCTA ANGOTOCTA ANGOTOCTA COCCAGCAGE COC	AGGTCCCTCG CAGACTGGCT GGGCATCGCC GGGCATCGCC GGCATGCCC GGCCGCCGCC GGCCGCCGCC GGCCGCGCCGC	GGCCCAGACC GCCAGACC GCCAGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCGCC GTGCACCAC GGGCCTCGCC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACA	CTOGCTGOCA CACTITTOGGO TOGGOGDAGA CACTITTOGGO TOGGOGDAGA CCCGOGGOGGO TOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGG	480 540 600 600 600 720 780 840 900 1020 1140 1220 1320 1320 1560 1560 1620 1680 1740 1860
555 60 65 70	CACCOSALCOS CARGALASCA CACCACACA CACCACACA CACCACACACA CACCAC	CHOCOGOGO COORDINATION OF THE COORDINATION OF	COCCAGCAGE COCCAGCAGE COCCAGCAGE ANGOTOCTA ANGOTOCTA ANGOTOCTA COCCAGCAGE COC	AGGTCCCTCG CAGACTGGCT GGGCATCGCC GGGCATCGCC GGCATGCCC GGCCGCCCCCC GGCCCGCCCCCC GGCCCGCCC	GGCCCAGACC GCCAGACC GCCAGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCGCC GTGCACCAC GGGCCTCGCC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACA	CTOGCTGOCA CACTITTOGGO TOGGOGDAGA CACTITTOGGO TOGGOGDAGA CCCGOGGOGGO TOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGG	480 540 600 660 720 780 840 900 900 9102 1140 1260 1380 1680 1680 1680 1860
555 60 655 70 75	CACCOSALCOS CARGALASCA CACCACACA CACCACACA CACCACACACA CACCAC	CYGGGGGGG CYGGGGGGG CYGGGGGGG GAGCCCACA ACTGCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAG CAGCAGCT CCCAGCAG GCAGCTTCC CCCAGCAG GCAGCTTCC CCCAGCAG GCAGCTTCC CCCAGCAG CCCACCC CCCTCCAGA GCAGCTCC CCCTCCAGA CCCACCC CCCTCCAGA CCCACCC CCCTCCAGA CCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCCACCC CCCCCACCC CCCCCACCC CCCCCC	COCCAGCAGE COCCAGCAGE COCCAGCAGE ANGOTOCTA ANGOTOCTA ANGOTOCTA COCCAGCAGE COC	AGGTCCCTCG CAGACTGGCT GGGCATCGCC GGGCATCGCC GGCATGCCC GGCCGCCCCCC GGCCCGCCCCCC GGCCCGCCC	GGCCCAGACC GCCAGACC GCCAGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCGCC GTGCACCAC GGGCCTCGCC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACA	CTOGCTGOCA CACTITTOGGO TOGGOGDAGA CACTITTOGGO TOGGOGDAGA CCCGOGGOGGO TOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGG	480 540 600 660 720 780 840 900 900 9102 1140 1260 1380 1680 1680 1680 1860
55 50 55 70	CACCOSACOSO CONTRACTOR	CYGGGGGGG CYGGGGGGGGGGGGGGGGGGGGGGGGGGG	COCCAGCAGCAC COCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	AGGTCCCTCG CAGACTGGCT GGGCATCGCC GGGCATCGCC GGCATGCCC GGCCGCCCCCC GGCCCGCCCCCC GGCCCGCCC	GGCCCAGACC GCCAGACC GCCAGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCGCC GTGCACCAC GGGCCTCGCC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACA	CTOGCTGOCA CACTITTOGGO TOGGOGDAGA CACTITTOGGO TOGGOGDAGA CCCGOGGOGGO TOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGG	480 540 600 660 720 780 840 900 900 9102 1140 1260 1380 1680 1680 1680 1860
55	CACCOSACOSO AGONECICO AGONECACIÓN BELLIAGIEST AGONECACIÓN AGONECACIÓN BELLIAGIEST AGONECACIÓN BELLIAGIEST AGONECACIÓN BELLIAGIEST AGONECACIÓN BELLIAGIEST AGONECACIÓN BELLIAGIEST AGONECACIÓN BELLIAGIEST AGONECACIÓN BELLIAGIEST AGONECACIÓN BELLIAGIEST AGONECACIÓN BELLIAGIEST AGONECACIÓN BELLIAGIEST BELLIAGIEST BELLIAGIEST BELLIAGIEST BONECACIÓN BELLIAGIEST BELLIAGIEST BONECACIÓN BELLIAGIEST BONECACIÓN BELLIAGIEST BONECACIÓN BELLIAGIEST BONECACIÓN BONE	CYGGGGGGG CYGGGGGGG CYGGGGGGG GAGCCCACA ACTGCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAGA GATCCCAG CAGCAGCT CCCAGCAG GCAGCTTCC CCCAGCAG GCAGCTTCC CCCAGCAG GCAGCTTCC CCCAGCAG CCCACCC CCCTCCAGA GCAGCTCC CCCTCCAGA CCCACCC CCCTCCAGA CCCACCC CCCTCCAGA CCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCCACCC CCCCCACCC CCCCCACCC CCCCCC	COCCAGCAGC COCCAGCAGC GTACAGTCCT AAGCTCCTTAGC GTCTCTCCA GTCCTCTCCA GTCCTCTCCA GTCCTCTCCA GTCCTCTCCA GTCCTCTCCA GTCCTCTCCA GTCCTCTCCA GTCCTCTCCA GTCCTCTCCA GTCCTCCCC GTCCCCCC GTCCCCC GTCCCCCC GTCCCCCC GTCCCCC GTCCCCC GTCCCCC GTCCCCC GTCCCCC GTCCCCC GTCCCCC GTCCCCC GTCCC GTCC GTCCC GTCCC GT	AGGTCCCTOG GGGCATGGGG GGGCATGGGG GGGCATGGGG GGGCATGGGG GGGCATGGGG GGCGGCATGGG GGCGGCATGGG GGCGGCGGCATGGGGGCGCGCGGGGGGGGGG	GGCCCAGACC GCCAGACC GCCAGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGGACC GGCGCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCCTG GTGCAGTGAC GGGCCTCGCC GTGCACCAC GGGCCTCGCC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCGACCAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCACAC CTGCCCACAC CTGCCACA	CTOGCTGOCA CACTITTOGGO TOGGOGDAGA CACTITTOGGO TOGGOGDAGA CCCGOGGOGGO TOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGGOGG	480 540 600 600 600 720 780 840 900 900 91 1260 1320 1380 1550 1650 1650 1650 1660

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Coding sequence: 1..714 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCCAAGCC CACCYGGGTG COCTCTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120 TGGCCCACCC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC GOSCOCCIGO GOCCTGOCCO COGCGAAGGC COCCGGCCTG TCCTGGCGTC CCCCGCCGGC 240 CACCTGCCGG GGGGACGCAC GGCCCGCTGG TGCAGTGGAA GAGCCCGGCG GCCGCCGCCG 300 10 exacement appropriate engacement appropriat engagement engagement CGCGCGCGC GGGCTGGGGG CCCGGGCAGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420 CGCCTGCGCT COCAGCTGCT GCCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCCGACGAG CTGGTGCGTT TCCGCTTCTG CAGCGGCTCC TGCCGCCGCG CGCGCTCTCC ACACGACCTC 540 600 660 720 GCTCCAGGGC TTTGCAGACT GGACCCTTAC COGTGGCTCT TCCTGCCTGG GACCCTCCCG CAGAGTOCCA CTAGCCAGCG GCCTCAGCCA GOGACGAAGG CCTCAAAGCT GAGAGGCCCC 840 TACCGGTGGG TGATGGATAT CATCCCGGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC AGAGCCCTCA CCCTGCGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 900 20 960 TTCGGACCCA CTTCTCACAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCCGCCC AGGCCCTGTA GGGACAGCAT 1020 TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC 1140 TCACTCATOS GAGCTGGCCC C 25 Seq ID NO: 607 Protein sequence Protein Accession #: NP 476501.1 30 MPGLISARGO PLLEVLPPOA HLGALFLPEA PLGLSAOPAL WPTLAALALL SSVAEASLGS APRSPAPREG PPPVLASPAG HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG RAARAGGPGS RARAAGARGC RLRSQLVPVR ALGLGHRSDE LVRFRFCSGS CRRARSPHDL SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG 35 Seq ID NO: 608 DNA sequence Nucleic Acid Accession #: NM_057090.1 Coding sequence: 29..715 40 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACTTGGA CTTGGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GGCGGCAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT 120 GTGGCCCACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC 100 COCCCCCCC AGCCCTGCCC CCCCGGAAGG CCCCCCGCCT GTCCTGGCGT CCCCCGCCGG CCACCTGCCG GGGGACGCA CGGCCCGCTG GTGCAGTGGA AGAGCCCGGC GGCCGCCGCC 240 300 GCAGCCTTCT CGGCCGGCGC CCCCGCGCGCC TGCACCCCCA TCTGCTCTTC CCCGCGGGGG CCGCGCGCGC CGCGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG CGCGGGGGCTT 420 COGCCTGCGC TOSCAGCTGG TGCCGGTGCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480 GCTGGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCCGCCGC GCGCGCTCTC CACACGACCT 540 CAGCCTGGCC ACCCTACTGG GCGCCGGGGC CCTGCGACCG CCCCCGGGCT CCCGGCCCGT 600 CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT 720 CHICAGGG CTTTGCAGAC TGGACCCTTA CONGTGGCTC TTCCTGCCTG GGACCCTCCC 780 GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGCCC 840 CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900 CAGAGCCCTC ACCCTGCGGA TCCCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC CTTCGGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG GGACCCCTCC 1020 TOTGATGARC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA 1000 60 TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCCTGTA 1140 CTCACTCATG GGAGCTGGCC CC Seq ID NO: 609 Protein sequence Protein Accession #: NP_476431.1 65 31 MELGLGGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVABASLG SAPRSPAPRE GPPPVLASPA GHLPGGRTAR WCSGRARRPP FOPSRPAPPP PAPPSALPRG GRAARAGGPG 120 70 SRARAGARG CRURSOLVPV RALGLIGHRSD ELVRFRYCSG SCRRARSPHD LSLASLLGAG ALRPPEGERP VSOPCCRPTR YEAVSFMOVN STWRTVDRLS ATACCCLG Seq ID NO: 610 DNA sequence Mucleic Acid Accession #: Eos sequence 75 Coding sequence: 1..1746 ATGCCACTGA AGCATTATCT CCTTTTGCTG GTGGGCTGCC AAGCCTGGGG TGCAGGGTTG 80 GCCTACCATG GCTGCCCTAG CGAGTGTACC TGCTCCAGGG CCTCCCAGGT GGAGTGCACC 120 GOGGIACOCA TROTGGCGGT GCCCACCCCT CTGCCCTGGA ACGCCATGAG CCTGCAGATC 180 CTCAACACGC ACATCACTGA ACTCAATGAG TCCCCGTTCC TCAATATCTC AGCCCTCATC GCCCTGAGGA TTGAGAAGAA TGAGCTGTCG CGCATCACGC CTGGGGCCTT CCGAAACCTG 300 GGCTCGCTGC GCTATCTCAG CCTCGCCAAC AACAAGCTGC AGGTTCTGCC CATCGGCCTC 360 TTOCMBGGCC TGGACAGCCT TGAGTCTCTC CTTCTGTCCA GTAGCCAGCT GTTGCAGATCC CAGCGGGCC ACTTCTCCCA GTGCAGCAGC CTCAAGGAGC TGCGATCACC CTGGAATACA TCCCTGAGG AGCCTTGGAC CACCTGGTAG GACTCACGAA GCTCAATCTG 420

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	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTYGGG	CAATCTCCAG TGATGGGCTT CCCTGGTCTC CTCCCAGCTG TGGGAATTCC	600
	CE COM COCCO	moma mosca a a	CACCOTTCACC	CATAMOCOCA	TOTAL COURT	TONTOGOGOTT	660
	GICCICCGGC	IGIAIGMAA	CAGGCICACG	GMINICCCCM	TOGGCACTIT	IGNIGGGCII	720
	GITARCUIGU	AUGARCIOGC	TCIACAGCAG	MACCAGALIG	CACIGCICIC	CCCIGGICIC	/40
-	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACAT	CTCCCAGCIG	780
5	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	900
	CTVCNNGCNCC	TOTOTOGG	CATUTECOOC	CCCARGCCCA	A CYTYCOGGA	COTTIGGOTO	900
	mi man an a ac	1010101000	more account	A DECEMBER CA	CCARCONCCC	GCTTTGGCTC CCAGTTGCAG CAACGGGCTA	960
	TATGACAACC	ACATCTCTTC	TCTACCCGAC	MITGICITUM	GCMACCICCG	CCMSTTGCAG	960
	GTCCTGATTC	TTAGCCGCAA	TCAGATCAGC	TTCATCTCCC	CGGGTGCCTT	CAACOGGCTA	1020
	ACCOUNTERED	GGGAGCTGTC TGGCCAACCT TCTTCGCCAA	CCTCCACACC	ARCGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
10	mmacco at man	macaga a agen	CCACAACAGC	MCCCMCCACA	ACATECOCCT	CNONCROCTO	1140
10	TICOSCATOL	TOGCCOULCET	GCMG/DICATC	TCCCTGCAGA	ACANICOCCI	CHOMCHOCIC	
	CCA3GGAATA	TCTTCGCCAA	CGTCAATGGC	CTCATGGCCA	TUCAGCIGCA	GAACHICCH	1200
	CTGGAGAACT	TGCCCCTCGG	CATCTTCGAT	CACCTGGGGA	AACTGTGTGA	GCTGCGGCTG	1260
	TATGACAATC	TGCCCCTCGG CCTGGAGGTG GGTTAGGGAC	TGACTCAGAC	ATCCTTCCGC	TOTGCARCEG	GCTCCTGCTC	1320
	**************	COMO LOCAL O	COLOR CITORIC	COMOMORON	marcaanrea	CARPORCOCA	1380
15	AMCCAGCCTA	GGTTMGGGAC	GCACACIGIA	CCIGIGIGII	TOMOCCOMOC	CAMIGICOOK	1300
13	GGCCAGTCCC	TCATTATCAT ACCCAGAAAC CTACCACTGA	CAATGTCAAC	GTTGCTGTTC	CAAGCGTCCA	TGTCCCTGAG	1440
	GTGCCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TOTATOTOTO	CTACCACTGA	GCTAACCAGC	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	100010101	CENCY MCV CCC	CACCCMETTOC	COCATOACOC	MAGCCCCNGNG	connervance	1620
	ATTCAGGTCA	CIGNIGACCO	CMGCGIIIGG	GOCKIONCCC	MOGCCCMUNG		1680
20	ATTGCCGCCA	TIGTAATIGG	CATTGTCGCC	Creeccrect	CCCTGGCTGC	CIGCOLCOC	Teac
20	TGTTGCTGCT	GCAAGAAGAG	GAGCCAAGCT	GTCCTGATGC	AGATGAAGGC	ACCCAATGAG	1740
	TOTTABAGAG	actagement	actionaction	GGAATGATGG	GACTIGGAGGA	CCTGGGAATT	1800
	TOT TABLES	accompanded	OULCOOK TOO	CCACCONTROC	OCCUPATION OF	CHARGE CHARGO CO.	1000
	TCATCTTCT	GCCTCCACCC	CIGGGICCAL	GONGCITICC	COLOMITOCI	CITICIOGCC	1000
	CTAGATAAAG	GTGTGCCTAC	CTCTTCCTGA	CTTGCCTGAT	TCTCCCGTAG	AGAAGCAGGT	1860
	CGTGCCGGGAC	CTTCCTACAA	TCAGGAAGAT	AGATCCAACT	GGCCATGGCA	TCTGACTACC COGGCTGGCC CTGCGTCGGC ACCCAATGAG CCTGGGAATT CTTTCTGGCC AGAAGCAGGT AAAGCCCTGG AATCCTCCCC CTGTAGACTC GCCCCTCCCC CTATGGCTTG	1980
25	CCATHECOS	TECHENCECE	TODOCTTOCT	TOGRADAGGGC	TOTTOTOTA	AATOCTCCCC	2040
	GOWITICOOK	TICALACCC	1000011001	TOUNUMOUC	retreered		
	ACCIGICATO	CARGAMICAGE	CITCCCTGCG	CCCMGGCCCC	CICCGGGCCI	CIGINGACIC	2100
	AGTTAGTCCA	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCTCTCG CTATGGCTTG GAAGGCAGGG AGCCGTCAAT CAGTTCCTGG GGAAGAAACA AACTTTGCTT TAAAAACAT TCCCTGTGTT STGCAGAAAA ACTGTGTAAA	2160
	CCTABGTATT	ATGUARGUEG	ATTTCCCTTC	TTTTGTTTCT	CTTGTTTGTG	CTATGGCTTG	2220
	1000100100	magagamenta	man a a common	0000000000	margar care	CNAGGCAGGG	2280
30	ACCCAGCATG	TOCCUTONA	TOPPORGITE	CCCCTTOMIT	ITCIGCICCI	GUNGGCNGGG	2340
30	TGAGTTCTCT	CCTCAAAGAA	GACTTCAAAC	CATTTAACTG	GTTTCTTAAG	AGCCGTCAAT	2340
	CAGCCTGGTT	TTGGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCCTGG	2400
	10101010101	OCCOPICATION.	OTOTOTO CACT	TOTALTTTT	AGGGGGGGGAAA	COLLEGE	2460
	AUACAUAAAA	CCCGTCATCA	OTOTOTOTOTO	***************************************	COLT TOURS	3.3.CEDWG-C-CTE	2520
	CCCCAGCACA	GUMAGCTUAG	CCITITAGAG	MAGGATATTT	CCMMCIGCA	MACTITIOCIT	2021
0.5	TGAAAAGTTT	AGCCCTTTAA	GGAATGAAAT	CATGTAGAAT	TTTGGACTTC	TAAAAACATT	2580
35	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCCTGGGGG	TCCCTGTGTT	2640
	CACCCCTACA	Opposition a	A A A TENTETTA A	TTGARGCATG	TONDOTOTAC	CTCCACAAAA	2700
	CACCCCIAGA	GIIIGIIIIA	AAATTTT AAA		1000010101	oroconoman.	2760
	GTGGGAACAT	GATAGIGIAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCIGIGIAAI	2/60
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCCAGA	2820
	GGAGATGGGG	GATAGTGTAT ACCCAGACCC GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCCATGA	GCCAGGACGG	2886
40							2044
70	TUCCUCCONCA	GICAGCCIGI	GCADAGGCCC	COTOGCCHOO	0010000000	GGAGACCTG GACTGCAGAG CGGAGGCCCC TTCATTCTTC AAGTGTAACG	3000
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATIT	TATTATATCT	GGAGACCCTG	3000
	AGAGACCCTG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCCTC	TECCCERCO	GCAAGTTGTC	TGCGGCTCAT	COGRAGGECCC	3120
	-cecorocac	CONCRETE	01000010001	COOMORTHON	COTTONNA MIN	THE COURSE OF THE COURSE	3180
45	TUUGUUTGGA	GCCTTCTATG	GACGIGATAT	OCCIDIATEL	GIIIIIMUII	TICATICITC	310
45	ACTTAGGGGA	AGTGAAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAACG	AAGTGTAACG	3240
	GARTCTACTC	TCTTTCTAAT	GTGGTAAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TOTAL OTTECHO	ABSTRUCTOR	A CAGCAGGGG	A CA COGGGGT	A CACCCATOG	GTCACACTGG	3360
	TOWNCT TOWN	MICICACII	TOTAL CARGOOD	mon concentrate	mma.coa.ommo	*Commomomor	3420
	GTCTGGGGGC	TCCCTGGAGC	TCCTCCTGCG	TGTGGTCTGG	TYAGGAGIYG	AGTIGTTIGC	3420
	TCCAGGGTTA	TTCTCCTCCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTC	3480
50	CTGCTATACA	CATATTCACA	TGGCGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
	CERCIPOCA CINA	CTCCCCCC CTC	TEACACTORA	ATGGAGAATT	TOMOGROPO	ACCRECISCOS	3600
	CICIOGAGO	CIGGCCCAGI	THOROTONA	VI GOVOVOTI	TCAGGIGGG	ACGICIOCCC	3000
	AGGAAAGAAC	TTCAGCTGAC	TCCACGGGGA	TCTGGAAATC	CAUGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	AGCTGGCAGC GTCACACTGG AGTTGTTTGC TCTGGCTTTC GTGTGTCTTTC CCCGATCCGC CCCATCCCGA TACCACCAT TCCAGGGCCA TCCAGGGCCA TCCAGGGGCCA TCCAGGGGCCA TCCAGGGGCCA TCCAGGGGCCA TCCAGGGGCCA	3720
	TOTOCTOTA	TTACCTCCCC	GCTCCACAAA	ACK CYPTOTCA	TOTOGRADATO	TACCACCAAT	3780
55		TIMOCICCO	managaman	ACALCIOIOA	monos osmoo	MCCFCCCCCV	3840
22	CCCGATCGGC	TOTTATTAGC	TCCCCGCTCC	ACAMBACACC	TOTONCATCC	ICCHOOCCON	3041
	CAGGAGCACG	TGCTGACCAG	TTTTCCCTTC	CAGTTCCTGC	ACAAAAAGTG	TCCAGAGGGC	3900
	TOTTTGCARA	CACTAGUGCA	CTTTGTAGCT	TTTCACCCTC	TGTCCCAGGG	AMTCTAGGAG	3900 3960
	101ma10000	CONCLORGE	1101010000	ATCCCCCCC	COTOTOTARO	GCATTTCCAC	4020
	MUNICIPAL	COTCAGAGIC	ANGAGATOTC	ALCCCCCCAG		0011110010	4086
10	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGGGGGGG	TCCAGGGCCA TCCAGAGGGC AATCTAGGAG GCATTTCCAC GGAAGTGAGC GGTGCCAACA AGACCTGTCG GCCAGGGCTG	4000
60	CCAGAGCATG	GCACATGAGC	ATCACCOGCT	GATGGTGGCC	TGCTGTGCCT	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGCCCAC	AGACCTGTGG	4200
	OGROCE CONG	TOLOTOCCE	CCAGATGTCT	TTGTGCATAG	acaca across	accagggmg	4260
	0010010010	10001000001	CCNONIOICI	11010011110			
	GAGGGAGGTG	GUARACCTCA	TCATCCGGTG	GOCCCIGCCA	ATCTIMACCC	AGMICCCITA	4360
	GGTATTCCTG	TGAGTGGCCT GGAAACCTCA GCAGTAGCCA	TGACATTGGA	GCACCTTCCT	CTCCAGCCAG	AGGCTGACCT	4380
65	GAGGGCCACT	GTCCTCAGAT	GACACCACCC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4500
	COMPRANCING	ACCTCTM3CC	TOTALCTURE	TYCCCATCAGA	OTGOTTOGET	GGLGCCLTTT2	4500
	CCITATOTOA	ACCICITOCC	2011001110	momomoon oo	A TOUT TOUR	OGRECO COLCO	4560
	GCCTCCTTTT	CITCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGA	GTCTCCTTTC	CAACAGGATG	ATGCATTTGC	TCAATTCTCA	4626
	GGGCTGGAAT	GMGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCAGTTTT	4680
70	Commitment of the committee of the commitment of	TACACOMCOM	TOLONOTOCO	ACCOCCATOR	OGNOWOODNO.	CUCCCACTUA	4740
, 0	CICICIOIT	AMOUNTECT	* OUCOUNCE	GCCCATCT		AGGCTGACCT GTGAGGGCCC GGAGCCATTG GCTGAGGAGC TCAATTCTCA GTTCAGTTT CTGGGAGTTA	4860
	GTGTTGGAGA	AGAAACAACA	AAAGCCAATT	AGAACCACTA	TTTTTAAAAA	GTGCTTACTG	4800
	TGCACAGATA	CTCTTCAAGC	ACTOGACOTG	GATTCTCTCT	CTAGCCCTCA	GCACCCCTGC	4860
	compactor and	COSCOMONAC	CCACTTCTC	TYGGGGTACAG	MOCACTTOC	TOTTOTAL	4920
	GUINGGHGIG	COCCICIAC	CONCILIBION	200001ACAG	MUNICALITY OF T	rocandrades	4980
75	GGTGTTCAAT	AGAAACAACA CTCTTCAAGC CCGCCTCTAC AGGCTGGGAG	TITTATTIAT	CYCTTCAAAC	TTIGTACAAG	MGCTCATGGC	4980
75	TTGTCTTGGG	CTTTCGTCAT TCATCAGAAC AACTCTTCCA	TARACCARAG	GAAATGGAAG	CCATTCCCCT	GITGCTCTCC	5040
	TTAGECTEGG	TEATEAGRAC	CTCACTTGGT	ACCATATAGA	TCARAGCTT	TGTAACCACA	5100
	COLDERATE	** CTCMOVAC	mocomments:	NAMACE ATTO		TOTATOOGRAM	5160
	GUANUMATA	MACTUTTUCA	LCCCTTMAAG	nnThunnTAG	TIGICCCTC	TOTAL GOODWAY	2100
	TGGGCTGTAT	GTATATTGTT	CTTCCTCCTT	AGAATTTAGA	GATACAAGAG	TICTACTIAG	5220
	AACTITICAT	GGACACAA TT	TOCACARCCT	TTCAGATGCT	GATGTAGAGC	TATTGGGAAA	5280
80	GNACTTCCAA	ACTOAGGA NO	TTTGCAGAGA	GCAGACAGCT	AGAGATAACT	TCATGGGAAA TATTGGGAAA CGGGACCCAG CAAAGATTCA AGTGGCCTAG CCGGGGAAAA	5340
30	CAMPAGE LOCAL	WICHOONNG		COMMUNICACI	A STATE A COST CO	CARACATEC	5400
	AGTTGGTCGA	CAGATGTTAG	ATGTATCCTA	GCTTTTAGCC	ATAAACCACT	CALANGATICA	5400
	GCCCCCAGAT	CCCACAGTCA	GAACTGAATC	TGCGTTGTTG	GGAAGCCAGC	AGTGGCCTTG	5460
	GGAAGGAACC	CARGOCTORO	GTTCAGACAG	GGTGGGGTT2C	CARGOCACTT	CCGGGGAAAA	5524
	-unnounnou			110000100	mammaman aa	***************************************	5584
0.5	CICCTTCCCC	CCCAGGITTC	LICTICICIT	NAGOMONGAT	TOTTCTCACC	MUCCUGGGGG	2201
85	CTTCATGCTG	CCTTCAAAGC	TAGATCATGT	TIGCCTIGCT	TAGAGAATTA	CTGCAAATCA	5640
	GCCCCAGTCC	TIGGCGATGC	ATTTACAGAT	TTCTAGGCCC	TCAGGGTTTT	AACCCGCTGC CTGCAAATCA GTAGAGTGTG	5700
	AGOOOTIGOTIC	GCCNGGGTTG	GGGGGTCT	CTTCTGCTYY	ATOCHGCTW	TAATCCATTT	576
	worren 10010	SUCHOOUTTO	ooooo1C101	C C. GC 100	~~~~~	111111111111111111111111111111111111111	570

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PCT/US02/12476

WO 02/086443 GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 611 Protein sequence Protein Accession #: BAB84587.1

5							
	1	11	21	31	41	51	
	1	1	1	1	1	1	
		VGCQAWGAGL					60
		SPFLNISALI					120
10		LLSSNQLLQI					180
		RVFQHLGNLQ					240
		YLSNNHISQL					300
		NVFSNLRQLQ					360
		SLONNRLRQL					420
15		ILPLRNWLLL					480
		POTPSYPDIT				GNTQAQSGLA	540
	IAAIVIGIVA	LACSLAACVG	CCCCKKRSQA	VIMONKAPNE	C		

Seq ID NO: 612 DNA sequence Nucleic Acid Accession #: XM_098151 Coding sequence: 1..447

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25	ATGATGCATT	TOCTCAATTC	TCAGGGCTGG	AATGAGCCGG	CTGGTCCCCC	AGAAAGCTGG	6
			TTTCCTCTCT				12
	TCTGGAGTGG	GAGCTGGGAG	TCAGTGTTGG	AGAAGAAACA	ACAAAAGCCA	ATTAGAACCA	18
	CTATTTTTAA	AAAGTGCTTA	CTGTGCACAG	ATACTCTTCA	AGCACTGGAC	GTGGATTCTC	24
			TGCGGTAGGA				30
30	CAGAGGCACT	TECTCTTCTG	CATGGTGTTC	AATAGGCTGG	GAGTTTTATT	TATCTCTTCA	36
	AACTTTGTAC	AAGAGCTCAT	GGCTTGTCTT	GGGCTTTCGT	CATTAAACCA	AAGGAAATGG	42
	AAGCCATTCC	CCTGTTGCTC	TCCTTAG				

Seq ID NO: 613 Protein sequence Protein Accession #: XP_098151 35

40	LFLKSAYCAQ	11 NEPAGPPESW ILFKHNTWIL GLSSLNORKW	SLALSTPAVG		60 120
	NFVQELMACL	GLSSLNORKW	KPFPCCSP		

31

41

11

Seq ID NO: 614 DNA sequence Nucleic Acid Accession #: NM_002658.1 Coding sequence: 77..1372

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	GAGCGACTCC	AAAGGCAGCA	ATGAACTTCA	TCAAGTTCCA	TCGAACTGTG	ACTGTCTAAA	180
	TGGAGGAACA	TGTGTGTCCA	ACAAGTACTT	CTCCAACATT	CACTGGTGCA	ACTGCCCAAA	240
		GGGCAGCACT					300
		CGAGGAAAGG					360
55		GTCCTTCAGC					420
		CATAATTACT					480
		CTARAGCCGC					540
		TCTCCTCCAG					600
		ATTATTGGGG					660
60		AGGCACCGGG					720
		GTGATCAGCG					780
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		CIGAAGATCC					960
65		TGCCTGCCCT					1020
		GGAAAAGAGA					1080
		CTGATTTCCC					1140
		ATGCTATGTG					1200
70		CCCCTCGTCT					1260
70		GGATGTGCCC					1320
		ATCCGCAGTC					1380
		CGGGCACCAC					1440
		GTAAGAAGAG					1500
76		GTGAACGACA					1560
75		GGCCAGGATG					1620
		TOGACTGAAG					1680
		GAGAGCCAGC					1740
		TTCCCAATTA					1860
80		CAGCGGTTTG					1920
80	ATTCCATGAA	TGTATCAGGA	AATATATATG	TGTGTGTATG	TTTGCACACT	TGTTGTGTGG	1920
		TARGTGTGAG					2040
		GACTGTGATG					2100
		TTGGGTCCCC					2160
85		AGCACTGTCT					2220
02							2220
		TTTATATTTC		TTTATATTTT	TGTAATTTTA	AKTAGGGGTG	2280
	ATCARTAAAA	TGTGATTTTT	CIGA				

WO 02/086443

Seg ID NO: 615 Protein sequence Protein Accession #: NP 002649.1

5	1	11	21	31	41	51	
	1	1	1	1	1	<u> </u>	
	MRALLARLLL	CVLVVSDSKG YEGNGHFYRG	SNELHQVPSN	CDCLNGGTCV	SNKYPSNIHW	CNCPKKPGGQ	120
	HCBIDKSKTC	PKCYVQVGLK	RASTITINGRP	CLPWNSATVL	QQTTHAHRSD	ALQLGIGANN VPI.BDBPVII	180
10	TCKNPDNRRR	PWFAAIYRRH	PEAGROWAND	COLTEDORIS	CATHCUTOVE	KIDKEKKKI	240
10	GGEPTTENQ	EMKFEVENLI	KUUSVIIVCU	OSDIOPCAVI	THEYPEREDIA	DEPTIOPICE.	300
	REMINISTRUG	TSCEITGFGK	DESCRIPTION OF THE	OT KWLAAKUT	CHBECOOPHY	YGSEVTTKML	360
	CAADDONYSD	SCOGDSGGPL	WOOTLOGDMITT.	TOTUSHORGE	ALKDEPGVYT	RVSHPLPWIR	420
	SHTKRENGLA		*CODQUIOTED	101101101100			
15	UII I I I I I I I I I I I I I I I I I I	-					
	Sec ID NO:	616 DNA 80	quence				
		d Accession		422.1			
	Coding sequ	ience: 202.	2907				
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	1	ī	1	ì	ĺ	1	
	CGCCAAAGGA	AAAGCCCCTT	GGATGAGAGG	CAGGCGCTTC	AGAGAAGCTA	AGAAAAGCAC	60
	CTCTCCGCGC	GCCCCACCTC	CTCCGCCTCG	CGCTCCTCCT	GAGCAGCGGG	CCCAGACTGC	120
	GCTCCGGCCG	CGGCCCTCGC	CCCGCGGAGC	CCTCCTACCC	CGGCCCGACG	CTCGGCCCGC	180
25	GACCTGCCCC	GAGCCCTCTC	CATGGAGGCA	GCCCGCCCCT	CCGGCTCCTG	GAACGGAGCC	240
	CTCTGCCGGC	TGCTCCTGCT	GACCCTCGCG	ATCTTAATAT	TTGCCAGTGA	TGCCTGCAAA	300
	AATGTGACAT	TACATGTTCC	CTCCAAACTA	GATGCCGAGA	AACTTGTTGG	TAGAGTTAAC	360
	CTGAAAGAGT	GCTTTACAGC	TGCAAATCTA	ATTCATTCAA	GTGATCCTGA	CTTCCAAATT	420
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30	TTTACCATAT	TACTTTCCAA	CACTGAGAAC	CAAGAAAAGA	AGAAAATATT	TGTCTTTTTG	600
	GAGCATCAAA	CAAAGGTCCT	AAAGAAAAGA	CATACTAAAG	AMMONGTIC:	MAGGGGGGG	660
	AAGAGAAGAT	AACAGGTTCA	TCCTTGTTCG	ATGCTAGAGA	ACTOCTIONS	CTATTCCATA	720
	CTTTTCCTTC	GAGTTGACCA	ATCTOACACG	A A TOTAL TOTAL	ATTOCCATALA	AGACACTGGA	780
35	AGAGGTCCTG	GTACTCGTCC	MONTOCICOS	CACCACRATIC	ANTOTOGRADA	CATAATTICC	840
55	MACTIGIATI	CTCCAGATGG	GTATACTCCA	GARCTTCCAC	TGCCCCTAAT	AATCAAAATA	900
	Chachman	ATGATAACTA	CCCLATTTTT	ACAGAAGAAA	CTTATACTTT	TACAATTTTT	960
	GAAAATTGCA	GAGTGGGCAC	TACTGTGGGA	CAAGTGIGTG	CTACTGACAA	AGATGAGCCT	1020
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40	CTATTTTCTA	TGCATCCAAC	TACAGGCGTG	ATCACCACAA	CATCATCTCA	GCTAGACAGA	1140
	GAGTTAATTG	ACARGTACCA	GTTGAAAATA	AAAGTACAAG	ACATGGATGG	TCAGTATTTT	1200
	GGTCTACAGA	CAACTTCAAC	TTGTATCATT	AACATTGATG	ATGTAAATGA	CCACTTGCCA	1260
	ACATTTACTC	GTACTTCTTA	TGTGACATCA	GTGGAAGAAA	ATACAGTTGA	TGTGGAAATC	1320
	TTACGAGTTA	CTGTTGAGGA	TAAGGACTTA	GTGAATACTG	CTAACTGGAG	AGCTAATTAT	1380
45	ACCATTTTAA	AGGGCAATGA	AAATGGCAAT	TTTAAAATTG	TAACAGATGC	CAAAACCAAT	1440
	GAAGGAGTTC	TTTGTGTAGT	TANGCCTTTG	aattatgaag	AAAAGCAACA	GATGATCTIG	1500
	CAAATTGGTG	TAGTTAATGA	AGCTCCATTT	TCCAGAGAGG	CTAGTCCAAG	ATCAGCCATG	1560
	AGCACAGCAA	CAGITACTGT	TAATGTAGAA	GATUAGGATG	AGGGCCCTGA	GYGYAACCCCT	1620 1680
50	CCAATACAGA	CTGTTCGCAT ACCCAGAAAC	GAAAGAAAAT	GCAGAAGTGG	GAACAACAAG	CARTGGATAT	1740
20	AAAGCATATG	GOGTCACCAT	ANGANGTAGE	AGTOGCATAA	GOTATAKONA	CLUMCION:	1800
	CUANCAGGGT	COGTCACCAT	CONTRACTOR	ATATATATA	TTACAGTOT	TOCATCAGAC	1860

GATAGAGAG CAGAGACCAT CAAAAATGGC ATATATAATA TTACAGTCCT TGCATCAGAC CAAGGAGGG GAACATGTAC GAGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAA

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ATTGTTGCGG TTGATCCTGA TGAGCCTATC CATGGCCCAC CCTTTGACTT TAGTCTGGAG AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA

ANTOGOTICA CAACCCAAAC TOTOGGGGCT TOTGCTCAGG GAGTTTGTGG CACCGTGGGA
TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAAGGAGG ACACCAGACC

TATTIGANGC ACANCCIANT GGAMANTIGT AGRICCTIG CITTANCATT ATCTCCAGIT

COTOTTCCT ATCAGAATGA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGA 60 AMGTOGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCATTGC TCTTTTGCAT CCTGTTTACG CTGGTCTGTG GGGCTTCTGG GACGTCTAAA CAACCAAAAG TAATTCCTGA TGATTTAGCC CAGCAGAACC TAATTGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG

55

85

65 TCGGAATCCT GCCGGGGGG TGGCCACCAT CACACCCTGG ACTCCTGCAG GGGAGGACAC
ACGGAGGTGG ACACCTGCAG ATACACTTAC TCGGAGTGG ACAGTTTTAC TCAGCCCGGT CITGGIGADA ARGIGIATOT GIGIARICAR GAIGARARIC ACARGORIGO CORAGACIAT GTCCTGACAT ATAACTATGA AGGAAGAGGA TCGGTGGCTG GGTCTGTAGG TTGTTGCAGT GAACGACAAG AAGAAGATGG GCTTGAATTT TTGGATAATT TGGAGCCCAA ATTTAGGACA 70 CTAGCAGAAG CATGCATGAA GAGATGAGTG TGTTCTAATA AGTCTCTGAA AGCCAGTGGC TITATGACTT TTAAAAAAA TTACAAACCA AGAATTTITT AAAGCAGAAG ATGCTATTTG TOGGGGTTTT TCCCCATTA TTTGGATGGA ATCCCTTTGG TCAAATGCAC ATTTACAGAG AGACCTATA AACAGTACA CAAATTTTC AATTTTACA TATTTTAAA TACCTATCT TCTATCCAAG GAGGATCAC GAGAATTAA AGTCCCCT ATTGTTACA TAGGGTATA 75 ATGACAACAG CCAATTTATA GTGCAATAAA ATGTAATTAA TTCAAGTOCT TATTATAGAC

ANTIANGIGE TOATGIGIG CITTOGAAACT GITTSTITTC CHARACATT ANGIGTGIAG ACTGCATTCT TOCTATTATT TTATTCTTGT ANTIGTGACCT TITCACTGTG CAAAGGGAGA TTTCTAGCCA GGCATTGACT ATTACAATTT CATT 80 Seg ID NO: 617 Protein sequence Protein Accession #: NP 077740.1

MEAARPSGSW NGALCRULL TLAILIFASD ACKNYTHUY SKLDAEKLVG RVNLKECFTA ANLIHSSDMD FOILEDGSVY TYNTILLSSE KRSPTILLSN TENGEKKKIP VPLEHOTKVL

1860 1920

1980

2040 2100

2220

2200

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2520 2580

2640 2700

2820

2880

2940

3000

3120 2100

3240

3300

WO 02/086443 KKRETKKKUL RRAKERWAPI PCSMLEHSIG PPPLPLQQVQ SDTAQNYTIY YSIRGDGUDQ SPRANLFYUSH DTONLYCTRP UDRGYESFE IIAFATTPDG YTPELDLULI ISIDENBUNT PIFTSETYTE TIEBURCHUST TUGQUCANDA DEPUTMETRIK MYSIIGQUPP SFTLEFSMEPT 300 TGVITTTSSO LDRRLIDKYO LKIKVODMDG OYPGLOTTST CIINIDDVND HLPTFTRTSY 360 UTSVERNITUD VEILBUTUED KOLVNITANNE ANYTILKGNE NGNEKIVIDA KINEGULCUV 420 KPLNYREKOO MILOIGUUNE APPSREASPE SAMSTATUTU NVEDODEGPE CNPPIOTVRM KENARUGTTS NGYKAYDPET RESEGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREARTI KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPPIPKK TVIICKPTMS SAEIVAVDPD EPIHGPPFDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFGSYVVPI TVRDRLGMSS 660 10 VTSLDVTLCD CITEMPOTHR VDPRIGGGGV OLGKWAILAI LLGIALLFCI LFTLVCGASG 720 TSKOPKVIPD DLAGONLIVS NTEAPGDDKV YSANGFTTOT VGASAQGVCG TVGSGIKNGG 780 OBTIEMVKGG HOTSESCRGA GHHTTLDSCR GCHTEVDNCR YTYSEWHSFT QPRLGEKVYL CNODENHKHA ODYVLTYNYE GRGSVAGSVG CCSERQEEDG LEFLONLEPK FRILAKACMK 15 Seg ID NO: 618 DNA sequence Nucleic Acid Accession #: NM 004949.1 Coding sequence: 202..2745 20 41 51 COCCAAAGGA AAAGCCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC CTCTCCGCGC GCCCCACCTC CTCCGCCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC GETECOGCCG COGCCCTCGC CCCGCGGAGC CCTCCTACCC CGGCCCGACG CTCGGCCCGC 180 25 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCCT CCGGCTCCTG GAACGGAGCC 240 CTCTGCCGGC TGCTCCTGCT GACCCTCGCG ATCTTAATAT TTGCCAGTGA TGCCTGCAAA 300 AATGTGACAT TACATGTTCC CTCCAAACTA GATGCCGAGA AACTTGTTGG TAGAGTTAAC CTGAAAGAGT GCTTTACAGC TGCAAATCTA ATTCATTCAA GTGATCCTGA CTTCCAAATT TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAGT TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTTG 480 30 540 GAGCATCARA CARAGGYCCT RAAGRAAAGA CATACTANAG RAARAGTTCT AAGGGGGGC MAGAGRAGAT GOGTCCART TCCTTGTTGS ATGCTAGRAA ACTCCTTGG TCCTTTTCCTTC AACQAGTTCA ATCTGACAGG GGCCARAACT ATACCATATA CTATTCCATA 600 720 AGAGGTCCTG GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA 790 35 ARCTIGIATE GENETIGEC TORRESTOR GAGGAGGET ANTICITIES GALANTIGC TITIGCARCA CICCAGATGG GIATACTCCA GRACTICCAC IGCCCCIANI ANTICARARIA 840 900 GAGGATGARA ATGATAACTA COCAATTTTT ACAGAAGAAA CTTATACTTT TACAATTTTT GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020 GACACGATGC ACACACGCCT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCCACC 1080 CTATTITCTA TGCATCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140 CHATTITITA TIGORICIARE TACAGGGIG ATCACCACA CALCACTOR CAGGACTACTOR GAGTTAATTG ACAAGTACCA GITGAAAATA AAAGTACAAG ACATGGATG TCAGTATTIT GGTTTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1200 ACATITACIC GIACTICITA IGIGACATCA GIGGAAGAAA ATACAGITGA IGIGGAAATC 1320 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAACTGGAG AGCTAATTAT 1380 45 ACCATTITAA AGGGCAATGA ARATGGCANT TITAAAATTG TAACAGATGC CAAAACCAAT 1440 GANGGAGTIC TITUTUTATU TANGCCITTU ANTENTANA ANARCANCA GATGATCITU CRAATIGGIU TAGITAATGA AGCICCATIT TOCAGAGAGG CIAGICCAAG ATCAGCCAIG 1500 1560 AGGACAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAACCCC CCAATACAGA CTGTTCGCAT GAAAGAAAT GCAGAAGTGG GAACAACAAG CAATGGATAT 1620 1600 50 ARAGCATATG ACCCAGARAC RAGRAGIAGC AGTGGCATAR GGTATARGAR ATTRACTGAT CCRACAGGGT GGGTCACCAT TGATGRARAT ACAGGATCAR TCRARGTTT CAGARGCCTG 1740 1800 GATAGAGAGG CAGAGACCAT CAAAAATGGC ATATATAATA TTAGAGTGCT TGGATCAGAC 1860 CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC AGCCCATTCA TACCTAAAAA GACAGTGATC ATCTGCAAAC CCACCATGTC ATCTGCGGAG 1980 55 ATTGTTGCGG TTGATCCTGA TGAGCCTATC CATGGCCCAC CCTTTGACTT TAGTCTGGAG 2040 AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100 COTCTTCCT ATCAGAATGA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160 GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220 GALANTGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGA 2280 60 GADDITISEC CONCRETO 13 PARTICOS ADMITISEC POSTROGATOS PORTUGATOS ANDITISECOS PORTUGATOS 2340 2400 2520 2580 65 TOGGARTOT GCCGGGGGG TGGCCACCAT CACACCCTGG ACTCCTGCAG GGGAGGACAC
ACGGAGGTGG ACACTGCAG ATACACTTAC TOGGAGTGGC ACAGTTTTAC TCAGCCCCGT 2640 2700 CTTGGTGAAG AATCCATTAG AGGACACACT CTGATTAAAA ATTAAACAAT GAAAGAAAGT GTATCTGTGT AATCAAGATG AAAATCACAA GCATGCCCAA GACTATGTCC TGACATATAA 2820 CTATGAAGGA AGAGGATCGG TGGCTGGGTC TGTAGGTTGT TGCAGTGAAC GACAAGAAGA 2880 70 AGATGGGCTT GAATTTTTGG ATAATTTGGA GCCCAAATTT AGGACACTAG CAGAAGCATG CATGAAGAGA TGAGTGTGTT CTAATAAGTC TCTGAAAGCC AGTGGCTTTA TGACTTTTAA 2940 3000 AAAAAATTAC AAACCAAGAA TITITTAAAG CAGAAGATGC TATITGTGGG GGTTFFTCTC NORMATTATTE GATGGAATAT TITTOGTCAA ATGCACATTI ACAGAGAGA ACTATAAACA AGTACACAAA TITTICAATT TITACATATI TITAAATTAC TIATOTTCTA TCCAAGGAGA 2180 75 TCTACAGAGA AATTAAAGTC TGCCTTATTT GTTACATTTG GGTATAATGA CAACAGCCAA 3240 TITATAGGE AATAANGE AATGAATGA AGCCEAT AGACCTATT TGAMGGEAA CCTANTGGAA AATGTAAGG ACCTTGCTT AACATTATC CCAGTTAAT AAGGCETAT 3300 GTGGTGCTTG GAAACTGTTG TTTTCCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT ATTATTTAT TETTGTAATG TGACCITTE ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480 80 TTGACTATTA CAATTTCATT Seq ID NO: 619 Protein sequence Protein Accession #: NP 004940.1 85 MEAARPSGSW NGALCRILLI TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECPTA

5	ANLIHSSDPD KKRHTKEKVL EPRNLFYVER PIFTEETYTF TGVITTISSQ VTSVEENTVD KPLNYEEKQQ KENAEVGTTS	RRAKRRWAPI DTGNLYCTRP TIFENCRVGT LDRELIDKYQ VEILRVTVED MILQIGVVNE NGYKAYDPET	PCSMLENSLG VDREQYESPE TVGQVCATDK LKIKVQDMDG KDLVNTANWR APFSREASPR RSSSGIRYKK	KRSFTILLSN PFPLFLQQVQ IIAFATTPDG DEPDTMETRL QYFGLQTTST ANYTILKGNE SAMSTATVTV LTDPTGWVTI	SDTAQNYTIY YTPELPLPLI KYSIIGQVPP CIINIDDVND NGNFKIVTDA NVEDQDRGPB DENTGSIKVF	YSIRGPGVDQ IKIEDENDNY SPTLFSMHPT HLPTFTRTSY KTNEGVLCVV CNPPIQTVRM RSLDREAETI	120 180 240 300 360 420 480 540
10	VTSLDVTLCD TSKQPKVIPD QETIEMVKGG	SLESSTSEVQ CITENDCTHR DLAOONLIVS	RMWRLKAIND VDPRIGGGGV NTEAPGDDKV	NDNSPFIPKK TAARLSYOND OLGKNAILAI YSANGPTTOT GGHTEVDNCR	PPFGSYVVPI LLGIALLFCI VGASAQGVCG	TVRDRLGMSS LFTLVCGASG TVGSGIKNGG	600 660 720 780 840
15	Seq ID NO: Nucleic Ac: Coding sequ	620 DNA se id Accession Lence: 46	1 # : NM_032	1545.1			
20	1	11	21	31	41	51	
20	1	11	21	1	1	Ĭ.	
25	CCATGT CAGG CTATCAAAGA GCACCGACAG GCAGGGCTGG CGCGCGGCCAC	CTTCTGTTTA GAGAAACATA TCACCGCTCA GGGCCGGAGG CGCTGCTGCA TTCACCGGCC	CGGTCAGTTT ACGGCGGTAG ACTGGACCTC AGCCGCTCCC GGAACGGCGG GCTACTGCGA	GACTCTCAAA GGCATTACAG AGAGGAAGTC CAGTCATTTC CTACTCCCGG TACCTGCGTG GCATGACCAG	ATCATCAATT ACCAAGGTTG GGAGAGGTGA GCTTTCGGAG CTGGGCAGCT AGGCGCAGTG	TUGGAAACAG CCACTCAGAA CTUGGAGCGC AGGGTGCGTC TCTGCGTGTG AATGCGGCGC	60 120 180 240 300 360 420
30	CCTGCACTGC CCACGCTCAC ACTCCTGCAC CGTCCTCCAG	CTCCCCCTCC GGGCCGAGCG CGCCTCCTGC CGGGAGCGGC	AGACGCCTGA CCGGGGGGGG GCCCGGATGC GCCCCTGCGG	CTGCCACCTC CCGCTGTGAC GCCCAGCCTG GCCCGCGCAC AAGGCCGGGA	COGARAGACT CTACTCTTGC CCTCGGTCCC CTTGGGCATC	TCCTGGCCTC TGCCCTGCGC TGGTCCCTTC GCCTTTAATT	540 600 660 720
35	TTCTATGTTG TTTTTATTGG AAAAAA	TAAATAATAG GTAATAAATA	ATGTGTTTAG TTTTCATGAA	TTTACCGTAA AGCGCCAAAA	GCTGAAGCAC	TGGGTGAATA	780 840
40	Seq ID NO: Protein Acc	621 Protes cession #: 1	In sequence IP_115934.1 21	31	41	51	
45	VTGSAEGWGP SECGALEHGA	EEPLPYSRAF WTLRACHLCR	GEGASARPRC CIFGALHCLP	ENGGREEVTK CRNGGTCVLG LQTPDRCDPK RRPCGRPGLG	SFCVCPAHFT DFLASHAHGP	GRYCEHDORR	60 120 180
50		622 DNA se id Accession Lence: 13	#: FGENES	H predicted	1		
55 60	TATGTGTCAG GAACCATGGC CAGTGCTGTT TGCACCTTCT TTTGTTGTGA	TOTGTOTOCT TOTGCCAGCC ACAATGACGC	CCTCTTGTGT GGCACCCAGG CATCGTGTCC TGAGCTCTGC TCAGGGTGTG	31 GACTACCCCA CCAAGGGAG TOTGGAGACA CTGAGCGAGA TGTCTTGATT AATTCCCAGT	TCATOGCTCC AGATCTACAA CCCGCCAATG CCTTTGGCCT	CCCCTTGGAG TGGTCCCCCC CACAAACGAT	60 120 180 240 300 360
	Seq ID NO: Protein Ac	623 Protes	in sequence FGENESH pre-	dicted			
65	MRFSVSGMRT QCCYNDAIVS SKCERGRIC	11 DYPRSVLAPA LSETRQCGPP	21 YVSVCLLLLC CTFWPCFBLC	31 PREVIAPAGS CLDSFGLTND	41 EPWLCQPAPR PVVKLKVQGV	51 CGDKIYNPLE NSQCHSSPIS	60 120
70	Seq ID NO: Nucleic Ac	624 DNA se id Accession Jence: 51	1 #: M18728	1.1			
75	CCTCAGCCCC	TCCCTGCAGA	TTGCATGTCC	31 CAGAGAAGAC CCTGGAAGGA	GGTCCTGCTC	ACAGCCTCAC	60 120
80	TTCTAACCTT ATGTCGCAGA GTTACAGCTG TAGGAACTCA	CTGGAACCCA GGGGAAGGAG GTACAAAGGC ACAAGCTACC	GTTCTTCTAC GAAAGAGTGG CCAGGGCCCG	CCAAGCTCAC TCGCCCACAA ATGGCAACAG CATACAGTGG AGAATGACAC	TATTGAATCC CCTGCCCCAG TCTAATTGTA TCGAGAGACA	ACCCCATTCA AATCCTATTC GGATATCTAA ATATACCCCA	180 240 300 360 420
85	TCATAAAGTC TGCCCAAGCC CCTTCACCTG	AGATOTTGTG CTCCATCTCC TGAACCTGAG	AGCAACAACT GTTCAGAACA	CAACCOGACA CCAACCCGT CAACCTACCT CCAATGGCAA	GTTCCATGTA GGAGGACAAG GTGGTGGGTA	TACCCGGAGC GATGCTGTGG AATGGTCAGA	480 540 600 660

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	ACCGCAGTGA	CCCAGTCACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCC	780 840
_	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
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	TATAGCAGCC	CTGGTGTATT	TTCGATATTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCCT	1140
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	CTGACTCATT	CITTATTCTA	TTTTAGTTGG	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920 1980
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	GTTAAGGAAG ACACAGGAGA	AAGATAGATC TTCCAGTCTA	CTTGAGTTAG	CATANTACAG	AAGTCCCCTC	TACTTTAACT	2340
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	1	11	21	31	41	51	
	Monnoappop	THABMKEATT	TACT.T.TUSOID	PTTAKITIES	TPENVARGER	VILLIAHNLPO	60
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	TLQVIKSCLV	NEEATGQFHV	YPELPXPSIS	SMNSNPVEDK	DAVAFTCEPE	VONTTYLWWV	180 240
	NGQSLFVSPR	LQLSNGNMTL					
		DODN'T NT. OCU	2 S CM DD 2 OVC	METHOTEOOR	TORI.PIPRIT	COMVESSION	300
4.5	TISPSKANYR	PGENLNLSCH TTVTMITVSG	AASNPPAQYS	WFINGTFQQS	TOELFIPNIT	VININGSYMCQ	300
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	TISPSKANYR AHNSATGLAR Seq ID NO: Nucleic Ac: Coding sequ	PGENLNISCH TTVTMITVSG 626 DNA se id Accession Lence: 1355	AASNPPAQYS SAPVLSAVAT equence 1 #: M1872: 1657	WFINGTFQQS VGITIGVLAR	TOELFIFRIT VALI	VIINISGSYMCQ	
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50	TISPSKANYR AHNSATGLNR Seq ID NO: Nucleic Ac: Coding sequ 1 GGAGCTCAAG CCTCAGCCCC	PGENLALSCH TTVTMITVSG 626 DNA se id Accession sence: 1355 11 	AASNPPAQYS SAPVLSAVAT equence 1 %: M18726 1657 21 AAGAGGTGGA	WFINGTFQQS VGITIGVLAR 3.1 31 CAGAGAAGAC CCTGGAAGGA	TQELFIFRIT VALI 41 AGCAGAGACC GGTCCTGCTC	VINNSGSYMCQ 51 ATGGGACCCC ACAGCCTCAC	
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50	TISPSKANYR AHNSATGLNR Seq ID NO: Nucleic Ac. Coding sequ 1 GGAGCTCAAG CCTCAGCCCC TTCTAACCTT ATGTCGCAGA GTTACAGCTG	PGRHANDSCH TTVTMITVSG 626 DNA sid Accession Lence: 1355 11	AASHPPAQYS SAPVLSAVAT equence 1 %: M187241657 21 AAGAGGTGGA TTGCATGTCC CCCA,CCACTG GTTCTTCTAC	WFINGTPOOS VGITIGVLAR 3.1 CAGAGAAGAC CCAGGAAGAC CCAGAAGCTCAC TCGCCCACAA	41 AGCAGAGACC GGTCCTGCTC TATTGAATCC CCTGCCCAGT	51 ATGGGACCC ACAGCCTCAC ACAGCCATTCA AATCGTATTG	60 120 180 240 300
50	TISPSKANYR AHNSATGLNR Seq ID NO: Nucleic Ac: Coding seq 1 GAGGTCAAG GCTCAGCCC TTCTAACCTT ATGTCGCAGA GTTACAGCTG TAGGAACTCA	PGRILNISCH TTVTMITVSG 626 DNA s: 626 DNA s: 61d Accession ience: 1355 11	AASHPRAQYS SAPVLSAVAT equence 1 %: M18724 1.1657 21 1 AAGAGGTGGA TTGCANGTCG CCCACCACTG GTTCTTCTAC GAAAGAGTGG CCAGGGCCG CCAGGGCCG CCAGGGCCG CCAGGGCCG CCAGGGCCG CCAGGGCCG CCAGGGCCG CCAGGGCCG CCAGGGCCG CCAGGGCCG CCAGGGCCG	WFINOTPOOS VGITIGVLAR 3.1	41 AGCAGAGACC GGTCCTGCTC CCTGCCCAG TCTAATTGAATCC	51 ATGGGACCCC ACAGCCTCAC AATGGTATTG GGATATGTAA AATGATGTAA	60 120 180 240
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50	TISPSKANYR AHNSATGLNR Seq ID NO: Nucleic Ac. Coding sequ GARGICAAG CCTCAGCCCC TTCTAACCTT TAGTGGCAGA GTACAGCTG TAGGAACTCA ATGCATCCCT TCATAAACTC TCATAAACTC	PGENIAUSCH TTVTMITVSG 626 DNA s: id Accession Lence: 1355 11	AASHPPAQYS SAPVLSAVAT equence 1 %: M187241657 21	MFINOTPOOS VGITIGVLAR 3.1 1 CAGAGAAGAC CCTGGAAGGA CCAGCCACA ATGGCACACA ATGGCACACA GATACAGTGA GAGATGACA CCACCACACA CCACCACACA CCACCACACA CCACCCCACACA CCACCCCCACACA CCACCCCCACACA CCACCCCCC	41 AGGAGAGACC GGTCCTGCTC TATTGAATCC CCTGCCCCAG TCGAGAGACA AGGATTCTAT GTTCCATCTA GGAGGACTAA GGAGGACTAA	51 ATGGGACCICA ACGCCATICA ACGCCATICA ACGCTATTG GGATATGTATG GGATATGTAA ATTATACCAA ACCCTACAAG TACCGGAGG	60 120 180 240 300 360 420 480 540
50	TISPSKANYR AHNSATGLAR Seq ID NO: Nucleic Ac. Coding sequ TOTAL GRACCTCAAG CCTCAAGCCCC TATGTGGCAGA GTIACAGGA GTIACAGGA ATGCAACTCA ATGCATCCAT TCATAAAGTC TGCCCAAGCC CCTTCACCTG CCTTCACCTG	PGENLAUSCH TTVTMITVSG 626 DNA s: id Accession lence: 1355 11	AASHPPAQYS SAFVLSAVAT equence 1 #: M187241657 21	MFINOTPOOS VGITIGVLAR 3.1	41 	51 ATGGGACCIC ACAGCCTCAC ACGCCATTCA ACGCCATTCA ACCCTACAAG ACCCTACAAG ACCCTACAAG ACCCTACAAG ACCCTACAAG AATGGTCAGA	60 120 180 240 300 360 420 480
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50 55 60	TISPSKANYE ANNSATGLER Seq ID NO: Rucleic Ac Coding seq CODING SEQ GAGGTCAAG GCTCAGCCCC TTCTAACCTT TAGTGTGAGA GTACAGCCC TAGTAACTC TGCCAAGCC CCTTCACTG GCCTCACTG GCCTCACGG GCTCCCGGG GCTCCAAGA ACCCCGGGG ACCGCCGGGG ACCGCCGGG	PGENLAUSCH 626 DNA s- id Accession Lence: 1355 11 1 CTCCTCTACA TCCCTGCAGA CTGGAACCGA GGGAAGCGA GGAACCGA GCTGACACAAGGC ACAAGCTACC ACGACCTACC TCCCATCTCC TGAACCTGAG GACCTGAG GACCTGAG GACCTGAG GACCAGGACCAG GACCAGTACCAG GACCAGTACCAG GACCAGTACCAG CCAGTCCAG	AASHPPAQYS SAPVLSAVAT Quence #: M18724 1657 21 AMAGGTGGA TTGCANGTCC CCA.CCACTG GAAAGAGTGG CCAGGGCCGA AACGTCACCC AATGAAGAATG GTCACACACACTG CTGCAAGCACTG GGCACACTG CTGCAAGCACTG CTGCAAGTGT CGTGAAGTGT CGTGAAGTGT	WFINOTPOOS VGITIGVLAR 3.1 CAGAGAAGAC CCTGGAAGGA CCAAGCTACA ATGGCAACAA ATGGCAACAA ATGGCACCAC CAACCGGACA ACGCACCAC CCAACGGGCA CCAACGGACA ATGTGAAAT TCTATGGCCC TCAATGGCAC AATTGGAACA TCTATGGACC	41 AGCAGAGACC GGTCCTGCTC TATTGAATCC CCTGGCCCAG TCTAATTGTA TCGAGAGACA AGGATTCTAT GTTCCATGTA GGGGGGAGA GGAGGACCA AGAGTCCTA AGAGTCCCA AGAGCCCA AGAGCCCA AGAGCCCA AGAGCCCA AGAGCCCA AGAGCCCA	51 ATGGGACCCA ACAGCCTCAC ACGCCATICA AATCGTATTG GGATACTANA ATTATACCCCA ACCCTACANG TACCCGGAGC GATGCTGTGG AATGGTCAGA ACTCTACTACA GGAGGTGCCA ACCATTTCCCC	60 120 180 240 300 420 480 540 600 660 720 780
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50 55 60	TISBSKANTA ANNSATCHAR Seq ID NO: Nucleic Ac. Coding seq: 1	FORMILA-SCH TYVINITIVS 626 DNA s. id. Accession Lennes: 1355 11 CTCCTCTACA TCCCTGCABA CTCGGABA CCGGABAGAG GTMACAAGA ACAACTTACC GGGABAGAG GTMACAAGAG GTMACAAGAG ACAACTTACC CCCATTCAC CCATTCACC CMATTACCGT CAACTACC CMATTACCGT CAACTACCC CMATTACCGT CAACTACCC CMATTACCGT CAACTACCC CMATTACCGT CAACTACCC CMATTACCGT CAACTACCT CMACTACCGC CCCAATCACC CCCAATCACC CCCAATCACC CCCAATCACC CCCAATCACC CCCAATCACC CCCCAATCACC CCCCAATCACC CCCCAATCACC CCCCAATCA	AASIPPAQYS Equence # H N1872(1657 21 ANGMOTIGA TTOSATOTICTAC GARAGAGTOG COCACCACTO COCACCACTO COCACCACTO COCACCACTO COCACCACTO COCACCACTO COCACCACTO COCACCACTO COCACCACTO COCACCACTO COCACCTO COC	MEINOTROGS VOITIGVIAR 3.1 3.1 CAGAGARAGA CCTGGARAGA CCTGGARAGA CCTGGARAGA CATACASTG CARACTCA CARACT	41	51 ATGGGACCCC ACAGCCTACA ANTOSTATTO GOGTATTATTO GOGTATTATTO GOGTATTATTO ACCTACAGA ACCTACAGA ACCTACAGA ACCTACAGA CACTACACAGA CACTACACACACACACACACACACACACACACACACACA	60 120 180 240 300 360 420 600 720 780 840 900 900 1020
50 55 60 65	TISBSKANYA ANNSATCHAR Seq ID NO: NUCleic Ac Coding Seq 1 GARGCICHAG CCTCAMCCCC TACTACACCC TACTACACCC TACTACACCC TACTACACCC TACTACACCC COTTACACCT CCTCAACCC CCTCAACCC CCTCAACCC CCTCAACCC CCTCAACCC CCTCAACCC CCTCAACCC CCTCAACCC CCTCAACCC CCTCAACCC CCTCAACCC CCTCAACCC CCCCAACCC CCCCAACCC CCCCAACCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCACCCC CCCCCACCCC CCCCCACCCC CCCCCACCCC CCCCCACCCC CCCCACCCC CCCCCACCCC	POBILIALISCE TYVINITYSS 626 DNA s: 1d Accession Lence: 1355 11	AASIPPAQYS SAPVLBAVAT equence 1 B: N1872i .1657 21 AMGAGGTGGA TTGCA.TGTCC CCCA.COA.CTG GTTGCA.TGTCC CCCA.COA.CTG GTTGCA.TGTCC CCCA.COA.CTG GTTGCA.CAG AMGAGGTGGA AMGAGGTGGA AMGAGGTGGA AMGAGGTGA GGAACCAATA GGATGTGGAACCAATA TGGTTTATACA GTGAAGGTTAAA CCG.CAGGCGAAA TGGTTTATACA TGGGAACTATA ACCA.CAGTCA TGGAACTATA ACCA.CAGTCA TGGAACTATA ACCA.CAGTCA TGGGAACTATA ACCA.CAGTCA	MPINOTPOGS VOITIGVIAR 3.1 3.1 CAGRANGAC CCTOGRANGA CCCAGCCACA AAGACCACA CCAACCCACA CAACCCACA CCAACCCACA CCAACCCACACA CCAACCCACACA CCAACCCACACA CCAACCCACACA CCAACCACACA CCAACCCACACA CCAACCCACACACA CCAACCCACACACACA CCAACCCACACACACACACACACACACACACACACACACA	41 1 AGOMANACC OCTOTATION TOMATON TOMA	S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S	60 120 180 240 300 420 480 540 600 600 720 780 840 900 960 1020
50 55 60	TISSENANTA ANNESATURA Seq ID NO: Nucleic Ac Coding seq: GRAGGTCAAG CCTCAAGCCC TYCTAACCTT AACGTAACTT AAGGAACTCA ATGCAACAGC CCTCAACCCC TGCCAAGCC CCTCAACCCC GCCCAAGCC CCTCAACCCC CCTCAACCCC TGCCAAGCC CCTCAACCCC TGCCCAAGCC CCTCAACCC TCTCAACCCC TCTCAACCCC TCTCAACCCC TCTCAACCCC TCTCAACCC TCTCAACCC TCTTCAACCC TCTTCAACCC TCTTCAACCC TCTTTTAACCC TCTTTTAACCC TCTTTTAACCC TCTTCTTAACCC TCTTTTTAACCC	PERILLI-SCH TYVINITUS 626 DIN s 626 DIN s 626 DIN s 626 DIN s 627	AASIPPAQYS Equence # H N1872(1657 21 ANGAGGIGGA TTGCATGTT GTTCTAC GARAGAGGGCCO AATGAAGAG GTCCTCTAC GARCACTGT GTCACTGT GARCACTACT GARCACTACT GARCACTACT GARCACTACT GARCACTACT GGARCACTACT RCACT GGARC	MEINOTROGS VOITIGVLAR 3.1 3.1 CAGAGARAGA CCTGGAAGGA CCTGGAAGGA CCTGGAAGGA CCTGGCAAGGA CATACAGTG CAAACGGA CAAACGAGA CAAACGGAAAGA CAAACGAAACA CAAACGGAAACA CAAACGGAAACA CAAACGGAAACA CAAACGGAAACA CAAACGGAAACA AATGGAAACT AATGGAAACT AATGGAAACT CAAACGGAAGGAACA CCAAACGCGAACCCGAACCGCGAACCCGAACCCGAACCCGAACCCGAACCCGAACCCGAACCGAACCCGAACCCGAACCCGAACCCGAACCCGAACCCGAACCCGAACCCGAACCCAACCGAACCCGAACCCCGAACCCCGAACCCCGAACCCCGAACCCCGAACCCCGAACCCCGAACCCCAACCCGAACCCCAACCCCGAACCCCAACCCCGAACCCCAACCCCGAACCCCAACCCCGAACCCCAACCCCGAACCCCAACCCCGAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCC	41	S1	60 120 180 240 300 360 420 480 540 600 720 780 840 900 1020 1020 1140
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50 55 60 65 70 75	TISBERNAMTRA ARMENATURAR Seq ID NO. Mucleic Ac. Coding sequity GRAGOTICANA GRA	## CONTROL OF THE PROBLEM SECTION OF THE PROB	AMSTEPAQUE SAPVILANATA SQUENCE 1 #1 H18721	SILVENTINGS VOITIOVIAN SILVENTINGS COMMANDA COMMANDA COMMANDA COMMANDA COMMANDA COMMANDA COMMANDA COMMANDA COMMANDA COMMANDA COMMANDA COMMANDA COMMONDA	41 ACTION OF THE PRINT OF THE	51 ATOMANOMENTO AND AND AND AND AND AND AND AND AND AND	660 120 180 300 424 480 480 660 660 780 1020 1120 1120 1120 1120 1120 1120 11
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5	TCTCACCTAG GTTAAGGAAG ACACAGGAGA TTTACAAAAA	/086443 GTGAGCGCAT AAGATAGATC TTCCAGTCTA AGTAACCTGA TTCCAATTTG ACTTGTAGAG	CAATTAAAA CTTGAGTTAG ACTAATCTGA ACAAAACCCA	AAATTAAAAC CATAATACAG TGTTAACCAA CTGTTCTTGT	CAATTTAAAA AAGTCCCCTC TGTATTTATT ATTGTATTCC	AAAAAAAGA TACTTTAACT TCTGTGGTTC CCAGGGGGAG	2220 2280 2340 2400 2460 2520
	Seq ID NO:	ACT 627 Protei	n sequence	IIIAIICAIA	AAT CACAAAT	Mindecari	2320
10	Protein Acc	cession #: A					
	1	11	21	31	41	51	
15	MDSFSQDVKT NPNVLHKIRD	RLLIMIRLLP PLVHPVTDIS	PPNLSLLMPA SIFNTAVCSN	SFAWQDDAVI VQWSFSELDF	SISQEVASEG	NLTECQIYLV	60
	Seq ID NO:	628 DNA se	quence				
20		ence: 2370.					
20	1	11	21	31	41	51	
	GGAGCTCAAG	CTCCTCTACA	AAGAGGTGGA	CAGAGAAGAC	AGCAGAGACC	ATGGGACCCC	60
25	CCTCAGCCCC	TCCCTGCAGA	TTGCATGTCC	CCTGGAAGGA	GGTCCTGCTC	ACAGCCTCAC	120 180
	ATGTCGCAGA	GGGGAAGGAG	GTTCTTCTAC	TCGCCCACAA	CCTGCCCCAG	AATCGTATTG	240
	GTTACAGCTG TAGGAACTCA	ACARGCTACC	GAAAGAGTGG CCAGGGCCCG	CATACAGTGG	TCGAGAGACA	ATATACCCCA	300 360
30	ATGCATCCCT	GCTGATCCAG AGATCTTGTG	AACGTCACCC	AGAATGACAC Chaccocaca	AGGATTCTAT	ACCCTACAAG TACCCGGAGC	420 480
50	TGCCCAAGCC	CTCCATCTCC	AGCAACAACT	CCAACCCCCT	GGAGGACAAG	GATGCTGTGG	540
	CCTTCACCTG	TGAACCTGAG CAGTCCCAGG	GTTCAGAACA CTGCAGCTGT	CAACCTACCT	CATGACCCTC	ACTOTACTOR	600 660
35	GCGTCAAAAG	GAACGATGCA CCCAGTCACC	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720 780
33	CCTCAAAGGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
	ACCCACCTGC	ACAGTACTCT CAACATCACT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900 960
40	CAGCCACTGG	CCTCAATAGG	ACCACAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGCTCCTG	1020
40	TATAGCAGCC	TGTGGCCACC CTGGTGTATT	TTCGATATTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCCT	1080 1140
	GAATTCTTCT	AGCTCCTCCA GAAGCCCTAT	ATCCCATTIT	ATCCCATGGA	ACCACTAAAA	ACAAGGTCTG	1200 1260
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	TGCCTCTTTC	GCTTGGCAGG ACAGAGTGTC	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
	AGATCCTTTA	GTGCACCCAG	TGACTGACAT	TAGCAGCATC	TTTAACACAG	CCGTGTGTTC	1620
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	GGAGGAGTCT	GTGCAGTTTC AGTTGTAGAA	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800 1860
	CTGACTCATT	CTTTATTCTA	TTTTAGTTGG	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920
55	CTCTTGGTAT	TACCCTCCTA TTTAAATGTC	ATAGTCATAC TGCATGCAGC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	GGCTGGAATT	ACAAAACTCA	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	TOTCACCTAG	CAAATGGTGG GTGAGCGCAT	TGAGCCAGTG	GTGCTAAATG	CTACATACTC	CAACTGAAAT	2220
60	GTTAAGGAAG	AAGATAGATC TTCCAGTCTA	CAATTAAAAA	AAATTAAAAC CATAATACAG	CAATTTAAAA	AAAAAAAAAA TACTTTAACT	2280
	TTTACARAAA	AGTAACCTGA	ACTAATCTGA	TOTTAACCAA	TGTATTTATT	TCTGTGGTTC	2400 2460
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80	1	11	21	31	41	51	
00	GCGGCGGGCG	CAGACAGCGG	COGGCGCAGG	ACGTGCACTA	TOGCTCGGGG	CTCGCTGCGC	60
	CGGTTGCTGC	GGCTCCTCGT	GCTGGGGGCTC	TOGCTGGCGT	TOCTGCGCTC	CGTGGCCGGG	120
85	AAGTGCATGG	ACTGCGCGTC	TTGCAGGGGG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240 300
65	CTGACCTTCG	CTCCTGCCCC TGCTGGGGCT	GCTTTCTGGC	TTTTTTGGTCT	GGAGACGATG	CCGCAGGAGA	360
	GAGAAGTTCA	CCACCCCCAT	AGAGGAGACC	GGCGGAGAGG	GCTGCCCAGC	TGTGGCGCTG	420

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	TTCTAGAGCC	AGTCTCTGCC	TCCCAGACGC	GGCGGGAGCC	AAGCTCCTCC	AACCACAAGG	540
	GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTCAGGG	GAACCTTCCA	600 660
5	ACRARACAGO	TTGCCCTGCC	TANGGAACTG	CAGCATTTGC	ACAGGGGAGG	GGGGTGCCCT	720
-	CCTTCCTTAG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC	780
	TCACTCAGAT	GTCCTGAAAT	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCCAACTC	840 900
10	CCCAAAGCGG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAATTTATT	960
10	aadaaataa	TCTTTAACTT	TAAAAAAAA	AAAAAAA			
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	Protein Acc	cession #: P	IP_057723.1				
15	1	11	21	31	41	51	
	1	RLLVLGLWLA	1	1	1	Parameter	60
	SDFCLGCAAA	PPAPFRLLWP	ILGGALSLTF	VLGLLSGFLV	WRRCRREKE	TTPIEETGGE	120
20	GCPAVAL IQ						
20	Seq ID NO:	632 DNA se	mence				
	Nucleic Ac	Ld Accession	#: NM 0031	316.1			
	Coding sequ	uence: 79	1538				
25	1	11	21	31	41	51	
	COOCEGGGTT	GGAAAATGAT	GGY FGFGGGG	GAGGTGGAGG	OGA COGA GTG	CTGAGAGGAA	60
	CCTGCGGAAT	CGGCCGAGAT	GGGGTCTGGC	GCGCGCTTTC	CCTCGGGGAC	CCTTCGTGTC	120
30	CGGTGGTTGC	TGTTGCTTGG	CCTGGTGGGC	CCAGTCCTCG	GIGCGGCGCG	GCCAGGCTTT	180 240
50		CCCCTAGGCC	CTATTCAAAA	CAAGTATCTT	ATGTTATTCA	GGCTGAAGGA	300
	AAAGAGCATA			AAAGACCTTT ACTGACCATC			360 420
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35	GGACTCAGAG		TTTAGAGAAT	GCGAGTTATG ATGGATGATG	GGATTGAACC	CCTGCAGAAC	540 600
	AGCTCTCATT	TTGAGCACAT CCAACAAGGA	TATAGAGAAA	GAAACTGCAA	AGGATGAAGA	GGAAGAGCCT	660
	CCCAGCATGA	CTCAGCTACT	TCGAAGAAGA	AGAGCTGTCT	TGCCACAGAC	COGGTATGTG	720
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45	ATGGCATTTG	TGGGAACAGT	GTGTTCAAGG	AGCCACGCAG	GCGGGATTAA	TGTGTTT3GA	1080
45			AGATTGTTCC	GTTGCTCATG TGTGGAGCAA	AGAGCTGCAT	CATGAATTCA	1140
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		GAGGAAACTG	CCTTCTTAAT	ATTCCAAAGC GGGGAAGAGT	CTGATGAAGC CTGACTGTGG	TACTCCAAAG	1320 1380
50	GAATGTGAAT	TOGACCCTTG	CTGCGAAGGA	AGTACCTGTA	AGCTTAAATC	ATTTGCTGAG	1440
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			ACCTGTATTT	GGAATTGTGC TTCCAGCTAG	CTGCTATTAT	TCAAACGCCT	1860 1920
	GGGATGGTTA	ACGAAGGCAC	AAAATGTGGT	GCTGGAAAGA	TCTGTAGAAA	CTTCCAGTGT	1980
60		CTGTTCTGAA	TTATGACTGT	GATGTTCAGA GAAAATGGCT	AAAAGTGTCA	TGGACATGGG	2040 2100
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		GCTTTAAGGT AAGCAGGAGC	ACGAAGTATT		AATCAAATAT	GTTGATTCAT TACAAAACCA	3360
	CTTGAGAATT	TCATGAGCAC	TTTAAAATCT	GAACTTTCAA	AGCTTGCTAT	TARATCATTT	3480
85	AGAATGTTTA	CATTTACTAA AGGCTGGAGA	GGTGTGCTGG	GTCATGTAAA	ATATTAGACA	CTANTATTT	3540 3600
	TTACTGTGGT	ATCTATGAGT	TATCATCTTA	GCTGTGTTAA	AAATGAATTT	TTACTATGGC	3660

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5	TGTGTATATA AAAAAAAAA Seq ID NO:	TACATATACA AAAAAAAAAA 633 Prote:	VVVV	TTACAATAAA	TAAAATACTT	GAAATTCTCA	3840
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10	PYSKOVSYVI	11 TLRVRWLLLL QAEGKEHIIH	LERNKOLLPE	DFVVYTYNKE	GTLITDHPNI	ONHCHYRGYV	60 120
15	DIEKETAKDE LLANYLDSMY AQLVLKKGFG RDCSCGAKSC LVDAGERCDC	SDCFGLRGLL EEEPPSMTQL IMLNIRIVLV GTAGMAFVGT IMNSCASGSR GTPKECELDP	LRRRRAVLPQ GLEIWINGNL VCSRSHAGGI NFSSCSAEDF CCEGSTCKLK	TRYVELFIVV INIVGGAGDV NVFGQITVET EKLTLNKGGN SFAECAYGDC	DKERYDMNGR LGNFVQWREK FASIVAHELG CLLNIPKPDE CKDCRFLPGG	NQTAVREEMI FLITRRRHDS HNLGMNHDDG AYSAPSCGNK TLCRGKTSEC	180 240 300 360 420 480 540
20	WGVDFQLGSD NCHCENGWAP DQLWRSYFRK	QFCQPDVFIQ GNCGFSGNEY VPDPGNVNEG PNCETKGYGG KRSQTYESDG PPPQPKVSSQ	TKCGAGKICR SVDSGPTYNE KNQANPSRQP	NFQCVDASVL NNTALROGLL GSVPRHVSPV	NYDCDVOKKC	HGHGVCNSNK	600 660 720 780
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20		ence: 56!					
30	CGGCAGTGAG	11 CTTCCCAGCC CTCCCGCTGG CTGCCTGCGG	TCCTGCTGGC	GCTGGT CCTC CGTGCTGACC	TGCCTAGOGC	CCCGGGGGGGG CGCGCGGCAA	60 120 180
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40	CCCCCAGCTG TANGAGACTG AAATATTTGA CTTCTGGTTT	AACCAGCAAT AGTTCTGCAA CTATTCTGTA AAACTTGTTT	GATAATGATG GCATCAGTTC TCTTTCATCC GCTGTGAACA	GCCTCTCTCA TACGGATCAT TTGACTAAAT ATTGTCGAAA	AAAGAGAAA CAACAAGATT TOGTGATTTT AGAGTCTTCC	ACAAAACCCC TCCTTGTGCA CAAGCAGCAT AATTAATGCT	540 600 660 720
45	TAAAAGCTTA			TTCAAGGCCC	CUAGCIUTTA	CCATTCACAA	780
50		ession #: 1	_				
50	1	11	21	31	41	51	
55	VSERGSLKQQ DVG6KGKVGR	LALVLCLAPR LREYIRWEEA LSAPGSQREG	ARNLLGLIBA RNPQLNQQ	GTVLTKMYPR KENRNHQPPQ	GNHWAVGHLM PKALGNQQPS	GKKSTGESSS WDSEDSSNFK	60 120
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70	GCCACCCTCA ACCATCCTCT AACACCCAAA TACACCTGCT	GGTGCACTAT ATGCTGGGAA CGCAGTACAG CGGTGCAGAC CCAAAATTGT	TGACAACOGG TGACAAGTGG CATCGAGATC AGACAACCAC	TGCCTGGATC CAGAACTIGG CCAAAGACCT	TGGCCTGGCT CTCGCGTGGT ATGTGTATGA CTAGGGTCCA	AAACCGCAGC CCTTCTGAGC CGAGGGCCCT CCTCATTGTG	480 540 600 660 720
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85	CTGCCTCTTC CGGGAAAGGC CCAATCAGAT GGGAGGGGAA	TGGTCTTGCA	CCTGCTTCTC ACCACCACCA GAAATTAGAA TTTGGGGGGA	AAATTTIGAT ACACAACAGC GAAACACAGC AAAGAGTTTT	ATTGGCAACA CTCATGGGAC AAAAAGAAA	CCTCCCCACC CCGACAGCAA AGAAATITGA TTGAAAATIG	1320 1380 1440 1500 1560

	1110.00	mac 4 12					
5	CCCGGCTTGG GGCTCAGCCT AAATTCAATC CCGGCCCAAG	AGTCCATAGA OGTGGGGCTG	AGCTGCATCG AGACTGCCCC GACGAACAGA CGGGCACTTT CAAAAAAAA	ATGAGACCTT	CCGGCCCAAG	CGTGGCGCTT	1620 1680 1740 1800
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20		638 DNA se id Accession uence: 203.	n #: NM_012	261.1			
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30	GGAAAATCTC TGGGACGACG GGCCAGCAAC	TCAGGCCTTT TGTCTCATGG TACGTAGATC	CAGAGTTTGC TGATCACAGA	TGAAAAAGAT AGCCAAATTT ACAGGCCGAT	ATATTTGTGG ATTGTACCTT ATCGCATTGA	TGCGGGAAAA ATGATGTGTG CCCGGGGGAGC	300 360 420 480
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40	GGAAGAAACC	TTGCCCCTGA	CCATGATCCT GTGAAGAGCA TTTTGGGGCT	CATCTTGGGC	CTCGTCATCA	TGGTAACACT	900 960
	ATCCCAGTAT CCAACTGGAT	AAGCACATGG CAGGTAGAAC	ACAAAATGAC GCTAGAGGCC AACAAAAGCA CCTGGGTATC	GTTAGGCAGG	CACCOCCTAT	GATACACCAA	1020 1080 1140 1200
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50	TCATGCTCCC	TGCAGCAAGA	GCTTATCCTA CCCCTGAAAG ATGTTTCACT GCAGAGTTGT CTGTGTGAGT	CCTACCOCCA	TCCAGCGACT	GCAGCACCAG	1500 1560 1620 1680 1740
55	TTCTCTGGC	639 Prote		CIGITITION	740110004171	10010101011	
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60			21 PHTMAQIMAE ITEQADIALT				60 120 180
65	PVKESHNNSK ECQAQQTISL LGLILGLVIM	ASSDPOKTVT VTLAIYHVHH	VQFVYDSSEK MILSAVHIQP KMTANQVQIP	FDIISDFVFS RDRSQYKHMG	EEHKCPVDER	BQLEETLPLI	240
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85	CTAATATAGT CAATTGACCA TGAAGATAAC	ATTTCCACTA TATTGTGAGC TATTGTATTT	TACGETTETE TITACTETTA AAAGAATCAC CTATCATACA TITATTAGTG	TTTTACCTGA TGGTTATTAG TTCCTTAAAG	TAAGTTATTG TCTTTCAATG TCTTACCGAA	AACCCTTTGG AATATTGAAT AAGGCTGTGG	660 720 780 840
35	ATTTCGTATG	GAAATAATGT	TTTATTAGTG	TCCTGTTGAG	GGAGGTATCC	TGTTGTTCTT	

		/086443 aggatgctat	PRA A CHIROPPA	OWNERS THE CA	A CIA CINCOCONICI	TOPOS PACOS	960
5	TTATCTGTGC CTAATATATT CATGATTTAC ATTCTGGTCA TGATTGCTAA AATGATCTGT CATTTAGTCC	AGAATATATT CTCTTCCTAT TCATTAAACT CTAAATATAC TTTACATAGA GCTCTGCAAA TCAAAATATA	TCCTTATTCA GGTTTTAGAT TTGATTTTGT ACTTTAGATA AATGTATTCT GTTTTGAAAA TACAGCATTG	GAATTTCTAA GTTTGATGTC ATGCTATTTT GATGAAGAAG CTTGGTTTTT TATATTTGAA CTAAGATTTT	ARATTTAAGT TTCTTAGTAT TTCACTATAG CCCAAAAACA TAAATAAAAG CAATTTGAAT CAGATATCTA	TCTGTAAGGG GGCATAATGT GATGACTATA GATAAATTCC CAAAATTAAC ATAAATTCAT TTGTGGATCT	1020 1080 1140 1200 1260 1320 1380
10	AAATTGCACT	TTGACCATTT TTTATTTTTT ATAAAGATT	TGTTATGAGG CCTGTGTGTC TCTAAACCAA	ATGTTGGTTT	TTGGTACTTG	TATTGTCATT	1440 1500
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20	1 MSLPSSRAAR KTIGKLQVPP	11 VPGPSGSLCA AGPQCSKVEV	21 LLALLLLLTP VASLKNGKQV	31 PGPLASAGPV CLOPEAPPLK	41 SAVLTELECT KVIQKILDSG	51 CLRVTLRVNP NKKN	60
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40	TGCCTGCACG CAGAAGTGCC	GCGCCGCCTC GCTGGGGGCG CCGCCTCTTG CCCGCCATCC CAGCCAGCCC	CTGCTGCGTG CCACCCTGAG CGCCACCAGG	CACTGCCCGG ACTTCTCCCC	AGAGACCCCG ATCCCGTGCA GCCAGCACGT	GCGCCCCAGG CCCTGGGACC CCAGAGCAAC	780 840 900 960
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50	RSVPRGEAAG PALGLDDDPD ERAGDETPDV	11 RAGGVGLLVL AVQELARALA APAAQLARAL DPELLRYLLG QVPARRLLPP	HLLEAERQER	ARAEAQEAED	QQARVLAQLL	RVWGAPRNSD YDDGPAGPDA	60 120 180 240
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75	CACTTGTTCT CCTGTGCCAG TTTCAGGTGG GCTCAGTTGA	AAACGACCGG TGGACTGGGC GTGCCTTGCG ATCAMGAAGT TTCAATAGAA	CRAGGTGAAG CTGGGTCCAG GAACGTTGTG TACCCATCTG	ACARTAGATG AATGTGGATG ATATTGTTTC TGCATGTTAT	CAATTTAATA AATACCCACT	AATGCAGCAT GAGGATTICA AGCAAAGGCT GAAAATGAAA	780 840 900 960 1020
80	ATTTTATGCT ATGTCTCAGC CTAGAAAAAT	GGTGACACCA GAAAGTTCAT ATCAATGCAC GGCATTTTTC ACCATACATT	CCTCTGAAGA AATAATATAG TCCCGTGACT AGCATCCACC	AATATCCTGT AAAAATTAAA TTCGTCTTGG CCGAAAGGAT	TTCCGTTGGA ATTTGGCTCA TCATAATCAA	TATCTTGTTG AACGATTTAT TACGTTGATA TGCAGTGACT	1080 1140 1200 1260 1320
85	ACAATTTAGA TCACTGAGTT AAGGAGGTTT	CTGCATGCCT TGAGAAAGCA TGACGCCATG AAGATTGCTG	GTTCATAGAC	ACATCCATGT AGAAGATCTC CTGTCTGTGA	GCTGTCTTTG TGGAAACATA AAGTCATATC	ACAGAGAACA GATACACCAG GGATGGCGAA	1380 1440 1500 1560

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	AAGTCACAGG	AGGAGACAAA	TTGCTCACGG	TCATGCCAGT	TGCTGGTTGT	ACACTOGAAC	3120
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	1	11	21	31	41	51	
	ī	1"	ī ·	ī	i	i	
45	MODELLER	AAFVCLQNDR	PODL SPIJA	WIRSTATICIC	OCEDNECASS	NAASCARCLA	60
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	GEVSTULKEG	YVDKTVSPYI	PERKIPODEI	CODYNI DOND	DUCATURE	TOUTTOORY	240
	SKUPKLGPGS	DTPEGGFDAM	DIMINATING	CODINDUCAL	LUCITUADO	AT DOUT BOTH	300
50	VHRUKISGNI	NNVYVKSTIM	DUANVCESHI	GWKKEAKKLL	DVMIDQISHL	MUDSKINGIV	360
30	VPNDGNCHLK	NNVYVKSTIM	EKPSLGQLSE	KLIDHNINVI	PAVQGKQFHW	TRUBLEPLEPG	420
	TIAGEIESKA	ANLANLUVEA	YOKLISEVKV	QVENQVQGIY	FNITAICPDG	SRKPGMEGCR	
		NVTVTMKKCD					480
	CVDETFLDSK	CFQCDENKCH	FDEDQFSSES	CKSHKDQPVC	SGRGVCVCGK	CSCHKIKLGK	540
	VYGKYCEKDD	FSCPYHHGNL	CAGHGECEAG	RCQCFSGWBG	DRCQCPSAAA	OHCANSKGOA	600
55	CSGRGTCVCG	RCECTDPRSI	GRECEHCPTC	YTACKENWNC	MOCLHPHNILS	QAILDQCKTS	660
	CALMEQQHYV	DOTSECFSSP	SYLRIFFIIF	IVTFLIGLLK	VLIIRQVILQ	WNSNKIKSSS	720
	DYRVSASKKD	KLILOSVCTR	AVTYRREKPE	EIKMDISKLN	AHETFRONF		
	Seg ID NO:	646 DNA 8	equence				
60		id Accession		318.1			
	Coding sequ	uence: 12	574 -				
	1	11	21	31	41	51	
	1	1	1	1	1	1	
65	ATGGAATCCG	AGGATTTAAG	TGGCAGAGAA	TTGACAATTG	ATTCCATAAT	GAACAAAGTG	60
	1010101000	*******	m	ON COMPACING	ATCA LOTTA AC	CHTCAATAAA	120

WO 02/086443 PCT/US02/12476

	GATTACATGA	GCTGTTTTAG	AACTCCAGTT	GTAAAGAATG	ACTITICACC	TGCTTGTCAG	1440
	TTGTCAACAC	CTTATGGCCA	ACCTGCCTGT	TTCCAGCAGC	AACAGCATCA	AATACTTGCC	1500
	ACTCCACTTC	AAAATTTACA	GGTTTTAGCA	TCTTCTTCAG	CAAATGAATG	CATTTCGGTT	1560
_	AAAGGAAGAA	TTTATTCCAT	TTTAAAGCAG	ATAGGAAGTG	GAGGTTCANG	CANGGTATTT	1620
5	CAGGIGITAA	ATGAAAAGAA	ACAGATATAT	GCTATAAAAT	ATGTGAACTT	AGAAGAAGCA	1680
	GATAACCAAA	CTCTTGATAG	TTACCGGAAC	GAAATAGCTT	ATTTGAATAA	ACTACAACAA	1740
	CACAGTGATA	AGATCATCCG	ACTITATION	TATGAAATCA	CGGACCAGTA	CATCTACATG	1800
	GTAATGGAGT	GTGGAAATAT	TGATCTTAAT	AGTTGGCTTA	AAAAGAAAAA	ATCCATTGAT	1860
	CCATGGGAAC	GCAAGAGTTA	CTGGAAAAAT	ATGTTAGAGG	CAGTTCACAC	AATCCATCAA	1920
10	CATGGCATTG	TTCACAGTGA	TCTTAAACCA	GCTAACTTTC	TGATAGTTGA	TOGAATGCTA	1980
	AAGCTAATTG	ATTTTGGGAT	TGCAAACCAA	ATGCAACCAG	ATACAACAAG	TGTTGTTAAA	2040
	GATTCTCAGG	TTGGCACAGT	TAATTATATG	CCACCAGAAG	CAATCAAAGA	TATGTCTTCC	2100
	TCCAGAGAGA	ATGGGAAATC	TAAGTCAAAG	ATAAGCCCCA	AAAGTGATGT	TTGGTCCTTA	2160
	GGATGTATTT	TGTACTATAT	GACTTACGGG	AAAACACCAT	TTCAGCAGAT	AATTAATCAG	2220
15	ATTTCTAAAT	TACATGCCAT	AATTGATCCT	AATCATGAAA	TTGAATTTCC	CGATATTCCA	2280
	GAGAAAGATC	TTCAAGATGT	GTTAAAGTGT	TGTTTAAAAA	GGGACCCAAA	ACAGAGGATA	2340
	TCCATTCCTG	AGCTCCTGGC	TCATCCCTAT	GTTCAAATTC	AAACTCATCC	AGTTAACCAA	2400
	ATGGCCAAGG	GAACCACTGA	AGAAATGAAA	TATGTTCTGG	GCCAACTTGT	TGGTCTGAAT	2460
	TCTCCTAACT	CCATTTTGAA	AGCTGCTAAA	ACTITATATG	AACACTATAG	TOGTGGTGAA	2520
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Seq ID NO: 647 Protein sequence Protein Accession #: NP_003309.1

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				YSQAIEALPP			120
	AIGEPDDARD	YFOMARANCK	KFAFVHISFA	QFELSQGNVK	KSKQLLQKAV	ERGAVPLEML	180
30	EIALRNLULQ	KKOLLSEEEK	KNLSASTVLT	AQESFSGSLG	HLONRNINSCD	SRGQTTKARF	240
	LYGENMPPOD	AEIGYRNSLR	QTNKTKQSCP	FGRVPVNLLN	SPECTVKTDD	SVVPCFMKRQ	300
				QNSHFKEPLW			360
	ESSLLAKLEE	TKEYQEPEVP	ESNOKOWOSK	RKSECINONP	AASSNHWQIP	ELARKVNTEQ	420
				CKTPSSNTLD			480
35				SSSANECISV			540
	OVLNEKKOIY	AIKYVNLEEA	DNOTLDSYRN	EIAYLNKLQQ	HSDKIIRLYD	YEITDQYIYM	600
	VMECGNIDLN	SWLKKKKSID	PWERKSYWKN	MLEAVHTIHO	HGIVHSDLKP	ANFLIVDGML	660
	KLIDFGIANO	MOPDITISVVK	DSQVGTVNYM	PPEAIKDMSS	SRENGKSKSK	ISPKSDVWSL	720
	GCILYYMTYG	KTPFOOIINO	ISKLHALIDP	NHEIEPPDIP	EKDLODVLKC	CLKRDPKORI	780
40	SIPELLAHPY	VOIOTHPVNO	MAKGTTEEMK	YVLGOLVGLN	SPNSILKAAK	TLYEHYSGGE	840
	SHNSSSSKTF	EKKRGKK		-			

Seq ID NO: 648 DNA sequence Nucleic Acid Accession #: NM_015507 Coding sequence: 241..1902

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				GAGAGAGGAG			180
	GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
				CIGCIGCICI			300
				TTGTTAGCAT			360
55				TACGGCTGGA			420
				TTTGGTGAGT			480
				TGCAGTCAAG			540
				AATACACACG			600
				ACCTGTGTGA			660
60				GAAGAAGGC			720
				GACTGTCTAG			780
				TGTGTGAACA			840
				ATCAGTGGAC			900
	AATGAATGTA	CTATGGATAG	CCATACGTGC	AGOCACCATG	CCAATTGCTT	CAATACCCAA	960
65				TATAAAGGCA			1020
				AGAGCACCTG			1080
				AAAAAGAAGG			1140
				GTGAACTTGC			1200
=0				GGTAAAAAAG			1260
70				AAAGCCCTGA			1320
				GTGAATGAAG			1380
				CTGGAACATA			1440
	GACTGCAGCT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	atagagaaga	TGATTTTGAC	1500
7.0				GGCTTCTATA			1560
75				CTTCTCCTAC			1620
				GCCCGAGACA			1680
				TGGGAGAAGA			1740
	TOGAAGACAG	GGAAAATTCA	GTTGTATCAA	GGAACTGATG	CTACCAAAAG	CATCATTTTT	1800
80	GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
80	TCAGGCTTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
				TTGATATTGC			1980
				ACCAACAGAA			2040
				AAATATCATA			2100
85				ATATGGAAAT			2160
0.0				TGAGCTTCTC			2220
				TGTTTGACTC			2280
	TATGACATCA	AAGATAGACT	TTTGCCTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340

5 Seq ID No: 649 Protein sequence Protein Accession #: NP_056322

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10	LSGHMLMPDA	TOVNSRTCAN	INCOYSCEDT	EEGPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
	GSFKCKCKOG	YKGNGLRCSA	KCHIGFELQY	RAPGTIKORI	KKLLAHENSM	KKKAKIKNVT	300
15	SLRGDVFFPK	VNEAGEFGLI	IVSRGGNSHG LVQRKALTSK	LEHROLNISV	DCSFNHGICD	WKQDREDDFD	360 420
			WKTGKIOLYQ				480 540
	SGLCPDSLLS			100-0-1			

20 Seg ID NO: 650 DNA sequence Nucleic Acid Accession #: NM_003506.1 Coding sequence: 259..2379

		id Accession Jence: 259.	1 #: NM_003	506.1			
	obasing seq						
~ ~	1	11	21	31	41	51	
25	1	ì	1	ì	1	1	
	GCAGCTCCAG	TCCCGGACGC	AACCCCGGAG	CCGTCTCAGG	TCCCTGGGGG	GAACGGTGGG	60
	TTAGACGGGG	DDDAADCOA	ACAGCGGCCT	TCGACCGCCC	CCCGAGTAAT	TGACCCAGGA	120
			AAAATGAGTA				180 240
30	ATCTTTGGAT	GGGGATCTTC	TGAGGATGCA	ANGAGTGATT	CATCCAAGCC	ATGIGGTANA	
30			GGAGATGTTT				300
			CTTCACCTGT				360 420
	ATGGCCTACA	ACATGACGTT	TTTCCCTAAT	CIGATOGGIC	ATTATORCCA	GMGTATTGCC	480
	GCGGTGGAAA	TGGAGCATTT	TCTTCCTCTC	GCAAATCIGG	ANTOTTCACC	AMPLATIONA	540
35	ACTITICATOR	GCAAAGCATT	AGTATATTCT	TOCATAGAAC	MANTICATOT	GGTTCCACCT	600
20	TGTCGTAAAC	TTTGTGAGAA	TGAATGTGAC	GATTGCAAAA	ANTIANTIGA	CACTITIOGG	660
							720
	GTAACTTTTG	ATCCACACAC	AGAATTTCTT TCCAAGGCAT	GGTCCTCAGA	AGNAMACAGA	ACCOMMITTER	780
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40			TATTGGAACA				900
40	CTAGAGITIG	CAAAAAGTTT	AATTGATGTT	GITTCAATAT	TTTGTCTTTG	CLCARCICIG	960
	TTCACATTCC	TTACTTTTTT	CAGCATTGTA	AGAAGATTCA	GATACCCAGA	GAGACCAATI	1020
	ATATATTACT	CTGTCTGTTA	TAAGGCAGAT	TCTCTTWIGT	ACTICATIOG	ATTITIOCIG	1020
			TTGCACOGTT				1140
45			GATTCTTACC				1200
45	GCTGGCACTG	TGTGGTGGGT	GCAAAAAGCA	ATTACTIGGT	TOT THOUTOU	MUCOCOCO DOCA	1260
	TOGAGTTGTG	ANGCCATCGA	GCTTCTTGCT	CONTRACTOR	ALGCIGITION	OF POSSESSION	1320
	CCAGGTTTCC	TGACTGTTAT	TTATGACCTG	CLONGCOMO	COLPORAGE	ACTOTOTOCCA	1380
	GGAGITIGUI	emenoment of	TGGGCTCTCT	CONTCOMPTAC	CHCCCOTTAT	TTCCTTAAAT	1440
50	CIGIGCCIII	GIGIGITIGI	ACATGATGGC	CITCITIAG	ARARACTERA	CARACTTATC	1500
50	ATGITCOAC	ANGICATACA	CGGCTTGTAT	COGRACCIONO	TAGTORCACT	TCTCGGATGT	1560
	TACCTCTATG	BOCKBOTORA	CAGGATTACC	TOGGGGGGTAA	CTTGGGTCTC	TGATCATTGT	1620
			TCCTTATCAG				1680
	TTATTTATCA	TARABATACCT	GATGACATTA	ATTIGTTIGGCA	TOTOTOTOT	CTTCTGGGTT	1740
55	CONNCIDENT	AGACATGCAC	AGAATGGGCT	GGGTTTTTTA	AACGAAATCG	CAAGAGAGAT	1800
-	CCANTCAGTG	DAAGTCGAAG	AGTACTACAG	GAATCATGTG	AGTTTTTCTT	AAAGCACAAT	1860
	TOTALACTTA	22020202020	GAAGCACTAT	BARCCAAGTT	CACACAAGCT	GAAGGTCATT	1920
	TCCAAATCCA	TOGGRACCAG	CACAGGAGCT	ACAGCAAATC	ATGGCACTTC	TOCAGTAGCA	1980
	ATTACTACCC	ATGATTACCT	AGGACAAGAA	ACTTYGACAG	AAATCCAAAC	CTCACCAGAA	2040
60	ACATCARTGA	GAGAGGTGAA	AGCGGACGGA	GCTAGCACCC	CCAGGTTAAG	AGAACAGGAC	2100
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	TCAGAACCAA	GCAGCCTCAA	AGGTTCCACA	TCTCTGCTTG	TTCACCCAGT	TTCAGGAGTG	2340
65	AGAAAAGAGC	AGGGAGGTGG	TTGTCATTCA	GATACTTGAA	GAACATTTTC	TCTCGTTACT	2400
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	TCAAGAATAA	TATGACTCAT	TTCACACAAA	GGTTAATGAC	AACAATATAC	CTGAAAACAG	2580
	AAATGIGCAG	GTTAATAATA	TTTTTTTAAT	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
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	TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTAAA	TCTTATCCTT	2760
	GTATCITTTT	ATACATATTT	GAAAATAAGC	TTATATGTAT	TTGAACTTTT	TTGAAATCCT	2820
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	ATTTCTAAGA	AAATTGTAAA	ATAGTCTTCT	TTTATACTGT	AAAAAAAGAT	ATACCAAAAA	2940
75	GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACITATTG	ATACCTTACC	ATCTAAAATG	3000
	TGTGATTTTT	ATAGTCTCGT	TTTAGGAATT	TCACAGATCT	AAATTATGTA	ACTGAAATAA	3060
	GGTGCTTACT	CAAAGAGTGT	CCACTATTGA	TTGTATTATG	CTGCTCACTG	ATCCTTCTGC	3120
			TAAAGGGTTA				3180
00			CCTTTTTTAA				3240
80	AACCACTTAC	AGTTGCTTAT	ATTTTTTTTTT	TTAACTITTG	TITCITAACA	TTTAGAATAT	3300
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Seq ID NO: 651 Protein sequence Protein Accession #: NP_003497.1

WO 02/086443 MEMFTFLLTC IFLPLLRGHS LPTCEPITVP RCMKMAYNMT FFPMLMGHYD QSIAAVEMEH FLPLANLECS PRIETFLCKA PVPTCIEQIH VVPPCRKLCE KVYSDCKKLI DTPGIRHPEB LECCRLOYCO ETVPVTFDEH TEPLGPQRKT EQUORDIGFW CPRILATISG GOYKFLGIDO CAPPCPMYF KEDBLEFAKS FIGTVSIFCL CATLFTLTF LIDVRFRYP ERPIIYYSVC 240 YSIVSLMYFI GFLIGDSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FFTMAGTVWW 300 VILTITUDELA AGREGICATE EDICATORE DI STOTO DE LA CONTROL DE 260 LYDLDASRYF VLLPLCLCVF VGLSLLLAGI ISLMHVRQVI QHDGRNQEKL KKFMIRIGVF SGLYLVPLVT LLGCYVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMIKY 480 LMTLIVGISA VFWVGSKKTC TEWAGFFKRIF RKRDPISBSR RVLQESCEFF LKHRISKVKHK 540 10 EVELVEDGER I EUTEKSMOT STGATANEGT SAVAITSHDY LGOSTLITEIO TSPETSMREV 600 VARIABLE PROPERTIES DALCTONING HOUNGKOOLG SUSESADERS RISPKSDITTS 660 TGLAGSNYLO VPSSSEPSSL KGSTSLLVHP VSGVRKEOGG GCHSDT Seq ID NO: 652 DNA sequence 15 Nucleic Acid Accession #: NM_014791.1 Coding sequence: 171..2126 20 TTOGCOGOGO GRAGCOGCON CARCCOGGO ATCGARAGA TTCTTAGGAA CGCCGTACCA 60 GCCGCGTCTC TCAGGACAGC AGGCCCCTGT CCTTCTGTCG GGCGCCGCTC AGCCGTGCCC TCCGCCCCTC AGCTTCTTT TCTAATTCC AATAAACTTG CAAGAGGACA ATCAAAAAATTA TATGAATATA ATGAAACTTA TOGGACAGT GGCTTTGCCA 120 AGGTCAAACT TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300 25 ARACACACT AGGGAGTGAT TTGCCCCGGA TCAARACGGA GATTGAGGCC TTGAAGAAC TGAGACATCA GGCATATATGT CAACTCTACC ATGTGCTTAGA GACAGCCAAC ARAATATTCA TGGTTCTTGA GTACTGCCCT GGAGGAGGC TGTTTGACTA TATRATTTCC CAGGATGGC 360 420 480 TOTCAGAAGA GGAGACCOGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540 ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC 30 660 ATAAATTAAA GCTGATTGAC TTTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAAT 720 CATATCTTGG ATCAGAGGCA GATGTTTGGA GCATGGGCAT ACTGTTATAT GTTCTTATGT 780 GTGGATTTCT ACCATTTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG GAAAATATGA TOTTCCCAAG TOGCTCTCTC CCAGTAGCAT TCTGCTTCTT CAACAAATGC 900 35 TGCRGGTGGA CCCAAAGAAA CGGATTTCTA TGAAAAATCT ATTGAACCAT CCCTGGATCA 0.60 TOCAMGATTA CAACTATCCT OTTGAGTGGC ANAGGAAGGA TCCTTTTATT CACCTGGATG ATGATTGGGT AGAGAACTA TCGTTACATTC AGAGAACGA TCGAGGAAGCA TAGAGAGGATT TAATTTCACT GTGGCAGTAT GATCACCTTA COGGTACCTA TCTTCTGCTT CTAGCCAGTA 1020 1080 AGGCTCGGGG AAAACCAGTT CGTTTAAGGC TITCTTCTTT CTCCTGTGGA CAAGCCAGTG 1200 40 CTACCCCATT CACAGACATC AAGTCAAATA ATTGGAGTCT GGAAGATGTG ACCGCAAGTG 1260 ATRARANTA NYNGGOGGA TRANTAGACT ATGATTGGTG TGARGATGAT TTATCHACAG GYGCTGCTAC CCCCCGARCA TCACAGITTA CCAMATACTG GACAGAATTA ARTGGGGTG AATCTAARTA ATRACTCCA GCCTTATGCA GACAGCTGC AARTAAATTA ARGAACRAAG 1320 1380 1440 AAAATGTATA TACTCCTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCCTGAGC 1500 45 CARAGACTCC AGTTACTAG AACCAGCATA AGAGAGAAAT ACTCACTACG CCARATCGTT 1560 ACACTACACC CTCAAAAGCT AGAAACCAGT GCCTGAAAGA AACTCCAATT AAAATACCAG 1620 1680 TARATTCARC AGGRACAGAC ARGTTARTGA CAGGTGTCAT TAGCCCTGAG AGGCGGTGCC GCTCAGTGGA ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG CCAAAGTGTT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1740 50 GCAAAAGGAA GGGTTCTGCC AGAGACGGC CCAGAAGACT AAAGCTTCAC TATAATGTGA 1860 CTACAACTAG ATTAGTGAAT COAGATCAAC TGTTGAATGA AATAATGTCT AFTCTTCCAA AGAAGCATGT TGACATTGTGA CAAAAGGGTT ATACACTGAA GTGTCAAACA CAGTCGGAT TTGGGAAAGT GACATGGAA TTTGAATTAG AAGTGTGCCA GGTTCAAAAA CCCGATGTGG 1920 1980 TGGGTATCAG GAGGCAGCGG CTTAAGGGGG ATGCCTGGGT TTACAAAAGA TTAGTGGAAG 2100 55 ACATCCTATC TAGCTGCAAG GTATAATTGA TOGATTCTTC CATCCTGCCG GATGAGTGTG 21.60 GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGGAA 2220 CTACCACTT GTTCTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAAACAAAA GATATTATTT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTTTT 2280 2340 TAATCATGTG GTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 60 AATGTAAGCT CTTAACTATG TCTCTTTGTA ATGTGTAATT TCTTTCTGAA ATAAAACCAT 2460 TTOTOTOTATAT Seg ID NO: 653 Protein sequence Protein Accession #: NP 055606.1 65 31 MEDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDENTIGSD LPRIKTEIBA LKNLRHQHIC QLYHVLETAN KIPMVLEYCP GGELFDYIIS QDRLGEEETR VVFRQIVSAV 70 AYVHSQGYAH RDLKPENLLF DEYHKLKLID PGLCAKPKGN KDYHLQTCCG SLAYAAPELI 280 OGKSYLGSEA DVWSMGILLY VLMCGFLPFD DDNVMALYKK IMRGKYDVPK WLSPSSILLL 240 OOMLOVDPKK RISMKNLLEH PWIMODYNYP VEWOSKNPFI HLDDDCVTRL SVHHRNNROT 300 MEDLISLMOY DELTATYLLL LAKKARGKPV RLRLSSFSCG OASATPPIDI KSNNWSLEDV 360 TASDKNYVAG LIDYDWCEDD LSTGAATPRT SOFTKYWTES NGVESKSLTP ALCRTPANKL 75 KNKENVYTPK SAVKNEBYFM PPEPKTPVNK NOHKREILTT PNRYTTPSKA RNQCLKETPI 480 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540 LTRSKRKGSA RDGPRRLELH YNVTTTRLVW PDQLLNEIMS ILPKKHVDFV OKGYTLKCOT QSDFGKYTMQ FELEVCQLQK PDVVGIRRQR LKGDAWVYKR LVEDILSSCK V 80 Seg ID NO: 654 DNA sequence Nucleic Acid Accession #: NM 000582 Coding sequence: 88..990 85 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA AACGCGGACC AAGGAAAACT CACTACCATG AGAATTGCAG TGATTTGCTT TTGCCTCCTA 120

	WO 02	/086443					
	GGCATCACCT	GTGCCATACC	AGTTAAACAG	GCTGATTCTG	GAAGTTCTGA	GGAAAAGCAG	180
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	CAGAATCTCC	TAGCCCCACA	GACCCTTCCA	AGTAAGTCCA	ACGAAAGCCA	TGACCACATG	300 360
5	BACGACTCTG	ATGATGTAGA	TGACACTGAT	GATTCTCACC	AGTCTGATGA	CATTGACTCG GTCTCACCAT	420
-	TCTGATGAAT	CTGATGAACT	GGTCACTGAT	TTTCCCACGG	ACCTGCCAGC	AACCGAAGTT	480
	TTCACTCCAG	TTGTCCCCAC	AGTAGACACA	TATGATGGCC	GAGGTGATAG	TGTGGTTTAT	540 600
	GGACTGAGGT	CAAAATCTAA	CATGGAAAGC	GAGGAGTTGA	ATGGTGCATA	CAAGGCCATC	660
10	CCCGTTGCCC	AGGACCTGAA	CGCGCCTTCT	GATTGGGACA	GCCGTGGGAA	CAAGGCCATC GGACAGTTAT	720
							780 840
		AAGCCAATGA					900
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15	TTAGATAGTG	CATCTTCTGA	GGTCAATTAA	AAAGGAGAAAA	AATACAATTT	CTCACTTTGC	1020
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	ATTAGTTTAG	TTTGTGGCTT	CATGGAAACT	CCCTGTAAAC	TAAAAGCTTC	ATGCTTCTT GTGTTTGATA AGGGTTATGT TGTTATTCTC AAAAGAGAAT	1200
••	CTATGTTCAT	TCTATAGAAG	AAATGCAAAC	TATCACTGTA	TTTTAATATT	TGTTATTCTC	1260
20	TCATGAATAG	AAATTTATGT	AGAAGCAAAC	AAAATACTTT	TACCCACITA	AAAAGAGAAT	1320
	ATAACATTIT	TGGTGTGAAT	AATCTTTTTT	TOTTOMATOT	AGIGIATATI	TGGTGGTGTC	1440
	AATTGCTTAT	TTGTTTTCCC	ACGGTTGTCC	AGCAATTAAT	AAAACATAAC	CTTTTTTACT	1500
25	GCCTAAAAAA	алалалала	AAAA				
25	Seq ID NO:	655 Protei	n semience				
	Protein Ac	ession #: N					
30	1	11	21	31	41	51	
20	MRIAVICECL	LGITCAIPVK	OADSGSSEEK	QLYNKYPDAV	ATWLNPDPSQ	KONLLAPOTL	60
	nevenpeunu	MUDMUDERUD	DUVDSODETD	SMINSONVIDE	DDSHOSDESH	HSDESDELVT	120
	DFPTDLPATE	VFTPVVPTVD	TYDGRGDSVV	YGLRSKSKKF	RRPDIQYPDA	TDEDITSHME LYKRKANDES	180 240
35	NEHSDVIDSO	ELSKVSREFH	SHEFHSHEDM	LVVDPKSKEE	DKHLKFRISH	ELDSASSEVN	
	Seq ID NO:	656 DNA se Ld Accession	equence	108.1			
	MUCTOTO NO.	ra vocessror	1 4. 111-003	10011			
			1401				
40	Coding sequ	ience: 76	1401				
40				21	41	51	
40	1	11	21	31	41	51 	
	1 agggTGGGAG	11	21 -	GAGACCCAGC	GGCCCGGGTT	GGAGCGTCCA	60
40 45	1 GGGGTGGGAG GCCCTGCAAC	11 GOOGAGGGGG GGATCATGGT	21 ACCTCCGCAC GCAGCAGGCG	GAGACCCAGC GAGAGCTTGG	GGCCCGGGTT AAGCGGAGAG	GAGOGTOCA CAACCTGCCC	120
	1 - - - - - - - - - - - - -	11 GGGGAGGGG GGATCATGGT TGGACACGGA	21 ACCTCCGCAC GCAGCAGGCG GGAGGGCGAA	GAGACCCAGC GAGAGCTTGG TTCATGGCTT	GGCCCGGGTT AAGCGGAGAG GCAGCCCGGT	GGAGOGTOCA CAACCTGCCC GGCCCTGGAC	60 120 180 240
	1 - - - - - - - - - - - - -	11 GGGGAGGGG GGATCATGGT TGGACACGGA	21 ACCTCCGCAC GCAGCAGGCG GGAGGGCGAA	GAGACCCAGC GAGAGCTTGG TTCATGGCTT	GGCCCGGGTT AAGCGGAGAG GCAGCCCGGT	GGAGOGTOCA CAACCTGCCC GGCCCTGGAC	120 180 240 300
45	1 	11 GGGGAGGGG GGATCATGGT TGGACAGGGA CAGACTGGTE GGTCCAAGAT TCTCCAAGAG	21 j ACCTCCGCAC GCAGCAGGCG GGAGGGCGAA CAAGACGGCG CGAACGCAGG GCTGGGCAAG	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TCGGGCCACA AAGATCATGG CGCTGGAAAA	GGCCCOGGTT AAGCGGAGAG GCAGCCCGGT TCAAGCGGCC AGCAGTCTCC TGCTGAAGGA	OGAGOGTOCA CAACCTGCCC GGCCCTGGAC GATGAACGCG GATGAACGCG CAGCGAGAAG	120 180 240 300 360
	1 	11 	21 ACCTCCGCAC GCAGGAGGGGAA CAAGACGGCG CGAACGCAGG GCTGGGCAAG GGAGCGGCTAAA	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TCGGGCCACA AAGATCATGG CGCTGGAAAA CGGCTCAAGC	GGCCCGGGTT AAGCGGAGAG GCAGCCCGGT TCAAGCGGCC AGCAGTCTCC TGCTGAAGGA ACATGGCCGA	GAGGGTCCA CAACCTGCCC GGCCCTGGAC GATGAACGCG GACATGCAC CAGCGAGAAG CTACCCCGAC CAGCGCCAGC	120 180 240 300 360 420 480
45	1 GGGGTGGAG GCCTGCAAC CGGGAGGGCG TTCATGGTAT AACGCCGAGA ATCCCGTTCA TACAAGTACC	11 GGGGAGGGG GGATCATGGT TGGACACGGA CAGACTGGTG GGTCCAAGAG TCCGGGAGGC GGCCCGGGA AGAACACGGAA	21 ACCTCCGGAC GCAGGAGGCG GGAGGGCGAA CRAGACGCGA GCTGGGCAAG GCAGCGGCAAG GGAGCGGCTG AAAGCCCAAA	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TCGGGGCACA AAGATCATGG CGCTGGAAAA CGGCTCAAGC ATGGACCCCT AGGGGGGGGA	GGCCCGGTT AAGCGGAGAG GCAGCCGGT TCAAGCGGCC AGCAGTCTCC TGCTGAAGGA ACATGGCCGA CGGCCGAGCC GCGCGGGGGGG	GGAGOGTCCA CAACCTGCCC GGCCCTGGAC GGCCCTGGAC GATGAACCCG CACCTGCAC CAGCGAGAAG CTACCCGAC CAGCGGCCAGC AGGCGCGGC	120 180 240 300 360 420 480 540
45	1 	11 GGGGAGGGG GGATCATGGT TGGA.CACGGA CAGACTGGTG GGTCCAAGAT TCTCCAAGAT TCTCGAGAGG GGCCCGGAA AGAAGAGGG CTTCCAACAG	21 ACCTCCGCAC GCAGCAGGCG GGAGGGCGAA CAAGACGCAG GCTGGGCAAG GGAGCGCCTG AAAGCCCAAA GGCGGCGCGC CTCCCAGCAGA	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TCGGGCACA AAGATCATGG CGCTGGAAAA CGGCTCAAGC ATGGACCCCT ATGGACCCCGTA AAATGCGGCA	GGCCCGGTT AAGCGGAGAG GCAGCCCGGT TCAAGCGGCC AGCAGTCTCC TGCTGAAGGA ACATGGCCGA ACATGGCCGA GCGCGGGCGG AGCTCAAGGC	GAAGOGTCCA CAACCTGCCC GGCCTGGAC GATGAACGCG GATGAACGCG CAGCGAGAAG CTACCCGAC CAGCGGCAGC CAGCGGCGCGCC CCCCGCGGCCCCCCCC	120 180 240 300 360 420 480 540 600
45	1 GGGGTGGAG GCCTGCAAC CGGGAGGCGC AGAGCGACC ATCCGTTCA TACAAGTAC TACAAGTACC CAGAGCCAG GGTGCCAAG GGGGGGGCA	11 	21) ACCTCCGCAC GCAGCAGGCG GGAGGGCGAA CRACACGAGG GCTGGGCAAG GGACGGCTAA GGCCGAGCAG CTCCAGCAAG GGGCAAGGCC	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TCGGGCCACA AAGATCATGG CGCTGGAAAA CGGCTCAAGC ATGGACCCCT GGCGGCGGGA AAATGCGGCA GCCCAGTCCC	GGCCCGGTT AAGCGAGAG GCAGCCCGGT TCAAGCGGCC AGCAGTCTCC TGCTGAAGGA ACATGGCCGA CGGCGGGGCG AGCTCAAGGC GCGCGGGCGG	GAAGOGTCCA CAACCTGCCC GGCCCTGGAC GATGAACGCG GATGAACGCG CAGCGAAG CTACCCGAAC CAGCGCCAGC AGGGCCGGGC CCCCGCGGCC	120 180 240 300 360 420 480 540
45	1 GGGGTGGGAG GCCTTGCAAC GGGAGGGGC GAGAGCGACC TTCATGGTAT AACGCCGAGA ATCCGGTCCA TACAAGTACC CAGAGCCCAG GGTGCCAAGA GGGGCGCCA GAGACTACG ACGATAAGT	11 GGGAAGGGG GGATCATGGT TGGACACGGGA CAGACTGGTG GGTCCAAGAG TCCGAGAGA GGCCCGGAA AGAAGAGGG CCTCCAAGAG AGGGGGGCGC TGCTGGGCAG GGGTGTTTCT	21) ACCTCCGCAC GCAGCAGGCG GGAGGGGGAA CAAGACGCAG GCTGGGCAG GGAGGGGCTG AAAGCCCAAA GGCCGCGGC CTCCAGCAAG GGCAAGGCC CTCCAGCAAG GGCAAGGCC CCTGCGCGTG GGATGAGGAAG	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TCGGGCCACA AAGATCATGG CGCTGAAAA CGGCTCAAGC ATGAACCCGT GGCGCGCGGAAAA AAGATGCGGCA AAATGCGGCA AAATGCGGCA AAATGCGGCA GCCCAGTCGC	GGCCCOGTT AAGCGGAGAG GCAGCCCGGT TCAAGCGGCC AGCAGTCTCC TGCTGAAGGA ACATGGCCGA CGCCCAACC GGCCCAACC GGGCGGGGG AGCTCAAGGC GGGCTGAGGC ACGACGACGA ACGACGACGA	GAGGGTCCA CAACCTGCC GGCCCTGGAC GATGAACCCG GATGAACCCG CAGGGAGAA CTACCCGAC CAGGGAGAA CTACCCGAC CAGGGCCAGC CCCGCGGCC GGCGGGGCC GGCGGGGCC GGCGGGGCCAGC CCCGCGGGCC GGCGGGGCCAGC CCCGCGGGCC GGCGGGCCAGC CCCGCGGGCC GGCGGGCCAGC	120 180 240 300 360 420 480 540 600 660 720 780
45	1 GGGTTGGAG GCCTGCAAC CGGGAGGGACC TTCATGGTAT AACGCCGAGA ATCCCGTTCA TACAAGTACC CAGAGCCCAG GGGGCCCAG GCGGCCCAGA ACGACTACG AACGACTACG AACGACTACG AACGACTACG	11 GGGGAGGGG GGATCATGGT TGGACACGGA CAGACTGGTG GGTCCAAGAT TCCCAAGAT TCCCGGAGG CGCCCGGAA AGAAGAGGG CCTCCAAGGG AGGCGGCG TGCTGGGCAG GGTGTTTCT TCAAACAGA	21 j ACCTCOGCAC GCAGCAGGGG GGAGGGCGAA CAAGACOGCGG GCTGGGCAAG GGAGCGCAG GGCCGAGCGGC CTCCAGCAAG GGGCAAGCCC CCTGGCGGTG GGATGAGGAG GGCCGAGCAGG GGCCGAGCAGG GGCCGAGCAGG GGCCGAGCAGG GGCCGAGCAGG GGCCGAGCAGG GGCCGAGCAGC GGCCGAGCAGAGCA	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TCGGGCCACA AGATCACACA AGATCACACA CGGCTCAAGC GGCGGCGGGA AAATGCGGCC GGCGGCCGGA GCCCAGCCC AGCGGCTCAG GAGAACACACG GAGAACGACG GAGAACGACG	GGCCCGGTT AAGCGGAGAG GCAGCCCGGT TCAAGCGGCC AGCAGTCTCC TGCTGAAGGA ACATGGCGGA AGCTCAAGGC GGGCGGGGG GGGACTACGG GGGACTACGG GGGCGGCGG ACGACGACGA ACCACGCCA	GAGCOTCCA CHACCTGCC GGCCTGGAC GATGRACGCG GATGRACGCG CAACTGCAC CAGCGAGAAG CTACCCGAC AGGCCAGC AGGCCAGC AGGCCAGC AGGCCAGC AGGCCAGC AGGCCAGC AGGCCAGC AGGCAGCAGC AGCAGAGTC CAACAGCTC CAACAGCTC	120 180 240 300 360 420 480 540 600 660 720 780 840
45	1 GGGGTGGRAG GCCCTGCARC GGGRAGGCGC GACAGCGAC TTCATGGTAT AACGCCGAGA ATCCGGTCCA GATGCCAGA GCGGCCAGA GCGGCCCAGA GCGGCCCAGA GCGGCCCAGA GCGGCCCAGA TCGGCCCAGA TCGGCCCAGA TCGGCCAGA	11 	21 ACCTCCGCAC QCACCAGGCG GGAGGGCGAA CAAAGCGAG GCACCCAAA GGCGCCAAA GGCGCGGC CTCCAGCAG CTCCAGCAG CTCCAGCAG GGCAAGCC CTCCAGCAG GGCAAGCC CTCCAGCAG GGCAAGCC GGCAAGCC GGCAACCCAG GCCCACCAG > GCCCACCAG GCCCACCAG GCCCACCACCAG GCCCACCACCAG GCCCACCACCAC GCCCACCACCACCAC GCCCACCACCACCAC GCCCACCACCACCAC GCCCACCACCACCACCAC GCCCACCACCACCACCAC GCCCACCACCACCACCAC GCCCACCACCACCACCACCAC GCCCACCACCACCACCACCACCAC GCCCACCACCACCACCACCACCACCACCACCACCACCACC	GAGACCCAGC GAGAGCTTGG TTCATGGCTCA AAGATCATGG COCTGGAAAA AAGATCATGG COCTGGAAAA AATGCACCCT GGCGCCGGAACGACG GCCCAGTCCG GACGACGAACG GACGACGACG GACGACGAACG GACGACGAACG GACGACGAACG GACGACGACGACG GACGACGACGACG GACGACGACGACG GACGACGACGACG GACGACGACGACG GACGACGACGACGACGACG GACGACGACGACGACGACCACC GACGACGACGACGACCACCACCACCACCACCACCACCACC	GGCCCGGTT AAGCGGACAG GCAGCCCGGT TCAAGCGGCC AGCAGTCTCC TGCTGAAGGA ACATGGCGA CGCCGAGGCG GGCACTAAGGC GGGCGGCGG ACGACGACGA ACACCACCACA ACCACCACA ACCACCACACA GCTACAACGC GCTACAACGC	GGAGGGTCCA CARCCTGGCC GGCCCTGGAC GGCCGTGGAC GACATGCAC CAGGGGCGGAC CAGGGCGAGC AGGGGCGGGC GGCGAGGAGAAG CGCGGGCC GGCGGGCC CGCGGGCC CGCGGGCC CGCGGGCC CGCGGGCCAGC CGCGGGCCAGC CGCGGGCCAGC CGCGGGCCAGC CGCGGGCCAGC CGCGGGCCAGC CGCGGGCCAGC CGCGGGCCAGC CGCGGGCCAGC CGCGGGCCAGC CGCCAAAGTG	120 180 240 300 360 420 480 540 600 720 780 840 900
45	1 GGGGTGGAG GCCTGCAAC GGGAGGGAC GAGAGGACC TCATAGTAT AACGCCGAGA ATCCGGTTCA ATCCGGTCA GGGACCCAG GGTGCCAAGA GCGACCAGA ACGCTAAGA CCGACCAAGA CCGACCAAGA CCGACCAAGA CCGCAGCA CCGCAGCA CCGCAGCA CCGCAGCA CCGCAGCA CCGCCAGCA CCGCCAGCA CCGCCAGCA CCGCCAGCA CCGCCAGCA CCGCCAGCA CCGCCAGCA CCAGCCCAGCA CCACCAC CCACCAC CCACCAC CCACCAC CCACCA	11 GGGGAGGGG GGRTCATGGT TGGACAGGGA GAGACTGGTG GGTCCRAGAT TCTCCRAGAG TCCCAGGA GGCCCGGAA AGAAGAGGG CCTCCRAGGG AGGGGGGGC TGCTGGGGC TGCTGGGGC TGCTGGGGC TCCAACAGGG CGGGGGGC CGGGGGAGCA CTACGCTGAG CGGGGGGAGCA	21 ACCTCCGCAC GCACCAGGCG GGAGGGGGAA CAAAACGCGG GCTGGGCAAG GGACCGCGCGC CTCCAGCAAG GGCCAACGC CTCCAGCAG CCCGCGCGCG CCTGCGCGCG CCTGCGCGCG CCTGCGCACAG GCCCTCGCACAAG CCCTCGCACAAG CCCTCGCACAAG CCCTTCGCACACAG CCCTTCGCACACAG CCCTTCGCACACAG CCCTTCGCACACAG CCCTTCGCACACAG CCCTTCGCACACAG CCCTTCGCACACAG CCCTTCGCACACACACC CAGCTTCGCACACACC CAGCTTCGCACACACACCTTCCGCACACACACCTTCCGCACACACA	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TCOGGGCCACA AAGATCATGG COCTGGAAAA ATGACCCT GGCGCAGGA AAATGCGGCA AAATGCGGCA GAGACCGGA AAATGCGGCA GACCAGTCCG GACGACGAGA GAGACGAGA GAGACGAGA GAGACGAGA GAGACGAGAGACGAGAGACGAGAGACGAGAGACGAGAGACGAGAGACGAGAGACGAGAGACGAGGAG	GGCCCOGGTT AAGCGGACAG GCAGCCCGGT TCAAGCGGACAG GCAGCCCGGT TCAAGCGCACAGCCCGGCACCACCCCACC	GGAGGGTCCA CAACCTGCC GGCCCTGGAC GATGAACGCG GCACATGCAC CAGGGGCGGGC CTACCCGGAC CAGGGGGGGGGC CCCGCGGGCC GGCGGGGCAC GGCGGGGCAC GGCGGGGCAC GCGGGGGGGCAC GCGAGGCAGGC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020
45 50 55	1 GSGGTGGGAG GCCTTGCAAC GSGGAGGGGC GAGAGCGACC TTCATGGTAT AACGCCGAGA ATCCCGTACA TACAAGTACC CAGAGCCACA GAGGACTACG AACGACTACG AACGACTACG AACGACTACG CAGACCCAGC CAGACCACC CAGACCACC CAGACCACC CAGACCAGC CAGACCACCAGC CAGACCACCAGC CAGACCACCAGC CAGACCACCAGC CAGACCACCACCAC CAGACCACACCAC CAGACCACCAC CAGACCACCAC CAGACCACCAC CAGACCACACCAC CAGACCACCAC CAGACCACCAC CAGACCACCAC CAGACCACCACCAC CAGACCACCAC CAGACCACCAC CAGACCACCAC CACACCACCACCAC CACACCACCACCAC CACACACCAC	11 GOGARGAGA GOGARGAGA GOGARGAGA CAGARGA CAGARGA CAGARGA CAGARGA GOCCOGGA AGAGAGA GOCCOGGA AGAGAGA GOCCOGGA AGAGAGA COCCOGGA AGAGAGA COCCOGGA AGAGAGA COCCOG	21 ACCTCCGCAC @CAGCAGGCG @GAGGGGGSAA CAAACGGCG GGAGGGGCGA AGGCCCAAA GGCGGAAGGCC CTCCAGCAAG GGCGAAGGCC CTCCAGCAAG GGCGAAGGCC GCCGAACGAC GCCGAACGAC GCCGACCAC GCCGACCAC GCCGACCAC GCCGACCAC GCCGACCAC GCCGACCAC GCCGACCAC CAGCTCGGCGCC CTCGGGGCGCC	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TTCATGGCTT TTCGGGCCACA AGATCATGG GCCTCAAGC ATGACCCCT GGGGGCGGGA AAATGCGGCA AGGGGCTCAAGC AGCGGCTCAG GACGACGAC GACGACGACG GACGACGACG GAGGCCGGGACGACGACGACG GAGGCCGGGACGACGACGACGACG GAGGCCGGC	GGCCCOGATT AAGCGGAGA GCAGCCCGGT TCAAGGGACGGGCA AGCAGTCTCC GGCGCCAAGCA ACATGGCCGA ACGTCAAGGA ACGTCAAGGA ACGTCAAGGA ACGTCAAGGA ACGCGACGA AACCACCGCA GCTACAAGGA AACCACCGCA GCTACAAGGA AACCACCGCA AACCACCGCA AACCACCGCA AACCACCG	GGAGGGTCCA GGACCTIGCC GGCCCTIGAC GAACCTIGCC GGCCCTIGAC GATGAACGCG GGATGAACGCG GAACATGCAC CAGGGAGAAA CTACCCGGAC CAGGGAGAAGAG CCCCGGGGCC CCCGGGGGC CCCGGGGGC CCCGGGGGC CCCGAAGTGC CCCAAGTTC CCAAGCTTC CCAAGGCTAC CTACAGGCT	120 180 240 300 360 420 540 600 660 720 840 900 960 1020 1080
45 50 55	1 GSGGTGGGAG GCCTTGCAAC GSGGAGGGGC GAGAGCGACC TTCATGGTAT AACGCCGAGA ATCCCGTACA TACAAGTACC CAGAGCCACA GAGGACTACG AACGACTACG AACGACTACG AACGACTACG CAGACCCAGC CAGACCACC CAGACCACC CAGACCACC CAGACCAGC CAGACCACCAGC CAGACCACCAGC CAGACCACCAGC CAGACCACCAGC CAGACCACCACCAC CAGACCACACCAC CAGACCACCAC CAGACCACCAC CAGACCACCAC CAGACCACACCAC CAGACCACCAC CAGACCACCAC CAGACCACCAC CAGACCACCACCAC CAGACCACCAC CAGACCACCAC CAGACCACCAC CACACCACCACCAC CACACCACCACCAC CACACACCAC	11 GOGARGAGA GOGARGAGA GOGARGAGA CAGARGA CAGARGA CAGARGA CAGARGA GOCCOGGA AGAGAGA GOCCOGGA AGAGAGA GOCCOGGA AGAGAGA COCCOGGA AGAGAGA COCCOGGA AGAGAGA COCCOG	21 ACCTCCGCAC @CAGCAGGCG @GAGGGGGSAA CAAACGGCG GGAGGGGCGA AGGCCCAAA GGCGGAAGGCC CTCCAGCAAG GGCGAAGGCC CTCCAGCAAG GGCGAAGGCC GCCGAACGAC GCCGAACGAC GCCGACCAC GCCGACCAC GCCGACCAC GCCGACCAC GCCGACCAC GCCGACCAC GCCGACCAC CAGCTCGGCGCC CTCGGGGCGCC	GAGACCCAGC GAGAGCTTGG TTCATGGCTT TTCATGGCTT TTCGGGCCACA AGATCATGG GCCTCAAGC ATGACCCCT GGGGGCGGGA AAATGCGGCA AGGGGCTCAAGC AGCGGCTCAG GACGACGAC GACGACGACG GACGACGACG GAGGCCGGGACGACGACGACG GAGGCCGGGACGACGACGACGACG GAGGCCGGC	GGCCCOGATT AAGCGGAGA GCAGCCCGGT TCAAGGGACGGGCA AGCAGTCTCC GGCGCCAAGCA ACATGGCCGA ACGTCAAGGA ACGTCAAGGA ACGTCAAGGA ACGTCAAGGA ACGCGACGA AACCACCGCA GCTACAAGGA AACCACCGCA GCTACAAGGA AACCACCGCA AACCACCGCA AACCACCGCA AACCACCG	GGAGGGTCCA GGACCTIGCC GGCCCTIGAC GAACCTIGCC GGCCCTIGAC GATGAACGCG GGATGAACGCG GAACATGCAC CAGGGAGAAA CTACCCGGAC CAGGGAGAAGAG CCCCGGGGCC CCCGGGGGC CCCGGGGGC CCCGGGGGC CCCGAAGTGC CCCAAGTTC CCAAGCTTC CCAAGGCTAC CTACAGGCT	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020
45 50 55 60	1 GGGGTGGAAC GGCCTGCAAC GGGAAGGGCC GGAAGGGAC TTCATGGTAT AA GGCCGAAC ATCCCGTTCA TACAAGTAC GGGCGCCCCC GAGACCCAA GAGACCCAA GAGACCAAC GAGACCCAAC GAGACCCAAC GAGACCCAAC GAGACCCAAC GAGACCCAAC GAGACCCAAC GAGACCAAC GAGACCAAC GAGACCAAC GAGACCAAC TTCAAGCAAC GAGACCAAC GAGACCAAC GAGACCAAC GAGACCAAC TTCAACCAAC GAGACCAAC GACACAACAAC GACACAACAAC GACACAAC GACACAAC GACACAAC GACACAAC GACACAAC GACACAACAAC GACACAACAAC GACACAACAAC GACACAACAAC GACACAACAAC GACACAACAAC GACACAACAACAAC GACACAACAACAACAAC GACACAACAACAACAAC GACACAACAACAACAACAACAACAACAACAACAACAACAA	11 GOODAGGGGC GARTCATGGT TGGA CAGGA GAGTCATGGT TGGA CAGGA GAGTCAGA TCTCCCAAGAT TCCCCAAGAT TCCCCAAGAT TCCCCAAGAT TCCCCAAGAT TCCCCAAGAT TCCCCAAGAT TCCCCAAGAT TCCCAAGAT TCCCAAGAT TCCCAACAT TCCCACCCC TCCCGGACAACAT TCCAACACAC TCCCGGACCACA CCAACACT TCCAACACC TCCCCCCCAACAC TCCCCCCCC	21 ACCTOSCAC GAAGAGGCC GAAGAGGCC GAAGAGGCC GAAGAGCCC GAAGCCAG GCTOGGCAAA GCCCGACCAAA GCCCGACCAAA GCCCGACCAC GCCCAACACACC CCTGCACCAC GCCCCCCCCCC	GAGACCCAGC GAGACCCAGC GAGACCCAGC GAGACCACA AGAATCATGG CTTCAGGCCTCAAGC GCCTCAAGC GCCTCAAGC GCCCAGTCCG GCGGGGGGGGAAA AGGGGCTCGGGGGGCGCA GCCCAGTCCG GAGAACACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGACGACG GAGCACGACG GAGCACCGCAC GCGCCAGC GCGCCACC GCGCCAGC GCGCCAGC GCGCCAGC GCGCCAGC GCGCCAGC GCGCCAGC GCGCCACC GCCCCACC GCCCCACC GCCCCACC GCCCCCCCC	GGCCOGGTT AACCGAAGA GCAGCCCGGT TCAAGCGGAA ACATGCCGA ACCATGCCGA ACCATGCCGA ACCATGCCGA AGCTAAGGC GGGCGGGCG GGGCGGCGA ACGACGACGA ACCACCGA ACCACCGA ACGACGACGA GCTACAACGT AGCGACGACGA GCTACAACGT CCCGCTCTTA CCCGCTCTTC CCACGCACGA	GRACOTECA CAACTIGUC GGCCTIGAA GATGAACGO GGATGAACGO GGACATGCAC CAG GGAGAA CTACCCGAC CAGCGAGAAA CTACCCGAC CCCGGGGGC GGCGGGGC GGCGGGGC GCCGGGGCAAGTG CCCGGGGCAAGTG CCCGGGGCCAAGTG CCCGGGGCCAAGTG CCCCGGGGCCAAGTG CCCCGGGGCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCAAGTG CCCCCAAGTG CCCCAAGTG CCCCCAAGTG CCCCCAAGTG CCCCCCCCCC	120 180 240 300 360 420 680 660 720 780 840 900 960 1020 1080 1140 1200
45 50 55	1 GGGGTTGGRAG GGCCTTGCAAC GGGAAGGGGC GGAAGGGAC TTCATGGTAT AA GGCCGAAG AT GCGGTTCA TACAAGTTCCA AA GGCGCAAG GGGACGCAC GAAGCGCAC GAAGCCGCA ACGGTCAAAT CACCGCCAAC GAAGCGCCAC GAAGTGCAAA TCCAAGCGCAC GAAGCGCAC GAAGCGCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAACACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAAGCACCAC GAACACCAC GAAGCACCAC GAAGCACCAC GAACACCACAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCACAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCACAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCACAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCACAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACCAC GAACACACAC	11 GOOGAGGGGC GGATCATGGT TGGA.CAGGA GGATCATGGT TGGA.CAGGA CAGACTGGTG GGTCCAAGAT TCCCCAAGAA TCCCCAAGAA TCCCCAAGAA AGAAGGGCC CCTCCCAAGAG GGGCCCCGGAA AGACTGGC CATCAAGAC CAGCCCCCAAGAA TCCCACCCC CAAGCAGCA TCCCAACCAGC TCCCAACCAGC TCTCCAACCAGC TCTCCAACCAGC TCTCCAACCACCA TCTCCAACCACCA TCTCCAACCACCA TCTCCAACCACCA TCTCCACCCCC TCTCAACCACCACCA TCTCCACCCCC TCTCCAACCACCACCACCACCACCACCACCACCACCACCA	21 j ACCTCCGCACAC gCAGCAGGGCC GGAGGGGGCAC CTCCAGCAGA GGCGGGCCC CCGGGCGCCC CCGGCCGCCC GGCGGC	GAGACOCAGO GAGAGOCTOG GAGAGOCTOG TTCATAGCT TCATAGCT TCATAGCT TCAGGCT TCAGGCT TCAGGCT TCAGGCT TCAGGCT TCAGGCT GAGACCACA AAGATCATC GGCGGCCCAG GCCCAGTCCG GAGACCACA GAGCGCT GAGACCACA GAGCGCCC GAGGGCGCAC CTCGCCGCAC CTCGCCCAC CAGCGCCAC AGCACCACA AGCATCAAAT GCGCCCAC AGCACCACA AGCATCAAAT GCGCCCAC AGCACCACA AGCATCAAAT GCGCCCAC AGCACCACAC AGCATCAAAT GCGCCCCAC AGCACCACAC AGCATCAAAT GCGCCCCAC AGCATCAAAT GCGCCCCAC AGCACCACAC AGCATCAAAT AGCATCAGCCCCAC AGCACCACAC AGCATCAAAT AGCATCAGCCCCAC AGCATCAAAT AGCATCAGCCCCAC AGCATCAAAT AGCATCAGCACAC AGCATCAGCACAC AGCATCAGCACCAC AGCATCACCACCAC AGCATCACCACCAC AGCATCACCACCACCAC AGCATCACCACCACACCA	GGCCOGGTT AACCGACAG GCAGCCGGTT TCAAGCGCGA AGCAGTCTCC TGCTGAAGGA GGCCGGAAGC GGCCGGAGCG GGCCGGAGCG GGGCGGGGGA ACGACGACGA ACCACCGCA GCTACAAGC GCTACAAGC GCTCTA AGGAGGAGA AGCACGCTCTA AGGAGCGACG CTACAAGCT CCGCCTCTA ACCACCTCTAAAG	GRAGOTTOCA CRACTISCOC GROCCTIGGAC GROCCTIGGAC GROCCTIGGAC GROCATICAC CAG CORRACAG CTACCCCGAC CCAG CORRACAG AGGGCCOGGC CCCCGGGGCC GCCGGGGCC CCCGGGGCC CCCGGGGCC CCCGGGGCC CCCGGGGCC CCCGGGGCC CCCGGGGCCAAGTTS CCCCCAAGCTTC CAGCAGCTC CAGCAGCGCC CAGCAGCGGGCC CAGCAGCGGGCC CAGCAGCGGGCC CAGCAGCGGGCC CAGCAGCGGGCC CAGCAGCGGGCC CAGCAGCGGGCC CAGCAGCGGGCCCAGCGGGCCCAGCGGGCCCAGCGGGCCCAGCGGGCCCAGCGGGCCCCAGCGGGCCCCAGCCGGCCCCCAGCCGGGCCCCCAGCGGGCCCCCAGCGGGCCCCCAGCGGGCCCCCAGCGGGCCCCCC	120 180 240 300 360 420 540 660 720 780 940 900 960 1020 1140 1260 1260
45 50 55 60	1 GGGGTGGGAG GGGGGGGGGGGGGGGGGGGGGGGGGG	11	21 ACCTCGSCAC GCAGGAGGCG GGAGGGGGGAGGGGGGGGGGGGGGGGGG	GRANCCACC GRAGOTTOS TTCATOCIC GRAGOTTOS TTCATOCIC GRAGOTTOS TTCATOCIC GRAGOTTOS ANGATCATOS GRAGOTTOS ANGATCATOS GRAGOTTOS ANGATCATOS GRAGOTTOS ANGATCATOS GRAGOTTOS ANGATCATOS GRAGOTTOS G	GGCCCGGCTTCAAAA ACCACCCCCCCCCCCCCCCCCCCC	DIAGOSTICA CNACTISCOC CNACCTIS	120 180 240 300 360 420 480 540 660 720 840 900 960 1020 1140 1200 1260 1380
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45 50 55 60 65	1 GGGGTGGGAG GCCTGCAAC GGGAGGGGGGGGGGGGGGG	11 G000A000000 G0ATCATGOT TOSA CACCION TOSA	21 ACCTCOSCAC @CAGCAGGCO @GCOGCO CAGCAGGCO @GCOGCO CAGCAGCC @GCOGCO CAGCAGCC CAGCACC CAG		GGCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GRAGOSTICO CANACTICOCC CANACTIC CANACTI	120 180 240 360 420 420 660 720 780 940 960 1020 1140 1200 1240 1320 1440 1550 1560 1680 1740 1680 1740 1680 1740 1680 1740 1680 1740 1860 1860 1920
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10	1	11	21	31	41	51	
	CTGCCACCTG	GGGCGGTGCG	GCAGCAAGTG GGCCCGGAGC CGAGCTGCGG	CCGGAGCCCG	GGTAGCGCGT	AGAGCCGGCG	60 120 180
15	CCCTGTTCCT GCTTCATCCA CCATTTTTGGG	GCTGCGCTCC CCGGCGCCTC CTTGCCCCAC	GCAGCTGGGG GCCCTGGCGG CGCCGGGGC TA CAACGCCA	ACTTCAGCCT AGCGGCGGGA CCCACCTCCA	GGACAACGAG GATGCAGCGC GGGCAAGCAC	GTGCACTCGA GAGATCCTCT AACTCGGCAC	240 300 360 420
20	GCCAGGGCTT	CTCCTACCCC	TACAAGGCCG	TCTTCAGTAC	CCAGGGCCCC	CCTCTGGCCA	480
20	TGGAACATGA TTTCCAAGAT ACATCCGGGA	CAAGGAATTC CCCAGAAGGG ACGCTTCGAC	CTCACCGACG TTCCACCGAC GAAGCTGTCA AATGAGACGT	GCTACCACCA CGGCAGCCGA TCCGGATCAG	TCGAGAGTTC ATTCCGGATC CGTTTATCAG	COGTTTGATC TACAAGGACT GTGCTCCAGG	600 660 720
25	AGCACTTGGG AGGAGGGCTG GGCACAACCT	CAGGGAATCG GCTGGTGTTT GGGCCTGCAG	GATCTCTTCC GACATCACAG CTCTCGGTGG CGGCACGGC	TGCTCGACAG CCACCAGCAA AGACGCTGGA	CCACTGGGTG TGGGCAGAGC	TGGGCCTCGG GTCAATCCGC ATCAACCCCA	780 840 900 960
	TOTTCARGGO	CACGGAGGTC	CACTTCOGCA	GCATCCGGTC	CACGGGGAGC	AAACAGCGCA	1020
30	AGAACAGCAG	CAGCGACCAG	AGGCAGGCCT	GTAAGAAGCA	CGAGCTGTAT	GTCAGCTTCC	1140
	AGGGGGGAGTG	TGCCTTCCCT	TGGATCATCG CTGAACTCCT	ACATGAACGC	CACCAACCAC	GCCATCGTGC	1200 1260
	AGACGCTGGT	CCACTTCATC	AACCCGGAAA CTCTACTTCG	CGGTGCCCAA	GCCCTGCTGT	GCGCCCACGC	1320 1380
35	ACAGAAACAT	GGTGGTCCGG	GCCTGTGGCT	GCCACTAGCT	CCTCCGAGAA	TTCAGACCCT	1440
	CTGCCTTTTG	TGAGACCTTC	CCCTCCCTAT	CCCCAACTTT	GCCAGGAACC AAAGGTGTGA	GAGTATTAGG	1500 1560
	AAACATGAGC TCCTACAAGC	AGCATATGGC	TTTTGATCAG	TTTTTCAGTG	GCAGCATCCA	ATGAACAAGA	1620 1680
40	acconggented	GTCATTGGCT	GGGAAGTCTC	AGCCATGCAC	GGACTCGTTT	CCAGAGGTAA	1740
	TTATGAGCGC GGGCACATTG CAATAAAACG	GTGTCTGTGC	GGCCACCCAG GAAAGGAAAA	CCGTGGGAGG TTGACCCGGA	AGTTCCTGTA	ATAAATGTCA	1800 1860
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50	ILGLPHRPRP LQDSHFLTDA IRERFDNETF	HLQGKHNSAP DNVMSFVNLV RISVYOVLOE	LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLPL	AVEBGGGFGG YHHREPRFDL LDSRTLWASE	QGFSYPYKAV SKIPEGEAVT EGNLVFDITA	RREMOREILS FSTOGPPLAS AAEFRIYKDY TSNHWVVNPR	60 120 180 240
50 55	ILGLPHRPRP LQDSHFLTDA IRERFDNETF HNLGLQLSVE ONRSKTPKNO	HLQGKHNSAP DMVMSFVNLV RISVYQVLQE TLDGQSINPK EALRMANVAE MNATNHAIVQ	MFMLDLYNAM EHDKEFFHPR	AVEEGGEPGG YHHREPRFDL LDSRTLWASE QNKQPFMVAP KKHELYVSFR	QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHFRS DLGWODWIIA	RREMOREILS FSTOGPPLAS AAEFRIYKDY TSHHWUVNPR IRSTGSKORS PBGYAAYYCE	120 180
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	TCAGAGCAGG	ACTGCCTGCC ATATTCTAAT	ACACTCTTTC	CACGAGGAGA	CCAAGGAAGA	TAGTGGGAGG	1860
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20	FVAAWAVARA	TLADARCWEL	SAGDIKWIYO	APILAAIGLN	FILPLNTVRV	LATKIWETNA	360
	VGHDTRKOYR	KLAKSTLVLV	LVFGVHYIVF	VCLPHSFTGL	GWEIRMHCEL	PFNSFOGFFV	420
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	GGCCGGTGGC	CCGGGCCCGV	CCACCCCAGC	TGCGCGTCGT	TACTGGCCAC	AAGTTTGCTC	60
35	TGGGCCAGCC	AAGTTGGCAA GCCGTTCCGG	CTTGGAAGCT	TCTCCCGGGC	TCTGGAGGAG	GGTCCCTGCT	120
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40	CAACCATAAA	GGAGTTGCTT	TCCGACACTG	TAACCCCAAT	GGAACATGGG	ATTTTATGCA	480
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	TCTGAATACG	GTTAGAGTTC	TAGCTACCAA	AATCTGGGAG	ACCAATGCAG	TTGGGCATGA	1200
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13	TTTGAGCTGT	TTGTAATGTA TACTACATTG	TACATGGCAT	GTGGGATCAA	TTARARATTT	GTTTTAAAAA	2580 2640
	T						
	Seq ID NO:	663 Prote	n semience				
80	Protein Ac	cession #: 1	P 005039				
			-			51	
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85	GNCFPENDGL	ICWPRGTVGK	ISAVPCPPYI	YDFNHKGVAP	RHCNPNGTWD	FMHSLNKTWA RLHCTRNYIH	120 180
	NYSDCLRFLQ MHT.FUSPMLR	PDISIGKQEP	VHAHIGUERL	RSLIMODDPO	NSIEATSVDK	SOYIGCKIAV	240

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	VMFIYFLATN	YYWILVEGLY AGDIKWIYOA	LHNLIFVAFF PILAAIGLNF	SDTKYLWOFI ILFLNTVRVL	LIGNGFPAAF ATKIWETNAV	VAANAVARAT GHDTRKOYRK	300 360
	LAKSTLVLVL	VFGVHYIVFV WNLSVDWKRT	CLPHSFTGLG	WEIRMHCELF	FNSFOGFFVS	IIYCYCNGEV	420 480
5	IASROPDSHI	TLPGYVWSNS	EQDCLPHSFH	EETKEDSGRQ	CEDDITMENTS IN	RPMESNPDTE	540
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35	Seq ID NO:	665 Prote	in seguence				
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	TTCGCTGTGA	GGTTGAGGCT	CCGGGCCCCGG	TACATGTGTA	CTGGCTGCTC	GATGGGGCCC	360
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00	AAGCCCGCAG	TGCCAACGCC	TCCTTCAACA	TCAAATGGAT	TGAGGCAGGT	CCTGTGGTCC	540
	TGAAGCATCC	AGCCTCGGAA	GCTGAGATCC	AGCCACAGAC	CCAGGTCACA	CTTCGTTGCC	600 660
	ATGGTCAGAG	GCACCCTCGG CAACCACACA	GTCAGCAGCA	AGGAGCGGAA	CCTGACGCTC	CGGCCAGCTG	720
65	GTCCTGAGCA	TAGTGGGCTG	TATTCCTGCT	GCGCCCACAG	TGCTTTTGGC	CAGGCTTGCA	780
	GCAGCCAGAA	CTTCACCTTG GGTAGTAGCG	AGCATTGCTG	ATGAAAGCTT	TGCCAGGGTG	GTGCTGGCAC	840 900
	AGCCACCCCC	GAGCCTGCAG	TGGCTCTTTG	AGGATGAGAC	TCCCATCACT	AACCGCAGTC	960
70	acceccents.	CCTCCCCACA	CCCACACTOT	TTGCCAACGG	GTCTCTGCTG	CTGACCCAGG	1020
70	TCCGGCCACG	CAATGCAGGG AGCCACACTT	CACCTAGGGG	AGATTGAAGA	CATGCCGCTA	TTTGAGCCAC	1140
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85							1980
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		TGTGTACAAC					3060
		CCCCGAGGCC					3120
		GCTGATGTGG					3180
20		AGTACTGGCA					3240
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		CAGTGAGATT					3360
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		CCTGGCTGGG					4080
25		CCCCACACTT				TTTTTCTTTT	4140
35	TGITTTTGTT	TTTACACTCG	CIGCICICAA	TAAATAAGCC	TITTITA		

Seq ID NO: 667 Protein sequence Protein Accession #: NP_002812

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45		GPEHSGLYSC					240
		OPPPSLOWLF					300
	CIGQGQRGPP	IILEATLHLA	BIEDMPLFEP	RVFTAGSEER	VTCLPPKGLP	EPSVWWEHAG	360
		QKGHELVLAN					420
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Seq ID NO: 668 DNA sequence Nucleic Acid Accession #: Bos sequence

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		CACACATACC					660
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		GGGACTTATT					900
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	ATGCTTCCCA	TIGGIGCIGI	GGTGATGGTT	TTTGGATTCG	TCATGGCTAT	TACAAATACT	1260

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5	Seq ID NO: Protein Acc	669 Protes	n sequence Sos sequence				
10	GFPLGILLLF IAMISYNIIA SLISTGLTTL	WVSYVTDFSL GDTLSKVFQR ILGIVMARAI	VLLIKGGALS IPGVDPENVF SLGPHIPKTE	GTDTYQSLVN IGRHFIIGLS DAWVFAKPNA	41 VVNSIIGSGI KTPGPPGYLL TVTFTLPLSL IQAVGVMSPA	LSVLQFLYPF YRNIAKLGKV FICHENSFLV	60 120 180 240 300
15	RFCYGVTVIL VLELNGVLCA	TYPMECFVTR	RVIANVFFGG	NLSSVFHIVV THSDKIMSCV	FTQGDLFENY TVMVITVATL MLPIGAVVMV FQ	VSLLIDCLGI	360 420
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25	AAGCAAGCTG	GGTTTCCTTT	GGGAATATTG	CTTTTATTCT	41 GAGGATTGCC GGGTTTCATA GAACAGATAC TCTCTGTTCT	CTACCAGTCT	60 120 180 240
30	TATCCTTTTA TTTCAARGAA GGACTTTCCA GGAAAGGTCT	TAGCAATGAT TCCCAGGAGT CAGTTACCTT CCCTCATCTC	AAGTTACAAT TGATCCTGAA TACTCTGCCT TACAGGTTTA	ATANTAGCTG AACGTGTTTA TTATCCTTGT ACAACTCTGA	GAGATACTTT TTGGTCGCCA ACCGAAATAT TTCTTGGAAT ACCCTTGGAT	GAGCAAAGTT CTTCATTATT AGCAAAGCTT TGTAATGCA ATTTGCAAAG	300 360 420 480 540
35	COCAATGCCA TTCTTAGITT ATGTCCATCG TTTACTGGCT ACATTTGGAA	TTCAAGCGGT ACAGTTCTCT TGATTTCTGT TCACCCAAGG GATTTTGTTA	CGGGGTTATG AGAAGAACCC ATTTATCTGT GGACTTATTT TGGTGTCACT	TCTTTTGCAT ACAGTAGCTA ATATTCTTTG GAAAATTACT GTCATTTTGA	TTATTTGCCA AGTGGTCCCG CTACATGTGG GCAGAAATGA CATACCCTAT	CCATAACTCC CCTTATCCAT ATACTTGACA TGACCTGGTA GGAATGCTTT	600 660 720 780 840
40	ATTGTTGTAA CTCGGGATAG	AGGTAATTGC CAGTGATGGT TTCTAGAACT	CATCACTOTA CATCACTOTA CAATGOTGTG	GCCACGCTTG CTCTGTGCAA	ATCTTTCATC TGTCATTGCT CTCCCCTCAT CACACTCOGA TTGGATTCGT ACTGCTTTCC	GATTGATTGC TTTTATCATT TAAGATTATG	900 960 1020 1080 1140
45	TCTCTCACAA ATTAGTATCT	ATACCTCAGA TTCAACTCGA	GTCTCATGTT GTAA	GAAATGTTCT CAGCAGACAA	ACTGCTTTCC CACAACTTTC	TACTITAAAT	1200 1260
50	Seq ID NO: Protein Acc	671 Prote: cession #: 1	in sequence Sos sequence 21	31	41	51	
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75	ACAGGTTTAA CACATACCAA GGGGTTATGT GAAGAACCCA TTTATCTGTA	CAACTCTGAT AAACAGAAGA CTTTTGCATT CAGTAGCTAA TATTCTTTGC	TCTTGGAATT CGCTTGGGTA TATTTGCCAC GTGGTCCCGC TACATGTGGA	GTAATGCAA TTTGCAAAGC CATAACTCCT CTTATCCATA TACTTGACAT	GGGCAATTTC CCAATGCCAT TCTTAGTTTA TGTCCATCGT TTACTGGCTT	ACTGGGTCCA TCARGCGGTC CAGTTCTCTA GATTTCTCTA CACCCAAGGG	420 480 540 600 660
80	GACTTATTTG GGTGTCACTG AATGTGTTTT ATCACTGTAG	AAANTTACTG TCATTTTGAC TTGGTGGGAA CCACGCTTGT	CAGAAATGAT ATACCCTATG TCTTTCATCG GTCATTGCTG	GACCTGGTAA GAATGCTTTG GTTTTCCACA ATTGATTGCC	TGACAAGAGA TTGTTGTAAC TCGGGATAGT	ATTITIGITAT GGTAATTGCC AGTGATGGTC TCTAGAACTC	720 780 840 900
85	AATGGTGTGC CTGTCTGAAG GGTGCTGTGG CATGGGCAGG	TCTGTGCAAC AACCAAGGAC TGATGGTTTT AAATGTTCTA	TCCCCTCATT ACACTCCGAT TGGATTCGTC CTGCTTTCCT	TTTATCATTC AAGATTATGT ATGCTATTA GACAATTTCT	CATCAGCCTG CTTGTGTCAT CAAATACTCA CTCTCACAAA TTAGTATCTT	GCTTCCCATT AGACTGCACC TACCTCAGAG	960 1020 1080 1140 1200

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5	Seq ID NO: Protein Ac	673 Protei cession #: E	in sequence los sequence	1					
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10	SYNIIAGDTL	SKVPQRIPGV VMARAISLGP	DERMANICKE	PAUDMATORY	CUMCERETCU	UNICOTAVOST.	180		
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	Nucleic Ac	id Accession	#: Eos se	quence					
	Coding sequ	uence: 111	140						
20	,	11	21	31	41	51			
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	COTOTOTOT	GEGCAACTCC	CCTCATTTTT	ATCATTCCAT	CAGCCTGTTA	TCTGAAACTG	900		
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-	1 MGYQRQEPVI	11 PPQVNKTFGF	21 PGYLLLSVLQ	31 PLYPFIAMIS	YNIIAGDTLS	KVPQRIPGVD MARATOT/JPH	120 180		
45 50	1 MGYQRQEPVI	11 PPQVNKTFGF	21 PGYLLLSVLQ	31 PLYPFIAMIS	YNIIAGDTLS	KVPQRIPGVD MARATOT/JPH	120		
-	1 MGYQRQEPVI PENVFIGRHF IPKTEDAWVF ICIFFATCGY VFFGGNLSSV SEEFRTHSDK	11 PPQVNKTFGF IIGLSTVTFT AKPNAIQAVG LTFTGFTQGD FHIVVTVMVI IMSCVMLFIG	21 PGYLLLSVLQ LPLSLYRNIA VMSFAFICHH LFENYCRNDD TVATLVSLLI	31 PLYPFIAMIS KLGKVSLIST MSFLVYSSLE LVTFGRFCYG DCLGIVLELM	YNIIAGDTLS GLTTLILGIV EPTVAKWSRL VIVILTYPME GVLCATPLIF	KVPQRIPGVD MARAISLGPH IHMSIVISVP CFVTREVIAN IIPSACYLKL	120 180 240		
-	1 MGYQRQEPVI PENVFIGRHF IPKTEDAWVP ICIFFATCGY VFFGGNLSSV	11 PPQVNKTFGF IIGLSTVTFT AKPNAIQAVG LTFTGFTQGD FHIVVTVMVI IMSCVMLFIG	21 PGYLLLSVLQ LPLSLYRNIA VMSFAFICHH LFENYCRNDD TVATLVSLLI	31 PLYPFIAMIS KLGKVSLIST MSFLVYSSLE LVTFGRFCYG DCLGIVLELM	YNIIAGDTLS GLTTLILGIV EPTVAKWSRL VIVILTYPME GVLCATPLIF	KVPQRIPGVD MARAISLGPH IHMSIVISVP CFVTREVIAN IIPSACYLKL	120 180 240 300		
-	1 MGYQRQEPVI PENVFIGRHF IPKTEDAWVF ICIFFATCGY VFFGGNLSSV SEEPRTHSDK HVQQTTQLST	11	21 PGYLLLSVLQ LPLSLYRNIA VMSPAFICHH LFENYCRNDD TVATLVSLLI AVVMVFGFVM	31 PLYPFIAMIS KLGKVSLIST MSFLVYSSLE LVTFGRFCYG DCLGIVLELM	YNIIAGDTLS GLTTLILGIV EPTVAKWSRL VIVILTYPME GVLCATPLIF	KVPQRIPGVD MARAISLGPH IHMSIVISVP CFVTREVIAN IIPSACYLKL	120 180 240 300		
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50 55	1 	11	21	31 	YNIIAGDTLS GLTTLILGIV EPTVAKWSRL VIVILTYPME GVLCATPLIF	KVPQRIPGVD MARAISLGPH IHMSIVISVP CFVTREVIAN IIPSACYLKL	120 180 240 300		
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50 55	1 MGYGROEPVI MGYGROEPVI MGYGROEPVI PENVFIGREF IPKTEDAWVP ICIFFATGGY VFFGGRILSV SEEPRIHSDK HVQQTTQLST Seq ID MO: Nucleic Ac. Coding sequence 1 AGGARTGING	11	21 PGYLLLSVLQ LPLSLYRMIA VMSPAFICHH LFENYCRNDD TVATLVSLIA AVVMVFGFVM PQUENCE 1 #: MM_006 074 21 CGCAGATGCA	31 FLYPFIAMIS KLGKVSLIST MSPLVYSSLE LVTFGRFCYG DCLGIVLELM AITHTQDCTH	YNIIAGDTLS GLTTLILGIV EPTVAKMSRL VIVILTYPME GVLCATPLIF GOEMFYCFPD 41 TGGCT00333	KVPCRIPGVD MARRISLIPPH HMSIVISVP CPVIREVIAN IIPBACYLKL NFSLIWISES	120 180 240 300 360		
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50 55 60	1 MGYQRQEPVI PENVFIGHEF FKTEDAWF ICIFFATOGY VFFGGHLESV VFFGGHLESV VFFGGHLESV VFFGGHLESV VFFGGHLESV VFFGGHLESV VFFGHLESV 	11	21 PGYLLLSVLQ LPLSLYRMIA VMSPAFICHH LFENYCRMDD LTVATLVSLLI AVVMVFGFVM Quence 1 #: MM_006 174 21 CGCAGATGCA CAGCCRAGGG	31 FLYPFIAMIS KLGKVSLIST MSFLVYSSLE LVTFGRFCVG DCLGIVLELM AITNTQDCTH 853.1 31 GAGGTTGAGG ACCTGGGGCC	YNIIAGDTLS GLTTLILGIV EPTVAKMSRL UTVILITYPME GVLCATPLIF GCEMFYCFPD 41 TGGCTGCCGG GGGCTGCTGC	EVPCRIPGVD MARRISLGPH IHMSIVISVF CFVTREVIAN IIPSACYLKL NFSLITHTSBS 51 ACTGGAAGTC CCCTCCAGGC GGGGAGGAGAC	120 180 240 300 360 60 120 180 240		
50 55	1 MOYOROGEPVI PENVFICARF ICIFFATOGY VFFGGHLESV VFFGGHLESV VFFGGHLESV VFGGH	11	21 PGYLLLSVLQ LPLSLYRMIA VMSFAFICHH LFERYCRNDD TVATLVSLLI AVVMVFGFVM 21 #: NM_006 74 21 GGCAGATGCA CAGCCAAGGA TCCTAGTGAAGGA TCCTAGTGAAGGA GTGGGGGGGGGG	31 	INITIAGETIS GUTTLILIAIV EPTVAKMSRL UTVILIVYPME GVLCATPLIF GCEMFYCFPD 41 I TGGCTGCGG GGGCTGCTGCC GGGCTGTGTAG CCCAGATGGC CCCAGATGGC CCCAGATGGC CCCAGATGGC	EVPORIPGUD MARAISLGPH IHNSIVISVE CPVTREVIAN IIBSACYLKI NFSLINTSES 51 Actiggaagic coctcoaggc G9G9AGGAC CAGCOCTOTT	120 180 240 300 360 60 120 180 240 300		
50 55 60	MOYORGEPVI PENVFIGHER LEXTEDANVP LCIFFATCOY VFFGGHLESV VFFGGHLESV SEERTHSDK RVQQTTQLST Seq ID NO: Coding sequence ACGGGCAGA ATOGGGCAGA ATOGGGCAGA CATGAGGATT CAGGATCATC CAGGATCATC CAGGATCATC	11	21 PGYLLLSVLQ LPLSLYRMIA MYSEAFICH LFENYCRNDD TVATLVSLLI TVATLVSLLI TVATLVSLLI CGCAGATGCA CGCCCAAGGA TCCTGCTTGC GTGGGGCGAC GTGGGGGCGAC GTGCATAGT	31 PLYPFIAMIS KLGKVSLIST MSPLVYSLIST MSPLVYSLIST MSPLVYSLIST AITMTQDCTH AITMTQDCTH 31 GAGGTTGAGG ACCTGGGGACA TCAGCACAG GCTCATCGCG	YNITAGDTLS GLITTLILGIV EPTVAKMSRL VIVILITYPHE GVLCATPLIF GQEMFYCFPD 41 TGGCTGCGG GGGTTGTAG GCCTGCCG GGGCTTGTAG CCCTGGCAGC CCCTGGCAGC CCAGATGGC	EVPOR I PSUD MARAI SLIGHE I HHSI SILY SE CPUTREVI AN I I PSACYLEL NF SLIMTSES 51 ACTSGRASTIC CCCTCCASGC GGSSRAGRAC CAGCCCTSTT TCCTGRACAGC	120 180 240 300 360 60 120 180 240 300 360		
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5	AHCLKPRYIV I SITWAVRPLT I NITDTMVCAS I DWIQETMKKN	HLGQHNLQKE LSSRCVTAGT VQEQGKDSCQ	EGCEQTRTAT SCLISGHGST GDSGGPLVCN	ESPPHPGFNN SSPQLRLPHT QSLQGIISWG	SLPNKDHRND LRCANITIIE QDPCAITRKP	IMLVENASPV HQKCENAYPG GVYTKVCKYV	120 180 240
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15	TTOGACAGA TTOCOCTOTO GACTOTOCOS GCCOSCTACO AATAACTOTO	GTGATGAGAA CCAGCGGCGA ATGGCAGCGA ACTGCAAGAA AAGACAACAG	GGAGTGCCCC CCATTGCATC TGAAGAGAAC CGGCCTCTGT TGATGAGGAA	AAGGCTAAGT ATTGGTCGCT TGCACAGCAA ATTGACAAGA AGCTGTGAAA CTTGTGTATT GTGGTGGCCC	TCCGGTGCAA ACCCTCTGCT GCTTCATCTG GTTCTCAAGA	TGGGTTTGAG TTGCTCCACC CGATGGACAG ACCCGGCAGT	180 240 300 360 420 480
20	CACCAGOGGA CTGCTGTCCC AATAATGGCA	AGCGGAACAA GCCTGGTGGT TCCAGTATGT	CCTCATGACG CCTGGACCAC GGCCAGCCAG	CTGCCCGTGC CCCCACCACT GCGGAGCAGA CAGAGGCCTG	ACCOGCTGCA GCAACGTCAC ATGCGTCGGA COTGGTATGA	GCACCCTGTG CTACAACGTC AGTAGGCTCC CCTTCCTCCA	540 600 660 720 780
25	COGTCCGGGA GACACCAGCC TCTGAGCCCA	ACAGCCOGGG GCCAGGGGAC	TGCCAGCTCC GCAGCCTGGC TGAAGAAGTA	AACCAAGCCG CAGGCAGCCA CCCCAGGAGG TAA			840 900
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35	DCPDGSDEEN GQVFVTSENQ LLSRLVVLDH PPYSSDTESL	CTANPLLCST	ARYHCKNGLC IIGSSVIFVL	KAKSKCGPTF IDKSFICDGQ VVALLALVLH ABQNASEVGS QAASSLLSVE	HQRKRNNLMT PPSYSEALLD	ORPAWYDLPP	60 120 180 240 300
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45	1 ATGAATCCTT	11 TOCAGAAAA	21 TGAGTCCAAG	31 GAAACTCTTT	41 TTTCACCTGT	51 CTCCATTGAA	60 120
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20	TATGGAATGA	AAGCTGTGC:	GATCCTGTAT	TICCIGIATI	100100n010	CATOCTOGGA	240
50	TATGGAATGA	AAGCTGTGC:	GATCCTGTAT	TICCIGIATI	100100n010	CATOCTOGGA	240 300 360
30	TATGGAATGA ACCTCCACAT GCAGCCATTG	CTATATACCI CTGACTCGT	GATCCTGTAT GATCCTGTAT TGCCTTCAGG	AGCCTCTGTT	TCATCTATCT	CATCCTGGGA CTCCTTGGTG	240 300 360 420
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55	TATGGAATGA ACCTCCACAT GCAGCCATTG TATGTGCTTG GTACACACAG AAACCCTGTG	CTATATACCI CTGACTOGTO CTGACTOGTO CCCATGTGA TCCTATCAT TGGCAGCTT	GATCGATAGE GATCCTGTAT TGCCTTCAGE GTTGGGAAA CAAGTCCTTC GATCGGCCTC TGGTGGAGA	AGCCTCTGTT ATCAAGACAA GGTGCCTTAC AGTCTAATAG CAGTTTGAAG	ATTITACTO	CATCCTGGGA CTCCTTGGTG AGGACAAGTG AGGAGGAACG AGAGGAACGG TTCTACATT	240 300 360 420 480 540 600
	TATGGAATGA ACCTCCACMT GCAGCCATTG TATGTGCTTG GTACACACAG AAACCCTGTG ACTAGATACT ATCACACCCA	AAGCTOTGC: CTATATACCI CTGACTCGTV GCCATGTGA' TCCTATCAT' TGCCAGCTT' TCTCAGTCT' TGCTGAGAG	CTTCATTGTC GATCCTGTAT TGCTTCAGC GTTGGGAAA CGAGTCCTTC GATCGGCTC TGGTGGAGA CTACCTGTCA AGATGTCCAI	AGCTCTGTT ATCAAGACAA GGTGCCTTAC AGTCTAATAG CAGTTTGAAG ATCAATGCAG ATCAATGCAG	ATTTACTCO TCATCTATCT CAATACTGGG CTTTGGGGAC AAAACATGG GGAGCTGAT AAGACTGCAA	CATCCTGGGA CTCCTTGGTG AGGACAAGTG AGGAGGCATC AGAGGAACGG TTCTACATTT TGCATTGGCT	240 300 360 420 480 540 600 660 720
55	TATGGAATGA ACCTCCACMT GCAGCCATTG TATGTGCTTG GTACACACAG AAACCCTGTG ACTAGATACT ATCACACCCA	AAGCTOTGC: CTATATACCI CTGACTCGTV GCCATGTGA' TCCTATCAT' TGCCAGCTT' TCTCAGTCT' TGCTGAGAG	CTTCATTGTC GATCCTGTAT TGCTTCAGC GTTGGGAAA CGAGTCCTTC GATCGGCTC TGGTGGAGA CTACCTGTCA AGATGTCCAI	AGCTCTGTT ATCAAGACAA GGTGCCTTAC AGTCTAATAG CAGTTTGAAG ATCAATGCAG ATCAATGCAG	ATTTACTCO TCATCTATCT CAATACTGGG CTTTGGGGAC AAAACATGG GGAGCTGAT AAGACTGCAA	CATCCTGGGA CTCCTTGGTG AGGACAAGTG AGGAGGCATC AGAGGAACGG TTCTACATTT TGCATTGGCT	240 300 360 420 480 540 600
	TATGGAATGA ACCTCCACH GCAGCCATTG GTACACACH GTACACACH AAACCCTGG ACTAGATAC ATTAGACACCC ATTAGGAGTTC ATTAGACATA TTTGGAGTTC ATATACAATA	AACACCCC CCAATGGTGA CTGACTCGTG GCCATGTGA TCCTATCAT TCCTATCAT TCCTGAGGGTCT TCCTGAGGGGC CAGGACTGC AACCACCCC	CTTCATTGTC CGATCTTCAGG GTTGGGAAAA CGAGTCCTTC GATCGGCTC TGGTGGAGAG CTACCTGTCC AGATGTGCAA CATGTCCAA CATGTCAAC CATGGTAAACCGTC CATGGTAAACCGTC CATGGTAAACCGTC CATGGTAAACCGTC CATGGTAAACCGTAAACCGTAAACCGTAAACCGTAAACCGTAAACCGTAAACCGTAAACCGTAAACCGTAAACCGTAAACCGTAAACCGTAAACCGTAAAAACCGTAAAACCGTAAAACCGTAAAAACCGTAAAAACCGTAAAAACCGTAAAAACCGTAAAAACCGTAAAAACCGTAAAAAACCGTAAAAAAAA	AGCTCATT	ATTITACTOC TCATCTATCT CAATACTGGG CTTTGGGGAC AAAACATG GGAGCTGAT AAGACTGCTA TGTTTGCAAT TTCCAAAG TTCCAAGACTGCAAT TTCCAAGACTGCAAT	CATCCTGGGA CTCCTTGGTG AGGACAATG AGGAGCATC AGAGGAACGG TTCTACATT TGCATTGGCT GGGAAGCAAA ATGTATCTGG ACAGCACTGG	240 300 360 420 480 540 600 660 720 780 840 900
55	TATGGAATGA ACCTCCACNT GCAGCCATTG TATGTGCTTG GTACACACAG AACCCTOTG ACTAGATACT ATTCACACCOCT ATTTAGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC AGAGTGGGAGGGTACTAT	ARGCTOTGC: CTGACTGTW GCCATGTGA' TCCTATCAT' TCCTATCAT' TCCTATCAT' TCCTATCAT' TCCTATCAT' TCCTATCAT' TCCTATCATC' CTGACATCTC' CAACCACCCC CCCAATCGTT' CCCAATCGTT' CCCATCGACATCTT' CCCATCTATA'	CTTCATTGT GATCCTCAG TGCTTCAG GTTGGGAAA TGCTTCAG GTTGGGAAA TGCTGTG TGATGGGAGA TCTGCTGGAGAA CCTGCTGAGAGAC CATGGTAAT CATGGTAAT CATGGCAA AATATCCAAA CCCATTGCA	MGCTCTOTT TTCAAGACAM GGTGCCTTAC GGTGCCTTACAG CAGTTTGAAG CAGTTTGAAG ATGTTTTGGAG GCACTTTTGGAG GCACTTGTTG ATAGTGGCT TCTGGAGACA GAGCCATTT	ATTITACTOC TCATCTATCT CAATACTGGG CTTTGGGGAC AAAACATGCG GGAGCTTGAT AAGACTGCTA TGTTTGCAAT TTCCAAAGCC TGGATGTAAA CTCTTTTGGA	CATOCTGGGA CTCCTTGGTG AGGACAATG AGGAGCATC AGAGGACGG TTCTACATT TGCATTGGCT GGGAAGCAAA ATGTATCTGG ACAGCACTGGC GGCACTGACC TCACATGGCT TGCATTGTTTTTTTTTT	240 300 360 420 480 540 600 660 720 780 840
55 60	TATGGAATGA ACCTCCACNT GCAGCCATTG TATGTGCTTG GTACACACAG AACCCTOTG ACTAGATACT ATTCACACCOCT ATTTAGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC ATATACAATA TTTGGAGTTC AGAGTGGGAGGGTACTAT	ARGCTOTGC: CTGACTGTW GCCATGTGA' TCCTATCAT' TCCTATCAT' TCCTATCAT' TCCTATCAT' TCCTATCAT' TCCTATCAT' TCCTATCATC' CTGACATCTC' CAACCACCCC CCCAATCGTT' CCCAATCGTT' CCCATCGACATCTT' CCCATCTATA'	CTTCATTGT GATCCTCAG TGCTTCAG GTTGGGAAA TGCTTCAG GTTGGGAAA TGCTGTG TGATGGGAGA TCTGCTGGAGAA CCTGCTGAGAGAC CATGGTAAT CATGGTAAT CATGGCAA AATATCCAAA CCCATTGCA	MGCTCTOTT TTCAAGACAM GGTGCCTTAC GGTGCCTTACAG CAGTTTGAAG CAGTTTGAAG ATGTTTTGGAG GCACTTTTGGAG GCACTTGTTG ATAGTGGCT TCTGGAGACA GAGCCATTT	ATTITACTOC TCATCTATCT CAATACTGGG CTTTGGGGAC AAAACATGCG GGAGCTTGAT AAGACTGCTA TGTTTGCAAT TTCCAAAGCC TGGATGTAAA CTCTTTTGGA	CATOCTGGGA CTCCTTGGTG AGGACAATG AGGAGCATC AGAGGACGG TTCTACATT TGCATTGGCT GGGAAGCAAA ATGTATCTGG ACAGCACTGGC GGCACTGACC TCACATGGCT TGCATTGTTTTTTTTTT	240 300 360 420 480 540 660 720 780 840 900 960 1020
55	TATGGATGA ACCTCACATI GCAGCCATTG TATGTGCTTG GTACACACAG AAACCCTGTG ACTAGATACT ATTGGAGTTC ATTAGACTAG TTTGGAGTTC CTAGACTAGT CAGACTAGT TTGGAGTTC CAGACTAGT CCAGACTAGT CCAGACTAGT CTGA	ARGETOTICE CTRATATACE CTRATATACE CTGACTOTIC GCCATOTGA' TOCCAGCT' TOCCAGCT' TOCCAGCT' TOCTAGAGG' CAGGACTIC ARCACCCC CCAATCGTT GCAGTGAGAG TOCTTGAGAG TOCTTGAGAG TOCTTGAGAG TOCTTGAGAG TOCTTTGAAA TOCGGGTTC ATCGTCTG	CTTCATTGT GATCCTTCAGG GTTGGGAAA; TGCCTTCAGG GTTGGGAGAG GTTGGGAGG TGAGTGGGGAG TGAGTGGGGAG TGAGTGGGGAG TGAGTGGGAG TGAGTGGGAG TGAGTGGGAG TGAGTGGGAG TGAGTGGAG TGAGTGGAG TGAGTGAG	MOCTOTATI MOCTOTATA MOCTOT	ATTITACTOC TCATCTATCT CCATACTGGG CTTTGGGGA AAAAACATGG GGAGCTIGAT AAGACTGCTA TGTTTGCAAT CTTCCAAAGCC TGGGGGTTTTA TGGATGTAAA CTGGATTTAAA CTCTTTTGG TGGGGGTTTT TGTTCATCC TCTGATCCC TCTGATCCC	CATCCTGGGA CTCCTTGGTG AGGACHAGTG AGGACHAGTG AGAGGACHC AGAGGACHC AGAGGACHA ATGTATCTGG AGGACCHA ATGTATCTGG AGGACCTGAC TCAGCACGGG TCAGCACGGG TTGTGTCTCAG CTTGTTTGAC TTGGAAATTG TAGGAAATA	240 300 360 420 480 540 600 660 720 780 840 900 960 1020
55 60	TATGGATGA ACCTCACAT GCAGCCATTG TATGTGCTTG GTACACACAG AAACCCTGTG ACTAGATACT ATTGGAGTTC ATTAGAATTC ATTAGAATTC ATTAGAATTC ATTAGAATTC ATTAGAATTC ATTAGAATTC ATTAGAATTC CTAGATGAT CCAGACTAGT TCACGATGGA CCAGGACTAGT TCACGATCGAT TTGCATTT GCTGTTCGTT	AMGCTOTGC CTGATTGGT GCCATCTGT TGCGAGCT TTGCAGCT TGCTGAGCT TGCTGAGCG CCAGCTGC CCATCGTT CCCATCGT TGCTGAGAG CCCACCGC CCATCGTT CCCATCGTT CCATCGTT TGCTGAGAG CCATCGTAGAG AGCTGAGA TCCTTTATA CTTTGCAAG TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTATA TCCTTTGCAAG TGATCCTAG TGATCCTAG	CTTCATTGT GATCCTTCAGG TGATCCTTCAGG GATCCTTCAGG CAAGTCCTTC GATCGGCATA CAAGTCCTTC GATCGGCATA CATCGAGAA CATCGAGAA CATCGAGAA CATCGAGAA ATATCCAAM CCCATTGCG CATCAGGAT AAATCCCTT TATCCAAGGAT AAATCCCT CATCAGGAT CATCGAGGAT CATCGAGGAT CATCGAGGAT CATCAGGAT CATCGAGAT CATCGAGAT C	MGCTCTGTT A TTCAAGACAA A TCTAAGACAA A AGTCTAATAG A TGTTTTTGGAG A TGTTTTTGGAG T TCTGGAGACA A TGTTTTTGGAG T TCTGGAGACA A TGTTTTTGGAGACA A TGTTTTTGGAGTTCTT T CGGAGTTAATAG A TTTTTGGAGTTCTT T CGGAGTAACA A TTTGCAGTTCT T CGGAGTAACA A TTTGCAGTTCAGAGACA A TTTGCAGTTCAGAGACA A TTTGCAGTTCAGAGACA A TTTGCAGTTCAGAGACA A TTTGCAGTTCAGAGACAA A TTTGCAGTTCAGAGACAA A TTTGCAGTTCAGAGACAA A TTTGCAGTTCAGAGACAA A TTTGCAGTTCAGAGACAA A TTTGCAGTTCAGAGACAA A TTTGCAGTTCAGAGACAA A TTTGCAGTTCAGAGACAA A TTTGCAGTTCAGAGACAA A TTTGCAGTTCAGAGACAAA A TTTGCAGTTCAGAGACAAA A TTTGCAGTTCAGAGACAAAAAAAAAAAAAAAAAAAAAA	ATTITACTOC TCATCTATCT CCATACTGGGA CTTTGGGAC CATTGGGAC CATTGGGAC AAAAACATGG GGAGCTTGAT AAGACTGCT TGTTTGCAAAGC TTGCAAAGC TTGCAAAGC TTGCAAAGC TTGCAATCTAAA CTCTTTGGA TTGCAACC TTGTCATCC TCTTATCC TCTTCATCC TTTTCCACT CGCAGCACTCA TTTTCCTACC TCACT TTTTCCTACC TCACT TTTTCCTACC TCACT TTTTCCTACC TCACT TTTTCCTACC TCACT TTTTCCTACC TCACT TTTCCTACC TCACT TTTTCCTACC TCACT TTTCCTACC TCACT TTTTCCTACC TCACT T	CATCCTOGGA CTCCTTGGTA CTCCTTGGTA AGGACAAGTA AGGACAAGTA AGGACAACTA CAGGACACAACTACACTT TCCATTGCATTT TCCATTGCAT TGCATTGCAT	240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140 1200 1260
55 60	TATGGATTA ACCTCCACHI GCAGCCATTA TATGTGCTTG GTACACACAG AAACCCTGTG ACTAGATACA TTTGGAGTTC ATATACAATA TTTGGAGTTC AGAGTGGAGG AGGGTACTAT TCAGGATGGA CCGGACCAG TTTGTCATT GCTGTTGGT ATAAATGAAA TCAGGAGAT CTGGCAGAT GTGGCAGAT GTGGCAGAT	AMGTOTIGE CTGATTACCI CTGACTGTY CGCATGTGY TCCCATGTCY TGCTGACCI TGCTGACCI TGCTGACCI CGCACCCC CCCACCCCC CCCCCC	CTTCATTGT CTTCATGT TGCTTCAGG TGATCCTTC GATCGCTCT GATCGCTCT GATCGCTCT GATCGCTCT GATCGCTCT GATCGCTCT CAGTGCAGA CCATGCT CATGCTCT CATGCTAT CATGCTAT CATGCTAT CATGCTAT CATGCTAT CATGCTAT CATGCTAT CATCAGGAT AATTCCAA CCATTGCC CATCAGGAT AATTCCAA CCATCAGGAT AATTCCAA CCATCAGGAT AATTCCAA CCATCAGGAT AATTCCAA CCATCAGGAT AATTCCAA CCATCAGGAT AATTCCAA CCATCAGGAT AATTCCAA CCAGTCAGGAT AATTCCAA CCAGTCAGGAT AATTCCAA CCAGTCAGGAT AATTCCAA CCAGTCAGGAT AATTCCAA CCAGTCAA CCAC	MOCTOTATION ATCARAGEMA ATCARAGEMA ATCARAGEMA ATCARTGAM ATCARTGAM ATCARTGAM ATCARTGAM ATCARTGAM ATCARTGAM ATCARTGAM ATCARTGAM ATCARTGAM ATCARTGAM ATCARTGAM ATCARTGAM ATTAGAM ATTAGAM ATTAGAM ATTAGAM ATTAGAM TTGG	ATTITACTION TOANTATION CASTACTIGGGA CITTIGGGGA GAGCTIGAT AAAACATG GGAGCTIGAT AAGACTGCT ATTITCCAAT TOCCAAAGC TOCCAATCACT TOCCAAAGC TOCCACT TOCC	CATCCTOGGA CTCCTTGGTA AGGACAMOTA AGGACAMOTA AGGACAMOTA AGGACAMOTA AGGACAMOTA AGGACAMA ATGTATCTOG GGGAACCAM ATGTATCTOG GGGACCTAACT TCACATTT TCATTATCTOG GGCACCTAC GGCACTGAC TCACAGGGT TOTGCTTCAG CTTGTTTCAC TAGGACAMA AGTCTTGAAT TCTCTTGAAT TCGAAACAMA AGTCTTGAAT TCGAAACAMA	240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140 1200
55 60 65	TATGGATTÓA ACOTCACAN GCAGCATTA GCAGCACAT GTACACACAG ANACCOTGTO ACTAGATAC ATTTGGAGTT ATTAGACTAG ATTTGGAGTT ATTAGACTAG ATTTGGAGTT CTAGACTAG AGGATGAT TCAGATGAG TTTGCATT CCAGGATGAG TTTGCATT CCAGGATGAG TTGCCATG CCGGCCACG TTGCCATG CGGCCACG CGGCCACG CGGCCACG CGCCACG CGCCCACG CGCCCACG CGCCCACG CGCCCACG CGCCCACG CGCCCACG CGCCACG CGCCCCCCCC	ANGITOTICS CTATATACCI CTAACTGTT GCCATGTGA TCCATGTA TCCAGGTT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCAGTCT TCTCTTATA TCTTTCAGA TGCGCCAG TGATCCTAG TGATCCTAG TGATCCTAG TGATCCTAG TGATCCTAG TGATCCTAG TGATCCTAG ATGATCCTAG TGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCTA	CTICATIGT CTICATIGT TGATCGTCAG TGATCGTTCAG TGATCGTTCAG TGATCGTTCAG TGATCGTTCAG TGATCGAGAA TCAGCTGTCAG TGATCGAGAA TCAGCTGTCAG TCAGGAGAA TCAGCAGGAA TCACAGAA TCACAGA	MAGCTCTOTT MICHAGOLA TICARAGCAN GOTGCCTTAC ATCTANTAGA ATCHATGAG ATCHATGAG TCHATGGAG GCACTTOTT TCHAGAGCAN CACTTOTT TCHAGAGCAN CACTTOTT TCHAGAGCAN ATTAGAACT ATTAGAACT TCHAGAGCAN TCHAGAGCAN TCHAGAGCAN TCHAGAGCAN CACTATTC GGAATTAC GCACTACC GTOGGAATT CCCACCAGC GTOGGAATT CCCACTACC GTOGGAATT CACTATTC CA	ATTITACTION TOATCTATCT CATACTGGG CATACTGGGG CATTGGGGG CATACTGGGGG CAAAACATGC GGAGCTTGAT AAAAACATGC TGGATTTAGAAGCC TGGATTAJA CTCTTTTGGGAT TTCCAAAGCC TGGAGTTTJ TCTTCTACC TGGAGTTTJ TCTTCTACC TCTTTGGG AAAACATT AACGCACCT AAAACAATT AACGCACCT CTCCTCACCC CTCCTCACCC	CATCCTGGGA CTCCTTGGTG CTCCTTGGTG AGGACAGTG AGGACAGTG TCTTACATTT TGCATTGGCT GGGAACCAG ATGTATCTOG ACAGCACTGG GGCACTGACC TCMCACGCGT TGTGTTCAC TCMCACGGGT TGTGTTCAC TCMCACGGGT TGTGTTCAC TGACACTGAC TGACACAGGG TGTGTTTGAC TGACACAGGGT TGTGTTCAC TTAGCAAAATAAA AGTCTTGATT GAGAAATAAA AGTCTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TGACACATTCT TGACTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TCTGTTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGATT TGACTGTGAT TGACTGTGAT TTGACTGTGAT TTGACTGTGAT TTGACTGTGAT TTGACTGTGAT TTGACTGTGAT TGACTGTGAT TTGACTGTGAT TGACTGTGAT TTGACTGTGAT TGACTGTGAT ACTGTGAT TGACTGTGAT TGACTGTGAT TGACTGTGAT TGACTGTGAT TGACTGAT TGACTGTGAT TGACTGTGAT TGACTGTGAT TGACTGTGAT TGACTGTGAT TGACTGAT TGACTGAT TGACTGAT TGACTGTAT TGACTGTAT TGACTGTAT TGACTGTAT TGACTTCAT TGACTGTAT TGACTTCAT TGACTTAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTTCAT TGACTT	240 300 420 480 540 660 720 840 900 1020 1080 1140 1290 1320 1320 1440
55 60	TATGGATTÓA ACOTCACAT GCAGCOATTA GTACACAGA AAACCCTOTO ACTAGATAC ATTTGGAGTT ATTAGATTA ATTAGATTA TTTTGAGTT CTAGATGATT CTAGATGATT TCAGATGAT ATAAATGAA TCGCAGAGAT TTGCCAGGAT TTGCCAGGAT TTGCCAGGAT TTGCCAGGAGAT TTGCCAGGAGAT TTGCCAGGAGAT TTGCCAGGAGAGGAG	ANGITOTICS CTATATACCI CTATATACCI CTATATACCI CTGATCGT TCCTATCAT TCCTATCAT TCCTATCAT CAGACACCC CAGACACCC CAGACACCC AACCACCC TCCTATATA CTTTGCAG TCCTTTATA TCCTTTATA TGCGGGTC ATGCGCGAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCTTCCATTCC TCCACTTCC TCCACTTCC ATGATCC AGAGATCGT AGACTGT AGACTGT TCCACTTCC AGAGATCGT AGACT AGACTGT	CTICATIGT GATCOTICAT TGCTTCAG TGCTTCAG TGCTTCAG GATCOTICAG CAG CAG CAG TGAGGAGA CAG CAG CAG CAG CAG CAG CAG CAG	MOCTOTATION MOCTOT	ATTITACTION TCANTACTIGGGA CATACTIGGGA CTITGGGGA AMAACATG GGAGCTIGAT AAGACTICAT TICCAAAGC TTGATTCAAAGC TTGATTCAAAGC TTGATTCAAAGC TTGATCAT TCTTCATCAC TCTCATCAC TTCATCAC TTTCATCAC TTCA	CATCCTGGGA CTCCTTGGTG CTCCTTGGTG AGGACAGTG AGGACAGTG TCTTACATTT TGCATTGGCT GGGGAACCAG ATGTATCTCG ACCCCTGGC TCCTGCCT TCACCTTT TCACTTGCT TCACTTGCT TCACTTGCT TCACTTGCT TCACCATGGC TCACCATGGC TCACCATGGC TCACCATGGC TCACCAGGGT TGTGCTTCAC TAGGAAATG TAGGAAATG TAGGAAATG TCTCTTGATA AGGCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTCTGAT TCTCTTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTCG GGGGTTTCT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTCG TCTCTCTCTCT TCTCTCTGAT TCTCTCTCTCT TCTCTCTCTCT TCTCTCTCTCT TCTCTCTCT TCTCTCTCTCT TCTCTCTCT TCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCT TCTCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTC	240 300 360 420 480 540 600 720 780 840 900 960 1020 1140 1200 1240 1320 1380
55 60 65	TATGGATTÓA ACOTCACAT GCAGCOATTA GTACACAGA AAACCCTOTO ACTAGATAC ATTTGGAGTT ATTAGATTA ATTAGATTA TTTTGAGTT CTAGATGATT CTAGATGATT TCAGATGAT ATAAATGAA TCGCAGAGAT TTGCCAGGAT TTGCCAGGAT TTGCCAGGAT TTGCCAGGAGAT TTGCCAGGAGAT TTGCCAGGAGAT TTGCCAGGAGAGGAG	ANGITOTICS CTATATACCI CTATATACCI CTATATACCI CTGATCGT TCCTATCAT TCCTATCAT TCCTATCAT CAGACACCC CAGACACCC CAGACACCC AACCACCC TCCTATATA CTTTGCAG TCCTTTATA TCCTTTATA TGCGGGTC ATGCGCGAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCCTAG ATGATCTTCCATTCC TCCACTTCC TCCACTTCC ATGATCC AGAGATCGT AGACTGT AGACTGT TCCACTTCC AGAGATCGT AGACT AGACTGT	CTICATIGT GATCOTICAT TGCTTCAG TGCTTCAG TGCTTCAG GATCOTICAG CAG CAG CAG TGAGGAGA CAG CAG CAG CAG CAG CAG CAG CAG	MOCTOTATION MOCTOT	ATTITACTION TCANTACTIGGGA CATACTIGGGA CTITGGGGA AMAACATG GGAGCTIGAT AAGACTICAT TICCAAAGC TTGATTCAAAGC TTGATTCAAAGC TTGATTCAAAGC TTGATCAT TCTTCATCAC TCTCATCAC TTCATCAC TTTCATCAC TTCA	CATCCTGGGA CTCCTTGGTG CTCCTTGGTG AGGACAGTG AGGACAGTG TCTTACATTT TGCATTGGCT GGGGAACCAG ATGTATCTCG ACCCCTGGC TCCTGCCT TCACCTTT TCACTTGCT TCACTTGCT TCACTTGCT TCACTTGCT TCACCATGGC TCACCATGGC TCACCATGGC TCACCATGGC TCACCAGGGT TGTGCTTCAC TAGGAAATG TAGGAAATG TAGGAAATG TCTCTTGATA AGGCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTTGAT TCTCTCTGAT TCTCTTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTCG GGGGTTTCT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTGAT TCTCTCTCG TCTCTCTCTCT TCTCTCTGAT TCTCTCTCTCT TCTCTCTCTCT TCTCTCTCTCT TCTCTCTCT TCTCTCTCTCT TCTCTCTCT TCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCT TCTCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTCTCT TCTC	240 300 420 480 540 660 720 780 840 960 1020 1140 1220 1320 1320 1440 1500 1500
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55 60 65	TATOGATOR ACTOCACAT GCAGCATTO TATOSTICTE ACTACACAT ACTACACAT TOGACATOR ACTACACAT TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACATOR TOGACAGAT TOGACACAT TOGACACAT TOGACACAT TOGACACAT TOGACACAT TOGACACAT TOGACACAT	AMGINISCI CTRANTACI CTRANT	CHICATIST GATCORTAL GATCOR	MOCTORIAL TO MARCHANGE AND A MOCTORIAL TO THE MARCHANGE AND A MOCTORIAL TO MARCHANGE AND A MARCHANGE A	TOTANGAM TOTANG	CATCOTOGGA CTCCTTOGGA CTCCTTOGGA AGGACAGT AGGACA	240 300 420 480 540 660 720 780 900 1020 1140 1220 1320 1340 1440 1500 1560 1680 1740 1800
55606570	TATOGANTON ACCOCCAGO TATOGACO TATOCACO TATOGACO TATOGACO TATOGACO TATOGACO TATOCAC TAT	AMGENTACIO TRANSPORTACIO TRANSPORTACI TROCATORI TOCTATOL	CHTICATISTIC ANTOCINE GATCORTAL GATC	ANCHORUST ANCH ANCHORUST ANCHORUST ANCHORUST ANCHORUST ANCHORUST ANCHORUST A	ANTIPOLITICA TO THE PROPERTY OF THE PROPERTY O	CATCTTOGAN TOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOTOGAN TOTOGAN	240 300 420 480 540 660 720 840 960 1020 1080 1140 1260 1320 1440 1500 1660 1740 1860 1740 1860
55 60 65 70 75	TATOGANTON ACCICAGNO GAGCOATTO TATOGACTE TATOGACTE TATOGACTE ACTABRITHET ACTABRITHET ACTABRITHET ACTABRITHET TOTABACTE TOTABRITHET TOTABRITH TOTABRITH TOTABRITHET TOTABRITH TOTABRITH TOTABRITH TOTABRITH TOTABRITH TOTABRITH	AMACHITICE CTATATACE CTATATACE CTATATACE CTATATACE TOCATOM TOC	OTTICATION OTTICATION	AGCCCCOTTO	ATTITUCTAC TEATRITY T	CATCTIOGGA CONTINUENT AGRACATO AG	240 300 420 480 540 660 720 840 900 1080 1140 1260 1320 1440 1560 1560 1680 1740 1860 1740 1860 1980
55606570	TATOGANTON TO CONTROL	AMACHITICA CTATATACA CTATATACA CTATATACA CTATATACA CTATATACA CATAT	GTICATION ATTOCHMAN TOCHTOCA ATTOCHMAN CONTROL CONTR	ABCONTOCTION TONDACION TON	AFTITUCTOC AFTITUCTOC AFTITUCTOC CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACT CONTROL C	CATCTIOGGA CONTINUENT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGACANT	240 300 360 420 480 540 660 720 960 1080 1140 1200 1260 1320 1340 1500 1560 1680 1740 1680 1740 1800 1800 1800 1900
55 60 65 70 75	TATOGRAFICA ACTICOLATIO GCAGOLTTO GCAGOLTTO GCAGOLTTO GCAGOLTO GCAGOLTO GCAGOLTO GCAGOLTO GCAGOLTO ACTACACACAC ACTACACACAC ACTACACACAC ACTACACACAC	AMACHINICA CTATATACA CATTACA C	CHTICATIONT GATCOTTAL	ASCINICATION A TOCAGOLOGY A TOC	AFTITUCTOC AFTITUCTOC AFTITUCTOC CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACT CONTROL C	CATCTIOGGA CONTINUENT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGAGACANT AGACANT	240 300 360 420 480 540 660 720 840 960 1020 1080 1120 1280 1320 1320 1320 1440 1500 1620 1620 1680 1740 1860 1920 1980 1980 1980 1980 1980 1980 1980 198
55 60 65 70 75	TATOGRAFICA ACTICOLATIO GCAGOLTTO GCAGOLTTO GCAGOLTTO GCAGOLTO GCAGOLTO GCAGOLTO GCAGOLTO GCAGOLTO ACTACACACAC ACTACACACAC ACTACACACAC ACTACACACAC	AMACHINICA CTATATACA CATTACA C	GTICATION ATTOCHMAN TOCHTOCA ATTOCHMAN CONTROL CONTR	ASCINICATION A TOCAGOLOGY A TOC	AFTITUCTOC AFTITUCTOC AFTITUCTOC CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACTISCO CANTACT CONTROL C	CATCTTOGGA CONTOTTOGGA AGGACALATO AGGAC	240 300 360 420 480 540 660 6720 780 960 1020 1140 1260 1320 1320 1440 1560 1620 1680 1740 1860 1790 1980 2040 2100

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GGCCGAGGGC AGCGGGAA GTTTCCCCGG ACCCTCAGG TTGCACTCCA 120 55 180 ATTCCGAGAG TTGCGGAAAC GCTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACCAGAG CTOGGAAGAT TOGAACACOG ACCTCGTCCC GGCCCCTGCA GTCCGGATAC TCACGCCAGA 300 AGTGCGGCTG GGATCCGGCG GCCACCTGCA CCTGCGTATC TCTCGGGCCG CCCTTCCCGA 360 GGGGCTCCCC GAGGCCTCCC GCCTTCACCG GGCTCTGTTC CGGCTGTCCC CGACGGCGTC 420 60 AAGGTCGTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC 480 GCCCGCGCTG CACCTGCGAC TGTCGCCGCC GCCGTCGCAG TCGGACCAAC TGCTGGCAGA 540 ATCTTOSTCC GCACGGCCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCCG CCAGGGGGCCG 600 CCGCAGAGGG CGTGCGCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG 660 TCTGCACACG GTCCGCGCGT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTCGCC 720 65 ACCIGIRACITIC CRACTICACCA TICTICATICGI COCCITICCCCO ACCCACTTICC COCCOGICARA 780 CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCCGACACGG AGCCAGCGCC 840 CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT 900 GTCGCTCCAG ACCTATGATG ACTTGTTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT 950 GOTCCTTCCA CTGTGCACCT GCGCGGGGGA GGCGACCTCA GTTGTCCTGC CCTGTGGAAT 1020 70 GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG
TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA 1080 ACTUTOTATT TATTTAAAAC TCTGGTGATA AAAATAAAGC TGTCTGAACT GTTAAAAAAA 75 Seg ID NO: 685 Protein sequence Protein Accession #: NP_004855.1 41 80 MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRASF PGPSELHSED SRFRELRKRY EDLLTRIRAN QSWEDSNTDL VPAPAVRILT PEVRIGSGCH LHIRISRAAL PEGLPEASRL 120 HRALPRLSPT ASSESSORTED LERGISLARP OAPALHLELS PPPSQSEQLL AESSSARPQL 180 ELHLEPOAAR GERRARANG DDCPLGPGRC CELHTVRASL EDLGWADWVL SPREVQVTMC 240

IGACPSOFRA ANMHAGIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTDT GVSLQTYDDL

Seg ID NO: 686 DNA sequence

85 LAKECHET

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Nucleic Acid Accession #: NM_002423.2 Coding sequence: 48..851

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	TGCTGTGTGC	TGTGTGCCTG	CTGCCTGGCA	GCCTGGCCCT	GCCGCTGCCT	CAGGAGGCGG	120
	GAGGCATGAG	TGAGCTACAG	TGGGAACAGG	CTCAGGACTA	TCTCAAGAGA	TTTTATCTCT	180
	ATGACTCAGA	AACAAAAAAT	GCCAACAGIT	TAGAAGCCAA	ACTCAAGGAG	ATGCAAAAAT	240
10	TCTTTGGCCT	ACCTATAACT	GGAATGTTAA	ACTCCCGCGT	CATAGAAATA	ATGCAGAAGC	300
	CCAGATGTGG	AGTGCCAGAT	GTTGCAGAAT	ACTCACTATT	TCCAAATAGC	CCAAAATGGA	360
	CTTCCAAAGT	GGTCACCTAC	AGGATCGTAT	CATATACTCG	AGACTTACCG	CATATTACAG	420
	TGGATCGATT	AGTGTCAAAG	GCTTTAAACA	TGTGGGGCAA	AGAGATOCCC	CTGCATTTCA	480
		ATGGGGAACT					540
15		ATTTGATGGG					600
		AGATGCTCAC					660
		CCTGTATGCT					720
		TAATGCAGTG					780
••		GGATGATATT					840
20		GAAACTTCAG					900
		TCAGAATIGA					960
		GCAGTTGGTT					1020
		TGTGTCTTAT				ATGTCAATAA	1080
25	ATGTTACATA	CACAAATAAA	TAAAATGTTT	ATTCCATGGT	AAATTTA		

Seq ID NO: 687 Protein sequence Protein Accession #: NP_002414.1

- - Seq ID NO: 688 DNA sequence Nucleic Acid Accession #: NM_005221.3 Coding sequence: 1..870

	1	11	21	31	41	51	
	1	1	1	1	1		
		TGTTTGACAG					60
		CCGCAGCTAT					120
45		ATTCTGACTA					180
		CTTCCTATGG					240
		COGGGAGCTA					300
		ACGGCGGCGC					360
		AGCCCGAGGT					420
50		ATTCCAGCTT					480
		TGCCGGAACG					540
		GGTTTCAGAA					600
		AGCACAGTCC					660
		GGGAGCCCCA					720
22		CCAACCAGTC					780
		CCAGCTCAAT		CIGCCGCCGC	CGGGCTCCTT	ACAGCACCCG	840,
	CTGGCGCTGG	CCTCCGGGAC	ACTCTATTAG				

60 Seq ID NO: 689 Protein sequence Protein Accession #: NP_005212.1

	1	11	21	31	41	51	
	1	1	1	1	1	1	
	MTGVFDRRVP	SIRSODFQAP	POTSAAMHHP	SQESPTLPES	SATDSDYYSP	TGGAPHGYCS	60
65	PTSASYGKAL	NPYOYOYHGV	NGSAGSYPAK	AYADYSYASS	YHOYGGAYNR	VPSATNOPEK	120
	EVTEPEVRNV	NGKPKKVRKP	RTIYSSFOLA	ALORRFORTO	YLALPERAEL	AASLGLTQTQ	180
	VKIWFONKRS	KIKKIMKNGB	MPPEHSPSSS	DPMACNSPOS	PAVNEPOGSS	RSLSHHPHAH	240
	PPTSMOSPAS	SYLENSASMY	TSAASSINSH	LPPPGSLOHP	LALASGILY		

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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein neorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

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WHAT IS CLAIMED IS:

- 1 1. A method of detecting a lung cancer-associated transcript in a cell
 2 from a patient, the method comprising contacting a biological sample from the patient with a
 3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
 4 as shown in Tables 1A-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
 2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue 2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises 2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying 2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a 2 sequence as shown in Tables 1A-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 10. The method of claim 1, wherein the polynucleotide is immobilized on
 a solid surface.
- 11. The method of claim 1, wherein the patient is undergoing a therapeutic
 regimen to treat lung cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having lung 2 cancer.
- 13. A method of monitoring the efficacy of a therapeutic treatment of lung
 cancer, the method comprising the steps of:

treatment; and

WO 02/086443 PCT/US02/12476 (i) providing a biological sample from a patient undergoing the therapeutic 3 4 treatment; and 5 (ii) determining the level of a lung cancer-associated transcript in the 6 biological sample by contacting the biological sample with a polynucleotide that selectively 7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. 8 thereby monitoring the efficacy of the therapy. 1 14. The method of claim 13, further comprising the step of: (iii) comparing 2 the level of the lung cancer-associated transcript to a level of the lung cancer-associated 3 transcript in a biological sample from the patient prior to, or earlier in, the therapeutic 4 treatment. 1 15. The method of claim 13, wherein the patient is a human. 1 16. A method of monitoring the efficacy of a therapeutic treatment of lung 2 cancer, the method comprising the steps of: 3 (i) providing a biological sample from a patient undergoing the therapeutic 4 treatment; and 5 (ii) determining the level of a lung cancer-associated antibody in the biological 6 sample by contacting the biological sample with a polypeptide encoded by a polynucleotide 7 that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in 8 Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated 9 antibody, thereby monitoring the efficacy of the therapy. 1 The method of claim 16, further comprising the step of: (iii) comparing 2 the level of the lung cancer-associated antibody to a level of the lung cancer-associated 3 antibody in a biological sample from the patient prior to, or earlier in, the therapeutic 4 treatment. 1 18. The method of claim 16, wherein the patient is a human. 1 19. A method of monitoring the efficacy of a therapeutic treatment of lung 2 cancer, the method comprising the steps of: 3 (i) providing a biological sample from a patient undergoing the therapeutic

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(ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. The method of claim 19, further comprising the step of: (iii) comparing 20. the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. The method of claim 19, wherein the patient is a human. 21. An isolated nucleic acid molecule consisting of a polynucleotide 22. sequence as shown in Tables 1A-16. The nucleic acid molecule of claim 22, which is labeled. 23. The nucleic acid of claim 23, wherein the label is a fluorescent label 24. An expression vector comprising the nucleic acid of claim 22. 25. A host cell comprising the expression vector of claim 25. 26. 27 An isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. An antibody that specifically binds a polypeptide of claim 27. 28. 29. The antibody of claim 28, further conjugated to an effector component. The antibody of claim 29, wherein the effector component is a 30. fluorescent label. 31. The antibody of claim 29, wherein the effector component is a radioisotope or a cytotoxic chemical. The antibody of claim 29, which is an antibody fragment. 32.

2 effect.

2 effect.

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WO 02/086443 PCT/US02/12476 1 33. The antibody of claim 29, which is a humanized antibody A method of detecting a lung cancer cell in a biological sample from a 34. 1 patient, the method comprising contacting the biological sample with an antibody of claim 2 3 28. The method of claim 34, wherein the antibody is further conjugated to 1 35. 2 an effector component. 1 36. The method of claim 35, wherein the effector component is a 2 fluorescent label. A method of detecting antibodies specific to lung cancer in a patient, 1 the method comprising contacting a biological sample from the patient with a polypeptide 2 encoded by a nucleic acid comprises a sequence from Tables 1A-16. 3 38. A method for identifying a compound that modulates a lung cancer-1 2 associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the 3 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 4 5

80% identical to a sequence as shown in Tables 1A-16; and

(ii) determining the functional effect of the compound upon the polypeptide.

- The method of claim 38, wherein the functional effect is a physical 1 39.
- 40. The method of claim 38, wherein the functional effect is a chemical 1
- The method of claim 38, wherein the polypeptide is expressed in a 1 41. 2 eukaryotic host cell or cell membrane.
- The method of claim 38, wherein the functional effect is determined by 1 42. measuring ligand binding to the polypeptide. 2
 - The method of claim 38, wherein the polypeptide is recombinant. 43.

physiologically acceptable excipient.

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1 44. A method of inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a 2 3 therapeutically effective amount of a compound identified using the method of claim 38. 45. The method of claim 44, wherein the compound is an antibody. 1 46. The method of claim 45, wherein the patient is a human. 1 1 47. A drug screening assay comprising the steps of 2 (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom: 3 4 (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a 5 6 treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the 7 polynucleotide is a candidate for the treatment of lung cancer. 8 The assay of claim 47, wherein the control is a mammal with lung 1 48. cancer or a cell therefrom that has not been treated with the test compound. 2 1 49. The assay of claim 47, wherein the control is a normal cell or mammal. 1 50. A method for treating a mammal having lung cancer comprising administering a compound identified by the assay of claim 47. 2 1 51. A pharmaceutiPcal composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay of claim 47 and a 2